MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Wed Mar 3 20:18:30 2010
Length of input sequence	624 amino acids
Number of nanomers from input sequence	616
Number of nanomers with obligatory P1 anchor residue	198
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	62

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	LRRLEGHFT	156	2.4000	40.00
2	VVVMDALRR	14	1.7000	28.33
3	FVVACGTAY	307	1.4900	24.83
4	YMHAEGFAA	502	1.3000	21.67
5	YRGYDSSGI	25	1.2000	20.00
6	IVVMPSPKG	528	1.0700	17.83
7	VITADGYRI	220	1.0000	16.67
8	LQVFAASVA	595	0.5800	9.67
9	LVVAISQSG	353	0.4000	6.67
10	VALEGALKL	489	0.4000	6.67

11	YVGRRPAYV	6	0.3000	5.00
12	FLAQIAANY	415	0.2000	3.33
13	VARARGYDV	602	0.2000	3.33
14	FVGSVLAVL	148	0.1000	1.67
15	FVGSDVAAF	195	0.1000	1.67
16	LAQIAANYL	416	0.1000	1.67
17	VVMPSPKGS	529	-0.1000	0
18	LIEIPAVST	576	-0.1000	0
19	LRRMEYRGY	20	-0.1100	0
20	LALAQARGT	427	-0.1100	0
21	VIAATGPVA	458	-0.1300	0
22	LQPLLSTIP	586	-0.2100	0
23	LGLALAQAR	425	-0.3000	0
24	LAYMHAEGF	500	-0.4000	0
25	LLSTIPLQV	589	-0.4000	0
26	VRRRAGRLA	43	-0.4100	0
27	LREIDKVFV	300	-0.5000	0
28	FRYRDPVLD	341	-0.5000	0
29	IQTRGAVTI	551	-0.5000	0
30	YEYFMLKEI	260	-0.5200	0
31	YFMLKEIAE	262	-0.6000	0
32	IREIQTRGA	548	-0.6100	0
33	VGSVLAVLR	149	-0.6500	0
34	YAIEHWTRL	323	-0.7100	0
35	VRHAKEQKA	370	-0.8000	0
36	VLFLGRHVG	478	-0.8000	0
37	FTLVFANAD	163	-0.8500	0
38	VFVVACGTA	306	-0.8500	0
39	VCGIVGYVG	0	-0.9000	0
40	LAICNTNGS	381	-0.9000	0
41	YTRAGPEIG	400	-0.9000	0
42	LLGLALAQA	424	-0.9000	0
43	LGHFVGGRI	280	-0.9200	0
44	IALVDGGTL	33	-0.9500	0
45	VTIVIAEEG	557	-0.9500	0
46	FDGNDGLQA	231	-1.0600	0
47	VGRRPAYVV	7	-1.1000	0

48	IVGYVGRRP	3	-1.1100	0
49	MPDLVARVI	451	-1.1100	0
50	YVVVMDALR	13	-1.1500	0
51	VARVIAATG	455	-1.1500	0
52	VVHNGIIEN	99	-1.1600	0
53	LVFANADDP	165	-1.2000	0
54	VVACGTAYH	308	-1.2000	0
55	ICNTNGSQI	383	-1.3000	0
56	VFAASVARA	597	-1.3000	0
57	VLAICNTNG	380	-1.3100	0
58	YHELEAMPD	445	-1.3100	0
59	IIENFAVLR	104	-1.3600	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	LRRLEGHFT	156	3.4000	56.67
2	VVVMDALRR	14	2.7000	45.00
3	IVVMPSPKG	528	2.0700	34.50
4	VITADGYRI	220	2.0000	33.33
5	LQVFAASVA	595	1.5800	26.33
6	FVVACGTAY	307	1.4900	24.83
7	LVVAISQSG	353	1.4000	23.33
8	VALEGALKL	489	1.4000	23.33
9	VARARGYDV	602	1.2000	20.00
10	LAQIAANYL	416	1.1000	18.33
11	LGRHVGYPV	481	1.0000	16.67
12	VVMPSPKGS	529	0.9000	15.00
13	LIEIPAVST	576	0.9000	15.00
14	LRRMEYRGY	20	0.8900	14.83
15	LALAQARGT	427	0.8900	14.83
16	VIAATGPVA	458	0.8700	14.50
17	LQPLLSTIP	586	0.7900	13.17
18	LGLALAQAR	425	0.7000	11.67
19	LAYMHAEGF	500	0.6000	10.00

20	LLSTIPLQV	589	0.6000	10.00
21	VRRRAGRLA	43	0.5900	9.83
22	LREIDKVFV	300	0.5000	8.33
23	IQTRGAVTI	551	0.5000	8.33
24	IREIQTRGA	548	0.3900	6.50
25	VGSVLAVLR	149	0.3500	5.83
26	YMHAEGFAA	502	0.3000	5.00
27	YRGYDSSGI	25	0.2000	3.33
28	VRHAKEQKA	370	0.2000	3.33
29	FLAQIAANY	415	0.2000	3.33
30	VLFLGRHVG	478	0.2000	3.33
31	VFVVACGTA	306	0.1500	2.50
32	VCGIVGYVG	0	0.1000	1.67
33	FVGSVLAVL	148	0.1000	1.67
34	FVGSDVAAF	195	0.1000	1.67
35	LAICNTNGS	381	0.1000	1.67
36	LLGLALAQA	424	0.1000	1.67
37	LGHFVGGRI	280	0.0800	1.33
38	IALVDGGTL	33	0.0500	0.83
39	VTIVIAEEG	557	0.0500	0.83
40	VGRRPAYVV	7	-0.1000	0
41	IVGYVGRRP	3	-0.1100	0
42	MPDLVARVI	451	-0.1100	0
43	VARVIAATG	455	-0.1500	0
44	VVHNGIIEN	99	-0.1600	0
45	LVFANADDP	165	-0.2000	0
46	VVACGTAYH	308	-0.2000	0
47	ICNTNGSQI	383	-0.3000	0
48	VFAASVARA	597	-0.3000	0
49	VLAICNTNG	380	-0.3100	0
50	IIENFAVLR	104	-0.3600	0
51	VEVELASEF	333	-0.4000	0
52	VAEMPSTAL	57	-0.4100	0
53	VGYVGRRPA	4	-0.4600	0
54	LVDGGTLTV	35	-0.5000	0
55	LGQDQAVVI	213	-0.5000	0
56	VACGTAYHS	309	-0.5000	0

57	FRYRDPVLD	341	-0.5000	0
58	VRPYADHLI	569	-0.5000	0
59	VIVVMPSPK	527	-0.5500	0
60	LKHGPIALI	513	-0.6000	0
61	LRRELETAG	111	-0.6100	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	VVMDALRRM	15	6.2000	65.26
2	IVLDEQRLS	288	5.3000	55.79
3	FVGSDVAAF	195	4.1000	43.16
4	LPVIVVMPS	525	3.9000	41.05
5	LIEDGLPVI	520	3.7000	38.95
6	VGSDVAAFI	196	3.6000	37.89
7	LGQDQAVVI	213	3.6000	37.89
8	IVVMPSPKG	528	3.6000	37.89
9	VMPSPKGSA	530	3.5000	36.84
10	LAICNTNGS	381	3.3100	34.84
11	VVVMDALRR	14	3.3000	34.74
12	LREIDKVFV	300	3.3000	34.74
13	VHNGIIENF	100	3.2000	33.68
14	VVMPSPKGS	529	3.2000	33.68
15	LKHGPIALI	513	3.1000	32.63
16	VVHNGIIEN	99	3.0000	31.58
17	LLGHFVGGR	279	3.0000	31.58
18	LVAARRSTP	176	2.8700	30.21
19	LVVAISQSG	353	2.8000	29.47
20	LFLGRHVGY	479	2.7000	28.42
21	LVDGGTLTV	35	2.6000	27.37
22	LGIGDNEMF	187	2.6000	27.37
23	VVACGTAYH	308	2.4000	25.26
24	VLFLGRHVG	478	2.4000	25.26
25	LKLKELAYM	495	2.4000	25.26
26	LEGHFTLVF	159	2.2000	23.16

27	FVGSVLAVL	148	2.1600	22.74
28	YRHGETADD	139	2.1000	22.11
29	LAVLRRLEG	153	2.1000	22.11
30	FVGGRIVLD	283	2.1000	22.11
31	VVAISQSGE	354	2.0700	21.79
32	LVFANADDP	165	2.0000	21.05
33	LVLGIGDNE	185	2.0000	21.05
34	LLSNIREIQ	544	2.0000	21.05
35	IVIAEEGDE	559	2.0000	21.05
36	VFAASVARA	597	2.0000	21.05
37	VIVVMPSPK	527	1.9700	20.74
38	LGLALAQAR	425	1.9000	20.00
39	IEIPAVSTL	577	1.8300	19.26
40	IGVASTKTF	407	1.8000	18.95
41	LAAAEKGGY	252	1.7000	17.89
42	VAISQSGET	355	1.7000	17.89
43	VTIVIAEEG	557	1.7000	17.89
44	FAQSSTVLF	472	1.6000	16.84
45	VACGTAYHS	309	1.5500	16.32
46	IENFAVLRR	105	1.5000	15.79
47	YLLGLALAQ	423	1.5000	15.79
48	LEGALKLKE	491	1.5000	15.79
49	LAYMHAEGF	500	1.5000	15.79
50	VGYVGRRPA	4	1.4000	14.74
51	VGSVLAVLR	149	1.4000	14.74
52	FHIDWDLAA	246	1.4000	14.74
53	VFVVACGTA	306	1.4000	14.74
54	LLGLALAQA	424	1.4000	14.74
55	IREIQTRGA	548	1.4000	14.74
56	LVARVIAAT	454	1.3000	13.68
57	VAAHLVARA	130	1.2000	12.63
58	VLAICNTNG	380	1.2000	12.63
59	LLSTIPLQV	589	1.2000	12.63
60	LSTIPLQVF	590	1.2000	12.63
61	YVGRRPAYV	6	1.1000	11.58
62	MDALRRMEY	17	1.1000	11.58

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	IVLDEQRLS	288	3.9000	42.86
2	VVMDALRRM	15	3.7000	40.66
3	FVGSDVAAF	195	3.2000	35.16
4	YLLGLALAQ	423	3.2000	35.16
5	LPVIVVMPS	525	2.5000	27.47
6	VMPSPKGSA	530	2.5000	27.47
7	FHIDWDLAA	246	2.4000	26.37
8	FMLKEIAEQ	263	2.3000	25.27
9	FVGSVLAVL	148	2.2000	24.18
10	YRHGETADD	139	2.0000	21.98
11	FVGGRIVLD	283	2.0000	21.98
12	VVACGTAYH	308	1.9800	21.76
13	LAICNTNGS	381	1.9100	20.99
14	LIEDGLPVI	520	1.8000	19.78
15	VVMPSPKGS	529	1.8000	19.78
16	VGSDVAAFI	196	1.7000	18.68
17	LGQDQAVVI	213	1.7000	18.68
18	LLSNIREIQ	544	1.7000	18.68
19	LREIDKVFV	300	1.3000	14.29
20	VVHNGIIEN	99	1.2000	13.19
21	LKHGPIALI	513	1.2000	13.19
22	IVVMPSPKG	528	1.2000	13.19
23	YVGRRPAYV	6	1.1000	12.09
24	YMHAEGFAA	502	1.1000	12.09
25	YRGYDSSGI	25	1.0700	11.76
26	YRISDFDGN	226	1.0000	10.99
27	FRYRDPVLD	341	1.0000	10.99
28	VFAASVARA	597	1.0000	10.99
29	LVAARRSTP	176	0.8700	9.56
30	VIVVMPSPK	527	0.8700	9.56
31	VVVMDALRR	14	0.8000	8.79
32	FVVACGTAY	307	0.8000	8.79

33	YHSGLLAKY	315	0.7000	7.69
34	FAQSSTVLF	472	0.7000	7.69
35	LVDGGTLTV	35	0.6000	6.59
36	LLGHFVGGR	279	0.5000	5.49
37	VGYVGRRPA	4	0.4000	4.40
38	VFVVACGTA	306	0.4000	4.40
39	LVVAISQSG	353	0.4000	4.40
40	LLGLALAQA	424	0.4000	4.40
41	LFLGRHVGY	479	0.4000	4.40
42	IREIQTRGA	548	0.4000	4.40
43	VHNGIIENF	100	0.3000	3.30
44	VAAHLVARA	130	0.2000	2.20
45	YRDPVLDRS	343	0.2000	2.20
46	FLGRHVGYP	480	0.2000	2.20
47	VACGTAYHS	309	0.1500	1.65
48	LETAGVEFA	115	0.1000	1.10
49	VIAATGPVA	458	0.1000	1.10
50	YDVDKPRNL	608	0.1000	1.10
51	FRPFHIDWD	243	-0.1000	0
52	VRHAKEQKA	370	-0.1000	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	IVLDEQRLS	288	4.6000	52.27
2	VVMDALRRM	15	4.4000	50.00
3	LAICNTNGS	381	3.6000	40.91
4	VVMPSPKGS	529	3.4000	38.64
5	LPVIVVMPS	525	3.2000	36.36
6	LLSNIREIQ	544	3.1000	35.23
7	VVACGTAYH	308	2.9800	33.86
8	VGSDVAAFI	196	2.7000	30.68
9	YLLGLALAQ	423	2.7000	30.68
10	LGQDQAVVI	213	2.5800	29.32
11	VVVMDALRR	14	2.3000	26.14

12	FVGSDVAAF	195	2.2000	25.00
13	LKHGPIALI	513	2.2000	25.00
14	LREIDKVFV	300	2.1800	24.77
15	LVDGGTLTV	35	2.1000	23.86
16	VMPSPKGSA	530	2.1000	23.86
17	VFAASVARA	597	2.0000	22.73
18	FHIDWDLAA	246	1.9000	21.59
19	VVHNGIIEN	99	1.8800	21.36
20	VLFLGRHVG	478	1.8000	20.45
21	VHNGIIENF	100	1.7000	19.32
22	LVAARRSTP	176	1.6000	18.18
23	VIVVMPSPK	527	1.6000	18.18
24	LETAGVEFA	115	1.5000	17.05
25	LVVAISQSG	353	1.5000	17.05
26	IPAVSTLLQ	579	1.5000	17.05
27	LLGLALAQA	424	1.4000	15.91
28	LIEDGLPVI	520	1.4000	15.91
29	LVFANADDP	165	1.3000	14.77
30	FMLKEIAEQ	263	1.3000	14.77
31	LFLGRHVGY	479	1.2800	14.55
32	VAAHLVARA	130	1.2000	13.64
33	FVGSVLAVL	148	1.2000	13.64
34	LAVLRRLEG	153	1.2000	13.64
35	VGYVGRRPA	4	1.1000	12.50
36	VLRRELETA	110	1.1000	12.50
37	LGIGDNEMF	187	1.1000	12.50
38	IREIQTRGA	548	1.1000	12.50
39	YRHGETADD	139	1.0000	11.36
40	LRRLEGHFT	156	1.0000	11.36
41	VRHAKEQKA	370	1.0000	11.36
42	LVLGIGDNE	185	0.9000	10.23
43	LKLKELAYM	495	0.9000	10.23
44	FVGGRIVLD	283	0.8800	10.00
45	LEGHFTLVF	159	0.8000	9.09
46	IVVMPSPKG	528	0.8000	9.09
47	VTIVIAEEG	557	0.7000	7.95
48	LLSTIPLQV	589	0.7000	7.95

49	LVARVIAAT	454	0.6000	6.82
50	LEGALKLKE	491	0.6000	6.82
51	IEIPAVSTL	577	0.6000	6.82
52	IENFAVLRR	105	0.5000	5.68
53	IGVASTKTF	407	0.5000	5.68
54	LGLALAQAR	425	0.5000	5.68
55	LQVFAASVA	595	0.5000	5.68
56	ITADGYRIS	221	0.4000	4.55
57	VVAISQSGE	354	0.4000	4.55
58	LDRSTLVVA	348	0.3800	4.32
59	YRISDFDGN	226	0.3000	3.41
60	IEHWTRLPV	325	0.3000	3.41
61	LLAKYAIEH	319	0.1600	1.82
62	YVGRRPAYV	6	0.1000	1.14

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	IVLDEQRLS	288	4.6000	52.27
2	VVMDALRRM	15	4.4000	50.00
3	LAICNTNGS	381	3.6000	40.91
4	VVMPSPKGS	529	3.4000	38.64
5	LPVIVVMPS	525	3.2000	36.36
6	LLSNIREIQ	544	3.1000	35.23
7	VVACGTAYH	308	2.9800	33.86
8	VGSDVAAFI	196	2.7000	30.68
9	YLLGLALAQ	423	2.7000	30.68
10	LGQDQAVVI	213	2.5800	29.32
11	VVVMDALRR	14	2.3000	26.14
12	FVGSDVAAF	195	2.2000	25.00
13	LKHGPIALI	513	2.2000	25.00
14	LREIDKVFV	300	2.1800	24.77
15	LVDGGTLTV	35	2.1000	23.86
16	VMPSPKGSA	530	2.1000	23.86
17	VFAASVARA	597	2.0000	22.73

18	FHIDWDLAA	246	1.9000	21.59
19	VVHNGIIEN	99	1.8800	21.36
20	VLFLGRHVG	478	1.8000	20.45
21	VHNGIIENF	100	1.7000	19.32
22	LVAARRSTP	176	1.6000	18.18
23	VIVVMPSPK	527	1.6000	18.18
24	LETAGVEFA	115	1.5000	17.05
25	LVVAISQSG	353	1.5000	17.05
26	IPAVSTLLQ	579	1.5000	17.05
27	LLGLALAQA	424	1.4000	15.91
28	LIEDGLPVI	520	1.4000	15.91
29	LVFANADDP	165	1.3000	14.77
30	FMLKEIAEQ	263	1.3000	14.77
31	LFLGRHVGY	479	1.2800	14.55
32	VAAHLVARA	130	1.2000	13.64
33	FVGSVLAVL	148	1.2000	13.64
34	LAVLRRLEG	153	1.2000	13.64
35	VGYVGRRPA	4	1.1000	12.50
36	VLRRELETA	110	1.1000	12.50
37	LGIGDNEMF	187	1.1000	12.50
38	IREIQTRGA	548	1.1000	12.50
39	YRHGETADD	139	1.0000	11.36
40	LRRLEGHFT	156	1.0000	11.36
41	VRHAKEQKA	370	1.0000	11.36
42	LVLGIGDNE	185	0.9000	10.23
43	LKLKELAYM	495	0.9000	10.23
44	FVGGRIVLD	283	0.8800	10.00
45	LEGHFTLVF	159	0.8000	9.09
46	IVVMPSPKG	528	0.8000	9.09
47	VTIVIAEEG	557	0.7000	7.95
48	LLSTIPLQV	589	0.7000	7.95
49	LVARVIAAT	454	0.6000	6.82
50	LEGALKLKE	491	0.6000	6.82
51	IEIPAVSTL	577	0.6000	6.82
52	IENFAVLRR	105	0.5000	5.68
53	IGVASTKTF	407	0.5000	5.68
54	LGLALAQAR	425	0.5000	5.68

55	LQVFAASVA	595	0.5000	5.68
56	ITADGYRIS	221	0.4000	4.55
57	VVAISQSGE	354	0.4000	4.55
58	LDRSTLVVA	348	0.3800	4.32
59	YRISDFDGN	226	0.3000	3.41
60	IEHWTRLPV	325	0.3000	3.41
61	LLAKYAIEH	319	0.1600	1.82
62	YVGRRPAYV	6	0.1000	1.14

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	IVLDEQRLS	288	4.6000	52.27
2	VVMDALRRM	15	4.4000	50.00
3	LAICNTNGS	381	3.6000	40.91
4	VVMPSPKGS	529	3.4000	38.64
5	LPVIVVMPS	525	3.2000	36.36
6	LLSNIREIQ	544	3.1000	35.23
7	VVACGTAYH	308	2.9800	33.86
8	VGSDVAAFI	196	2.7000	30.68
9	YLLGLALAQ	423	2.7000	30.68
10	LGQDQAVVI	213	2.5800	29.32
11	VVVMDALRR	14	2.3000	26.14
12	FVGSDVAAF	195	2.2000	25.00
13	LKHGPIALI	513	2.2000	25.00
14	LREIDKVFV	300	2.1800	24.77
15	LVDGGTLTV	35	2.1000	23.86
16	VMPSPKGSA	530	2.1000	23.86
17	VFAASVARA	597	2.0000	22.73
18	FHIDWDLAA	246	1.9000	21.59
19	VVHNGIIEN	99	1.8800	21.36
20	VLFLGRHVG	478	1.8000	20.45
21	VHNGIIENF	100	1.7000	19.32
22	LVAARRSTP	176	1.6000	18.18
23	VIVVMPSPK	527	1.6000	18.18

24	LETAGVEFA	115	1.5000	17.05
25	LVVAISQSG	353	1.5000	17.05
26	IPAVSTLLQ	579	1.5000	17.05
27	LLGLALAQA	424	1.4000	15.91
28	LIEDGLPVI	520	1.4000	15.91
29	LVFANADDP	165	1.3000	14.77
30	FMLKEIAEQ	263	1.3000	14.77
31	LFLGRHVGY	479	1.2800	14.55
32	VAAHLVARA	130	1.2000	13.64
33	FVGSVLAVL	148	1.2000	13.64
34	LAVLRRLEG	153	1.2000	13.64
35	VGYVGRRPA	4	1.1000	12.50
36	VLRRELETA	110	1.1000	12.50
37	LGIGDNEMF	187	1.1000	12.50
38	IREIQTRGA	548	1.1000	12.50
39	YRHGETADD	139	1.0000	11.36
40	LRRLEGHFT	156	1.0000	11.36
41	VRHAKEQKA	370	1.0000	11.36
42	LVLGIGDNE	185	0.9000	10.23
43	LKLKELAYM	495	0.9000	10.23
44	FVGGRIVLD	283	0.8800	10.00
45	LEGHFTLVF	159	0.8000	9.09
46	IVVMPSPKG	528	0.8000	9.09
47	VTIVIAEEG	557	0.7000	7.95
48	LLSTIPLQV	589	0.7000	7.95
49	LVARVIAAT	454	0.6000	6.82
50	LEGALKLKE	491	0.6000	6.82
51	IEIPAVSTL	577	0.6000	6.82
52	IENFAVLRR	105	0.5000	5.68
53	IGVASTKTF	407	0.5000	5.68
54	LGLALAQAR	425	0.5000	5.68
55	LQVFAASVA	595	0.5000	5.68
56	ITADGYRIS	221	0.4000	4.55
57	VVAISQSGE	354	0.4000	4.55
58	LDRSTLVVA	348	0.3800	4.32
59	YRISDFDGN	226	0.3000	3.41
60	IEHWTRLPV	325	0.3000	3.41

61	LLAKYAIEH	319	0.1600	1.82
62	YVGRRPAYV	6	0.1000	1.14

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	VVMDALRRM	15	5.2000	54.74
2	FVGSDVAAF	195	5.1000	53.68
3	IVLDEQRLS	288	4.3000	45.26
4	FVGSVLAVL	148	3.1600	33.26
5	YRHGETADD	139	3.1000	32.63
6	FVGGRIVLD	283	3.1000	32.63
7	LPVIVVMPS	525	2.9000	30.53
8	LIEDGLPVI	520	2.7000	28.42
9	VGSDVAAFI	196	2.6000	27.37
10	LGQDQAVVI	213	2.6000	27.37
11	FAQSSTVLF	472	2.6000	27.37
12	IVVMPSPKG	528	2.6000	27.37
13	YLLGLALAQ	423	2.5000	26.32
14	VMPSPKGSA	530	2.5000	26.32
15	FHIDWDLAA	246	2.4000	25.26
16	LAICNTNGS	381	2.3100	24.32
17	VVVMDALRR	14	2.3000	24.21
18	LREIDKVFV	300	2.3000	24.21
19	VHNGIIENF	100	2.2000	23.16
20	VVMPSPKGS	529	2.2000	23.16
21	YVGRRPAYV	6	2.1000	22.11
22	FVVACGTAY	307	2.1000	22.11
23	FRYRDPVLD	341	2.1000	22.11
24	LKHGPIALI	513	2.1000	22.11
25	VVHNGIIEN	99	2.0000	21.05
26	LLGHFVGGR	279	2.0000	21.05
27	YHSGLLAKY	315	2.0000	21.05
28	YRGYDSSGI	25	1.9700	20.74
29	LVAARRSTP	176	1.8700	19.68

30	YRISDFDGN	226	1.8000	18.95
31	LVVAISQSG	353	1.8000	18.95
32	LFLGRHVGY	479	1.7000	17.89
33	LVDGGTLTV	35	1.6000	16.84
34	LGIGDNEMF	187	1.6000	16.84
35	FMLKEIAEQ	263	1.6000	16.84
36	VVACGTAYH	308	1.4000	14.74
37	WTRLPVEVE	328	1.4000	14.74
38	YTRAGPEIG	400	1.4000	14.74
39	VLFLGRHVG	478	1.4000	14.74
40	LKLKELAYM	495	1.4000	14.74
41	FLAQIAANY	415	1.3000	13.68
42	LEGHFTLVF	159	1.2000	12.63
43	FLGRHVGYP	480	1.2000	12.63
44	WATHGRPTD	76	1.1000	11.58
45	LAVLRRLEG	153	1.1000	11.58
46	YMHAEGFAA	502	1.1000	11.58
47	VVAISQSGE	354	1.0700	11.26
48	YDVDKPRNL	608	1.0600	11.16
49	FAVLRRELE	108	1.0000	10.53
50	LVFANADDP	165	1.0000	10.53
51	LVLGIGDNE	185	1.0000	10.53
52	FIEHTREAV	203	1.0000	10.53
53	FRPFHIDWD	243	1.0000	10.53
54	LLSNIREIQ	544	1.0000	10.53
55	IVIAEEGDE	559	1.0000	10.53
56	VFAASVARA	597	1.0000	10.53
57	VIVVMPSPK	527	0.9700	10.21
58	YFMLKEIAE	262	0.9000	9.47
59	LGLALAQAR	425	0.9000	9.47
60	IEIPAVSTL	577	0.8300	8.74
61	IGVASTKTF	407	0.8000	8.42
62	YVVVMDALR	13	0.7000	7.37

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	IVLDEQRLS	288	4.6000	52.27
2	VVMDALRRM	15	4.4000	50.00
3	LAICNTNGS	381	3.6000	40.91
4	VVMPSPKGS	529	3.4000	38.64
5	LPVIVVMPS	525	3.2000	36.36
6	LLSNIREIQ	544	3.1000	35.23
7	VVACGTAYH	308	2.9800	33.86
8	VGSDVAAFI	196	2.7000	30.68
9	YLLGLALAQ	423	2.7000	30.68
10	LGQDQAVVI	213	2.5800	29.32
11	VVVMDALRR	14	2.3000	26.14
12	FVGSDVAAF	195	2.2000	25.00
13	LKHGPIALI	513	2.2000	25.00
14	LREIDKVFV	300	2.1800	24.77
15	LVDGGTLTV	35	2.1000	23.86
16	VMPSPKGSA	530	2.1000	23.86
17	VFAASVARA	597	2.0000	22.73
18	FHIDWDLAA	246	1.9000	21.59
19	VVHNGIIEN	99	1.8800	21.36
20	VLFLGRHVG	478	1.8000	20.45
21	VHNGIIENF	100	1.7000	19.32
22	LVAARRSTP	176	1.6000	18.18
23	VIVVMPSPK	527	1.6000	18.18
24	LETAGVEFA	115	1.5000	17.05
25	LVVAISQSG	353	1.5000	17.05
26	IPAVSTLLQ	579	1.5000	17.05
27	LLGLALAQA	424	1.4000	15.91
28	LIEDGLPVI	520	1.4000	15.91
29	LVFANADDP	165	1.3000	14.77
30	FMLKEIAEQ	263	1.3000	14.77
31	LFLGRHVGY	479	1.2800	14.55
32	VAAHLVARA	130	1.2000	13.64
33	FVGSVLAVL	148	1.2000	13.64
34	LAVLRRLEG	153	1.2000	13.64
35	VGYVGRRPA	4	1.1000	12.50
36	VLRRELETA	110	1.1000	12.50

37	LGIGDNEMF	187	1.1000	12.50
38	IREIQTRGA	548	1.1000	12.50
39	YRHGETADD	139	1.0000	11.36
40	LRRLEGHFT	156	1.0000	11.36
41	VRHAKEQKA	370	1.0000	11.36
42	LVLGIGDNE	185	0.9000	10.23
43	LKLKELAYM	495	0.9000	10.23
44	FVGGRIVLD	283	0.8800	10.00
45	LEGHFTLVF	159	0.8000	9.09
46	IVVMPSPKG	528	0.8000	9.09
47	VTIVIAEEG	557	0.7000	7.95
48	LLSTIPLQV	589	0.7000	7.95
49	LVARVIAAT	454	0.6000	6.82
50	LEGALKLKE	491	0.6000	6.82
51	IEIPAVSTL	577	0.6000	6.82
52	IENFAVLRR	105	0.5000	5.68
53	IGVASTKTF	407	0.5000	5.68
54	LGLALAQAR	425	0.5000	5.68
55	LQVFAASVA	595	0.5000	5.68
56	ITADGYRIS	221	0.4000	4.55
57	VVAISQSGE	354	0.4000	4.55
58	LDRSTLVVA	348	0.3800	4.32
59	YRISDFDGN	226	0.3000	3.41
60	IEHWTRLPV	325	0.3000	3.41
61	LLAKYAIEH	319	0.1600	1.82
62	YVGRRPAYV	6	0.1000	1.14

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	LAICNTNGS	381	3.7000	43.02
2	FHIDWDLAA	246	3.3000	38.37
3	VVACGTAYH	308	3.0800	35.81
4	FVGSDVAAF	195	3.0000	34.88
5	VVVMDALRR	14	2.2000	25.58

6	LPVIVVMPS	525	2.2000	25.58
7	LEGHFTLVF	159	2.0000	23.26
8	IVVMPSPKG	528	1.8000	20.93
9	FAQSSTVLF	472	1.7800	20.70
10	YRISDFDGN	226	1.7000	19.77
11	LVVAISQSG	353	1.6000	18.60
12	YLLGLALAQ	423	1.6000	18.60
13	IVLDEQRLS	288	1.5000	17.44
14	IREIQTRGA	548	1.5000	17.44
15	YRGYDSSGI	25	1.3000	15.12
16	VVMPSPKGS	529	1.3000	15.12
17	VVMDALRRM	15	1.2000	13.95
18	VALEGALKL	489	1.2000	13.95
19	VAAHLVARA	130	1.0000	11.63
20	YRHGETADD	139	1.0000	11.63
21	FVGSVLAVL	148	1.0000	11.63
22	VLAICNTNG	380	1.0000	11.63
23	YAIEHWTRL	323	0.9000	10.47
24	WTRLPVEVE	328	0.9000	10.47
25	LQPLLSTIP	586	0.9000	10.47
26	LLSTIPLQV	589	0.9000	10.47
27	VGSDVAAFI	196	0.8000	9.30
28	FMLKEIAEQ	263	0.8000	9.30
29	VASTKTFLA	409	0.8000	9.30
30	FLAQIAANY	415	0.8000	9.30
31	VVHNGIIEN	99	0.7800	9.07
32	IPAVSTLLQ	579	0.7000	8.14
33	VFAASVARA	597	0.7000	8.14
34	LGQDQAVVI	213	0.6800	7.91
35	IGVASTKTF	407	0.6000	6.98
36	MLKEIAEQP	264	0.4000	4.65
37	LVFANADDP	165	0.3000	3.49
38	LETAGVEFA	115	0.2000	2.33
39	LVDGGTLTV	35	0.1000	1.16
40	VLGIGDNEM	186	0.1000	1.16
41	LRRELETAG	111	-0.1000	0
42	LGIGDNEMF	187	-0.1000	0

43	VVITADGYR	219	-0.1000	0
44	LLGHFVGGR	279	-0.1000	0
45	VEVELASEF	333	-0.1000	0
46	YTRAGPEIG	400	-0.1000	0
47	LLGLALAQA	424	-0.1000	0
48	LAYMHAEGF	500	-0.1000	0
49	IPLQVFAAS	593	-0.1000	0
50	VAISQSGET	355	-0.2000	0
51	YVGRRPAYV	6	-0.3000	0
52	FASDTDTEV	122	-0.3000	0
53	YVVVMDALR	13	-0.4000	0
54	LEAMPDLVA	448	-0.4000	0
55	LQVFAASVA	595	-0.4000	0
56	FRPFHIDWD	243	-0.5000	0
57	LPVEVELAS	331	-0.5000	0
58	LGLALAQAR	425	-0.5000	0
59	YHELEAMPD	445	-0.5000	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	LAICNTNGS	381	4.7000	48.96
2	IREIQTRGA	548	4.6800	48.75
3	VRRRAGRLA	43	4.1000	42.71
4	VVACGTAYH	308	4.0800	42.50
5	LVVAISQSG	353	3.7000	38.54
6	LEGHFTLVF	159	3.4000	35.42
7	VVVMDALRR	14	3.2000	33.33
8	LAHRFAQSS	468	3.0000	31.25
9	VLDRSTLVV	347	2.9000	30.21
10	VVMPSPKGS	529	2.9000	30.21
11	LRRMEYRGY	20	2.7000	28.13
12	LPVIVVMPS	525	2.4800	25.83
13	VGRRPAYVV	7	2.4000	25.00
14	LVDGGTLTV	35	2.3000	23.96

15	LVARAYRHG	134	2.3000	23.96
16	IVVMPSPKG	528	2.2000	22.92
17	IPAVSTLLQ	579	2.2000	22.92
18	VAAHLVARA	130	2.1000	21.88
19	VASTKTFLA	409	2.1000	21.88
20	IQTRGAVTI	551	2.1000	21.88
21	VGGRIVLDE	284	1.9000	19.79
22	IGVASTKTF	407	1.9000	19.79
23	IENFAVLRR	105	1.8000	18.75
24	YLLGLALAQ	423	1.8000	18.75
25	LVARVIAAT	454	1.8000	18.75
26	IVLDEQRLS	288	1.7000	17.71
27	VFAASVARA	597	1.7000	17.71
28	LLAKYAIEH	319	1.6800	17.50
29	YVGRRPAYV	6	1.6000	16.67
30	FMLKEIAEQ	263	1.6000	16.67
31	LGLALAQAR	425	1.6000	16.67
32	LQVFAASVA	595	1.6000	16.67
33	FRYRDPVLD	341	1.5000	15.62
34	LALAQARGT	427	1.5000	15.62
35	VLAICNTNG	380	1.4800	15.42
36	VVMDALRRM	15	1.4000	14.58
37	YRGYDSSGI	25	1.3000	13.54
38	VRPYADHLI	569	1.2000	12.50
39	VAARRSTPL	177	1.1000	11.46
40	VRHAKEQKA	370	1.1000	11.46
41	LGRHVGYPV	481	1.1000	11.46
42	LLSTIPLQV	589	1.0000	10.42
43	VVHNGIIEN	99	0.9000	9.38
44	YRHGETADD	139	0.9000	9.38
45	VACGTAYHS	309	0.9000	9.38
46	IVGYVGRRP	3	0.8000	8.33
47	LKLKELAYM	495	0.7000	7.29
48	LQPLLSTIP	586	0.7000	7.29
49	LEAMPDLVA	448	0.6000	6.25
50	VLRRELETA	110	0.4000	4.17
51	LGIGDNEMF	187	0.4000	4.17

52	VLGIGDNEM	186	0.3800	3.96
53	FVGSDVAAF	195	0.2000	2.08
54	VITADGYRI	220	0.2000	2.08
55	LLGHFVGGR	279	0.2000	2.08
56	LKHGPIALI	513	0.2000	2.08
57	VIVVMPSPK	527	0.2000	2.08
58	LRRLEGHFT	156	0.1000	1.04
59	VGYVGRRPA	4	-0.1000	0
60	LETAGVEFA	115	-0.2000	0

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	LAICNTNGS	381	4.8000	54.55
2	VVACGTAYH	308	4.0800	46.36
3	VVVMDALRR	14	3.7000	42.05
4	LPVIVVMPS	525	3.4000	38.64
5	IVVMPSPKG	528	3.4000	38.64
6	LQVFAASVA	595	3.2000	36.36
7	IREIQTRGA	548	3.1000	35.23
8	VLAICNTNG	380	2.8000	31.82
9	IPAVSTLLQ	579	2.7000	30.68
10	LQPLLSTIP	586	2.6000	29.55
11	LVVAISQSG	353	2.4000	27.27
12	VIVVMPSPK	527	2.3000	26.14
13	YRGYDSSGI	25	2.2000	25.00
14	IENFAVLRR	105	1.8000	20.45
15	VFAASVARA	597	1.7000	19.32
16	VVMPSPKGS	529	1.6000	18.18
17	VLGIGDNEM	186	1.5000	17.05
18	LRRMEYRGY	20	1.3000	14.77
19	VASTKTFLA	409	1.1500	13.07
20	LLGLALAQA	424	1.1000	12.50
21	LEAMPDLVA	448	1.1000	12.50
22	VAEMPSTAL	57	1.0000	11.36

23	LAYMHAEGF	500	0.9000	10.23
24	IAVVHNGII	97	0.8000	9.09
25	LRRLEGHFT	156	0.8000	9.09
26	LAQIAANYL	416	0.8000	9.09
27	IEIPAVSTL	577	0.7000	7.95
28	VFVVACGTA	306	0.6000	6.82
29	IGVASTKTF	407	0.6000	6.82
30	LEGHFTLVF	159	0.5000	5.68
31	FVGSDVAAF	195	0.5000	5.68
32	VVAISQSGE	354	0.5000	5.68
33	LVFANADDP	165	0.4000	4.55
34	LETAGVEFA	115	0.3000	3.41
35	IVLDEQRLS	288	0.3000	3.41
36	LGLALAQAR	425	0.3000	3.41
37	VTIVIAEEG	557	0.3000	3.41
38	VRPYADHLI	569	0.3000	3.41
39	VARVIAATG	455	0.2000	2.27
40	VVHNGIIEN	99	0.1800	2.05
41	VGSVLAVLR	149	0.1000	1.14
42	LKELAYMHA	497	0.1000	1.14
43	IPLQVFAAS	593	0.1000	1.14
44	LVDGGTLTV	35	-0.1000	0
45	VAAHLVARA	130	-0.1000	0
46	LLSTIPLQV	589	-0.1000	0
47	VRHAKEQKA	370	-0.2000	0
48	LIEIPAVST	576	-0.3000	0
49	LLAKYAIEH	319	-0.3400	0
50	FTLVFANAD	163	-0.5000	0
51	FRPFHIDWD	243	-0.5000	0
52	FVVACGTAY	307	-0.5000	0
53	VVITADGYR	219	-0.6000	0
54	FHIDWDLAA	246	-0.6000	0
55	VAISQSGET	355	-0.6000	0
56	YLLGLALAQ	423	-0.6000	0
57	VGSDVAAFI	196	-0.7000	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	VVACGTAYH	308	4.3000	45.74
2	LAICNTNGS	381	3.8000	40.43
3	IVVMPSPKG	528	3.7000	39.36
4	YRGYDSSGI	25	3.4000	36.17
5	FTLVFANAD	163	3.2000	34.04
6	FRPFHIDWD	243	3.2000	34.04
7	WTRLPVEVE	328	3.2000	34.04
8	VLAICNTNG	380	3.1000	32.98
9	YRHGETADD	139	2.9000	30.85
10	VVVMDALRR	14	2.7000	28.72
11	LVVAISQSG	353	2.7000	28.72
12	VVAISQSGE	354	2.5000	26.60
13	IPAVSTLLQ	579	2.5000	26.60
14	FVGSDVAAF	195	2.4000	25.53
15	LPVIVVMPS	525	2.4000	25.53
16	YHELEAMPD	445	2.3000	24.47
17	LQVFAASVA	595	2.2000	23.40
18	YFMLKEIAE	262	2.1800	23.19
19	IREIQTRGA	548	2.1000	22.34
20	LQPLLSTIP	586	2.0000	21.28
21	FMLKEIAEQ	263	1.8000	19.15
22	VLGIGDNEM	186	1.6000	17.02
23	FVVACGTAY	307	1.6000	17.02
24	FRYRDPVLD	341	1.5000	15.96
25	LRRMEYRGY	20	1.4000	14.89
26	YRISDFDGN	226	1.3000	13.83
27	YLLGLALAQ	423	1.2000	12.77
28	VVHNGIIEN	99	1.1800	12.55
29	FLAQIAANY	415	1.1000	11.70
30	YVVVMDALR	13	1.0000	10.64
31	VAEMPSTAL	57	1.0000	10.64
32	FAQSSTVLF	472	1.0000	10.64
33	IENFAVLRR	105	0.8000	8.51

34	LAQIAANYL	416	0.8000	8.51
35	LAYMHAEGF	500	0.8000	8.51
36	LRRLEGHFT	156	0.7000	7.45
37	FVGGRIVLD	283	0.7000	7.45
38	IEIPAVSTL	577	0.7000	7.45
39	VFAASVARA	597	0.7000	7.45
40	VIVVMPSPK	527	0.6000	6.38
41	VVMPSPKGS	529	0.6000	6.38
42	VTIVIAEEG	557	0.6000	6.38
43	FVGSVLAVL	148	0.5000	5.32
44	IGVASTKTF	407	0.5000	5.32
45	VARVIAATG	455	0.5000	5.32
46	LEGHFTLVF	159	0.4000	4.26
47	FHIDWDLAA	246	0.4000	4.26
48	YTRAGPEIG	400	0.3000	3.19
49	IVIAEEGDE	559	0.3000	3.19
50	VASTKTFLA	409	0.1500	1.60
51	VVMDALRRM	15	0.1000	1.06
52	LLGLALAQA	424	0.1000	1.06
53	LEAMPDLVA	448	0.1000	1.06
54	LLAKYAIEH	319	-0.1200	0
55	LVFANADDP	165	-0.2000	0
56	VGGRIVLDE	284	-0.2000	0
57	YAIEHWTRL	323	-0.2000	0
58	YMHAEGFAA	502	-0.2500	0
59	FAVLRRELE	108	-0.3000	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	LAICNTNGS	381	3.8000	43.18
2	YRGYDSSGI	25	3.2000	36.36
3	VVACGTAYH	308	3.0800	35.00
4	VVVMDALRR	14	2.7000	30.68
5	LPVIVVMPS	525	2.4000	27.27

6	IVVMPSPKG	528	2.4000	27.27
7	LQVFAASVA	595	2.2000	25.00
8	IREIQTRGA	548	2.1000	23.86
9	VLAICNTNG	380	1.8000	20.45
10	IPAVSTLLQ	579	1.7000	19.32
11	LQPLLSTIP	586	1.6000	18.18
12	FVGSDVAAF	195	1.5000	17.05
13	LVVAISQSG	353	1.4000	15.91
14	VIVVMPSPK	527	1.3000	14.77
15	YVVVMDALR	13	1.0000	11.36
16	FMLKEIAEQ	263	1.0000	11.36
17	IENFAVLRR	105	0.8000	9.09
18	VFAASVARA	597	0.7000	7.95
19	VVMPSPKGS	529	0.6000	6.82
20	FTLVFANAD	163	0.5000	5.68
21	VLGIGDNEM	186	0.5000	5.68
22	FRPFHIDWD	243	0.5000	5.68
23	FVVACGTAY	307	0.5000	5.68
24	FHIDWDLAA	246	0.4000	4.55
25	YLLGLALAQ	423	0.4000	4.55
26	LRRMEYRGY	20	0.3000	3.41
27	YRHGETADD	139	0.2000	2.27
28	WTRLPVEVE	328	0.2000	2.27
29	VASTKTFLA	409	0.1500	1.70
30	LLGLALAQA	424	0.1000	1.14
31	LEAMPDLVA	448	0.1000	1.14
32	FAQSSTVLF	472	0.1000	1.14
33	LAYMHAEGF	500	-0.1000	0
34	IAVVHNGII	97	-0.2000	0
35	LRRLEGHFT	156	-0.2000	0
36	LAQIAANYL	416	-0.2000	0
37	YMHAEGFAA	502	-0.2500	0
38	IEIPAVSTL	577	-0.3000	0
39	VFVVACGTA	306	-0.4000	0
40	IGVASTKTF	407	-0.4000	0
41	YHELEAMPD	445	-0.4000	0
42	FVGSVLAVL	148	-0.5000	0

43	LEGHFTLVF	159	-0.5000	0
44	VVAISQSGE	354	-0.5000	0
45	LVFANADDP	165	-0.6000	0
46	LETAGVEFA	115	-0.7000	0
47	YRISDFDGN	226	-0.7000	0
48	IVLDEQRLS	288	-0.7000	0
49	LGLALAQAR	425	-0.7000	0
50	VTIVIAEEG	557	-0.7000	0
51	VRPYADHLI	569	-0.7000	0
52	YVGRRPAYV	6	-0.8000	0
53	YEYFMLKEI	260	-0.8000	0
54	VARVIAATG	455	-0.8000	0
55	VVHNGIIEN	99	-0.8200	0
56	YFMLKEIAE	262	-0.8200	0
57	VGSVLAVLR	149	-0.9000	0
58	LKELAYMHA	497	-0.9000	0
59	IPLQVFAAS	593	-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	VVACGTAYH	308	5.3000	56.38
2	LAICNTNGS	381	4.8000	51.06
3	IVVMPSPKG	528	4.7000	50.00
4	VLAICNTNG	380	4.1000	43.62
5	VVVMDALRR	14	3.7000	39.36
6	LVVAISQSG	353	3.7000	39.36
7	VVAISQSGE	354	3.5000	37.23
8	IPAVSTLLQ	579	3.5000	37.23
9	LPVIVVMPS	525	3.4000	36.17
10	LQVFAASVA	595	3.2000	34.04
11	IREIQTRGA	548	3.1000	32.98
12	LQPLLSTIP	586	3.0000	31.91
13	VLGIGDNEM	186	2.6000	27.66
14	LRRMEYRGY	20	2.4000	25.53

15	YRGYDSSGI	25	2.4000	25.53
16	FTLVFANAD	163	2.2000	23.40
17	FRPFHIDWD	243	2.2000	23.40
18	WTRLPVEVE	328	2.2000	23.40
19	VVHNGIIEN	99	2.1800	23.19
20	VAEMPSTAL	57	2.0000	21.28
21	YRHGETADD	139	1.9000	20.21
22	IENFAVLRR	105	1.8000	19.15
23	LAQIAANYL	416	1.8000	19.15
24	LAYMHAEGF	500	1.8000	19.15
25	LRRLEGHFT	156	1.7000	18.09
26	IEIPAVSTL	577	1.7000	18.09
27	VFAASVARA	597	1.7000	18.09
28	VIVVMPSPK	527	1.6000	17.02
29	VVMPSPKGS	529	1.6000	17.02
30	VTIVIAEEG	557	1.6000	17.02
31	IGVASTKTF	407	1.5000	15.96
32	VARVIAATG	455	1.5000	15.96
33	LEGHFTLVF	159	1.4000	14.89
34	FVGSDVAAF	195	1.4000	14.89
35	YHELEAMPD	445	1.3000	13.83
36	IVIAEEGDE	559	1.3000	13.83
37	YFMLKEIAE	262	1.1800	12.55
38	VASTKTFLA	409	1.1500	12.23
39	VVMDALRRM	15	1.1000	11.70
40	LLGLALAQA	424	1.1000	11.70
41	LEAMPDLVA	448	1.1000	11.70
42	IAVVHNGII	97	1.0000	10.64
43	VLYTRAGPE	398	1.0000	10.64
44	LLAKYAIEH	319	0.8800	9.36
45	LVFANADDP	165	0.8000	8.51
46	FMLKEIAEQ	263	0.8000	8.51
47	VGGRIVLDE	284	0.8000	8.51
48	VFVVACGTA	306	0.6000	6.38
49	FVVACGTAY	307	0.6000	6.38
50	VGYPVALEG	485	0.6000	6.38
51	LIEIPAVST	576	0.6000	6.38

52	FRYRDPVLD	341	0.5000	5.32
53	LEAVRHAKE	367	0.5000	5.32
54	VRPYADHLI	569	0.5000	5.32
55	LETAGVEFA	115	0.3000	3.19
56	YRISDFDGN	226	0.3000	3.19
57	IVLDEQRLS	288	0.3000	3.19
58	VAISQSGET	355	0.3000	3.19
59	LGLALAQAR	425	0.3000	3.19
60	IAATGPVAE	459	0.3000	3.19
61	VLFLGRHVG	478	0.3000	3.19
62	LVDGGTLTV	35	0.2000	2.13

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	FVGSDVAAF	195	4.9000	54.44
2	LAICNTNGS	381	4.1000	45.56
3	LEGHFTLVF	159	3.9000	43.33
4	VVVMDALRR	14	3.7000	41.11
5	FAQSSTVLF	472	3.6800	40.89
6	FHIDWDLAA	246	3.3000	36.67
7	IVVMPSPKG	528	3.2000	35.56
8	LVVAISQSG	353	3.0000	33.33
9	VVMDALRRM	15	2.7000	30.00
10	LPVIVVMPS	525	2.6000	28.89
11	YRISDFDGN	226	2.5000	27.78
12	VVACGTAYH	308	2.5000	27.78
13	IGVASTKTF	407	2.5000	27.78
14	VLAICNTNG	380	2.4000	26.67
15	WTRLPVEVE	328	2.3000	25.56
16	YRGYDSSGI	25	2.2000	24.44
17	VALEGALKL	489	2.1600	24.00
18	YRHGETADD	139	2.1000	23.33
19	FLAQIAANY	415	2.1000	23.33
20	FVGSVLAVL	148	1.9600	21.78

21	IVLDEQRLS	288	1.9000	21.11
22	LQPLLSTIP	586	1.9000	21.11
23	LLSTIPLQV	589	1.9000	21.11
24	YAIEHWTRL	323	1.8600	20.67
25	LGIGDNEMF	187	1.8000	20.00
26	VEVELASEF	333	1.8000	20.00
27	LAYMHAEGF	500	1.8000	20.00
28	VGSDVAAFI	196	1.7000	18.89
29	VVMPSPKGS	529	1.7000	18.89
30	VLGIGDNEM	186	1.6000	17.78
31	VVHNGIIEN	99	1.5800	17.56
32	LGQDQAVVI	213	1.5800	17.56
33	IREIQTRGA	548	1.5000	16.67
34	VVITADGYR	219	1.4000	15.56
35	MLKEIAEQP	264	1.4000	15.56
36	LLGHFVGGR	279	1.4000	15.56
37	LRRELETAG	111	1.3000	14.44
38	LVFANADDP	165	1.3000	14.44
39	FVVACGTAY	307	1.3000	14.44
40	YTRAGPEIG	400	1.3000	14.44
41	YVVVMDALR	13	1.1000	12.22
42	LVDGGTLTV	35	1.1000	12.22
43	VAAHLVARA	130	1.0000	11.11
44	LGLALAQAR	425	1.0000	11.11
45	YLLGLALAQ	423	0.9000	10.00
46	IENFAVLRR	105	0.8000	8.89
47	VASTKTFLA	409	0.8000	8.89
48	YVGRRPAYV	6	0.7000	7.78
49	FASDTDTEV	122	0.7000	7.78
50	LRRLEGHFT	156	0.7000	7.78
51	VFAASVARA	597	0.7000	7.78
52	FRPFHIDWD	243	0.6000	6.67
53	YHELEAMPD	445	0.6000	6.67
54	MHAEGFAAG	503	0.6000	6.67
55	FRYRDPVLD	341	0.5800	6.44
56	VAISQSGET	355	0.5000	5.56
57	LRRMEYRGY	20	0.4000	4.44

58	IIENFAVLR	104	0.3800	4.22
59	YFMLKEIAE	262	0.3800	4.22
60	LAQIAANYL	416	0.3600	4.00
61	WDLAAAEKG	250	0.3000	3.33
62	IPLQVFAAS	593	0.3000	3.33

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	LAICNTNGS	381	4.8000	54.55
2	VVACGTAYH	308	4.0800	46.36
3	VVVMDALRR	14	3.7000	42.05
4	LPVIVVMPS	525	3.4000	38.64
5	IVVMPSPKG	528	3.4000	38.64
6	LQVFAASVA	595	3.2000	36.36
7	IREIQTRGA	548	3.1000	35.23
8	VLAICNTNG	380	2.8000	31.82
9	IPAVSTLLQ	579	2.7000	30.68
10	LQPLLSTIP	586	2.6000	29.55
11	LVVAISQSG	353	2.4000	27.27
12	VIVVMPSPK	527	2.3000	26.14
13	YRGYDSSGI	25	2.2000	25.00
14	IENFAVLRR	105	1.8000	20.45
15	VFAASVARA	597	1.7000	19.32
16	VVMPSPKGS	529	1.6000	18.18
17	VLGIGDNEM	186	1.5000	17.05
18	LRRMEYRGY	20	1.3000	14.77
19	VASTKTFLA	409	1.1500	13.07
20	LLGLALAQA	424	1.1000	12.50
21	LEAMPDLVA	448	1.1000	12.50
22	VAEMPSTAL	57	1.0000	11.36
23	LAYMHAEGF	500	0.9000	10.23
24	IAVVHNGII	97	0.8000	9.09
25	LRRLEGHFT	156	0.8000	9.09
26	LAQIAANYL	416	0.8000	9.09

27	IEIPAVSTL	577	0.7000	7.95
28	VFVVACGTA	306	0.6000	6.82
29	IGVASTKTF	407	0.6000	6.82
30	LEGHFTLVF	159	0.5000	5.68
31	FVGSDVAAF	195	0.5000	5.68
32	VVAISQSGE	354	0.5000	5.68
33	LVFANADDP	165	0.4000	4.55
34	LETAGVEFA	115	0.3000	3.41
35	IVLDEQRLS	288	0.3000	3.41
36	LGLALAQAR	425	0.3000	3.41
37	VTIVIAEEG	557	0.3000	3.41
38	VRPYADHLI	569	0.3000	3.41
39	VARVIAATG	455	0.2000	2.27
40	VVHNGIIEN	99	0.1800	2.05
41	VGSVLAVLR	149	0.1000	1.14
42	LKELAYMHA	497	0.1000	1.14
43	IPLQVFAAS	593	0.1000	1.14
44	LVDGGTLTV	35	-0.1000	0
45	VAAHLVARA	130	-0.1000	0
46	LLSTIPLQV	589	-0.1000	0
47	VRHAKEQKA	370	-0.2000	0
48	LIEIPAVST	576	-0.3000	0
49	LLAKYAIEH	319	-0.3400	0
50	FTLVFANAD	163	-0.5000	0
51	FRPFHIDWD	243	-0.5000	0
52	FVVACGTAY	307	-0.5000	0
53	VVITADGYR	219	-0.6000	0
54	FHIDWDLAA	246	-0.6000	0
55	VAISQSGET	355	-0.6000	0
56	YLLGLALAQ	423	-0.6000	0
57	VGSDVAAFI	196	-0.7000	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	LAICNTNGS	381	3.7000	43.02
2	FHIDWDLAA	246	3.3000	38.37
3	VVACGTAYH	308	3.0800	35.81
4	FVGSDVAAF	195	3.0000	34.88
5	VVVMDALRR	14	2.2000	25.58
6	LPVIVVMPS	525	2.2000	25.58
7	LEGHFTLVF	159	2.0000	23.26
8	IVVMPSPKG	528	1.8000	20.93
9	FAQSSTVLF	472	1.7800	20.70
10	YRISDFDGN	226	1.7000	19.77
11	LVVAISQSG	353	1.6000	18.60
12	YLLGLALAQ	423	1.6000	18.60
13	IVLDEQRLS	288	1.5000	17.44
14	IREIQTRGA	548	1.5000	17.44
15	YRGYDSSGI	25	1.3000	15.12
16	VVMPSPKGS	529	1.3000	15.12
17	VVMDALRRM	15	1.2000	13.95
18	VALEGALKL	489	1.2000	13.95
19	VAAHLVARA	130	1.0000	11.63
20	YRHGETADD	139	1.0000	11.63
21	FVGSVLAVL	148	1.0000	11.63
22	VLAICNTNG	380	1.0000	11.63
23	YAIEHWTRL	323	0.9000	10.47
24	WTRLPVEVE	328	0.9000	10.47
25	LQPLLSTIP	586	0.9000	10.47
26	LLSTIPLQV	589	0.9000	10.47
27	VGSDVAAFI	196	0.8000	9.30
28	FMLKEIAEQ	263	0.8000	9.30
29	VASTKTFLA	409	0.8000	9.30
30	FLAQIAANY	415	0.8000	9.30
31	VVHNGIIEN	99	0.7800	9.07
32	IPAVSTLLQ	579	0.7000	8.14
33	VFAASVARA	597	0.7000	8.14
34	LGQDQAVVI	213	0.6800	7.91
35	IGVASTKTF	407	0.6000	6.98
36	MLKEIAEQP	264	0.4000	4.65
37	LVFANADDP	165	0.3000	3.49

38	LETAGVEFA	115	0.2000	2.33
39	LVDGGTLTV	35	0.1000	1.16
40	VLGIGDNEM	186	0.1000	1.16
41	LRRELETAG	111	-0.1000	0
42	LGIGDNEMF	187	-0.1000	0
43	VVITADGYR	219	-0.1000	0
44	LLGHFVGGR	279	-0.1000	0
45	VEVELASEF	333	-0.1000	0
46	YTRAGPEIG	400	-0.1000	0
47	LLGLALAQA	424	-0.1000	0
48	LAYMHAEGF	500	-0.1000	0
49	IPLQVFAAS	593	-0.1000	0
50	VAISQSGET	355	-0.2000	0
51	YVGRRPAYV	6	-0.3000	0
52	FASDTDTEV	122	-0.3000	0
53	YVVVMDALR	13	-0.4000	0
54	LEAMPDLVA	448	-0.4000	0
55	LQVFAASVA	595	-0.4000	0
56	FRPFHIDWD	243	-0.5000	0
57	LPVEVELAS	331	-0.5000	0
58	LGLALAQAR	425	-0.5000	0
59	YHELEAMPD	445	-0.5000	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	FVGSVLAVL	148	6.3000	54.31
2	FVGSDVAAF	195	6.0000	51.72
3	YRGYDSSGI	25	5.9000	50.86
4	LLSTIPLQV	589	5.3000	45.69
5	FAQSSTVLF	472	5.1200	44.14
6	LAQIAANYL	416	4.9000	42.24
7	VITADGYRI	220	4.6000	39.66
8	VALEGALKL	489	4.2000	36.21
9	YEYFMLKEI	260	4.1000	35.34

10	ICNTNGSQI	383	4.1000	35.34
11	IQTRGAVTI	551	4.1000	35.34
12	FVVACGTAY	307	4.0000	34.48
13	IALVDGGTL	33	3.7000	31.90
14	LEGHFTLVF	159	3.6200	31.21
15	LREIDKVFV	300	3.6000	31.03
16	YAIEHWTRL	323	3.5000	30.17
17	LGRHVGYPV	481	3.4000	29.31
18	IEIPAVSTL	577	3.3000	28.45
19	IAVVHNGII	97	3.2000	27.59
20	VAISQSGET	355	3.0000	25.86
21	LGQDQAVVI	213	2.9000	25.00
22	LVDGGTLTV	35	2.8200	24.31
23	VGRRPAYVV	7	2.8000	24.14
24	VAARRSTPL	177	2.8000	24.14
25	YMHAEGFAA	502	2.8000	24.14
26	VARARGYDV	602	2.8000	24.14
27	YVGRRPAYV	6	2.7000	23.28
28	VVMDALRRM	15	2.7000	23.28
29	LGHFVGGRI	280	2.7000	23.28
30	LVVAISQSG	353	2.7000	23.28
31	VASTKTFLA	409	2.6200	22.59
32	VVVMDALRR	14	2.6000	22.41
33	YRISDFDGN	226	2.6000	22.41
34	IAANYLLGL	419	2.6000	22.41
35	IGVASTKTF	407	2.5200	21.72
36	LAYMHAEGF	500	2.4000	20.69
37	VRPYADHLI	569	2.4000	20.69
38	LRRMEYRGY	20	2.3000	19.83
39	VAEMPSTAL	57	2.3000	19.83
40	LGIGDNEMF	187	2.3000	19.83
41	VLGIGDNEM	186	2.2000	18.97
42	YLLGLALAQ	423	2.2000	18.97
43	FTLVFANAD	163	2.1000	18.10
44	LKHGPIALI	513	2.1000	18.10
45	LSTIPLQVF	590	2.1000	18.10
46	LIEIPAVST	576	2.0000	17.24

47	YDSSGIALV	28	1.9000	16.38
48	VLYTRAGPE	398	1.9000	16.38
49	LRRLEGHFT	156	1.8000	15.52
50	FIEHTREAV	203	1.8000	15.52
51	FRYRDPVLD	341	1.8000	15.52
52	VLDRSTLVV	347	1.7200	14.83
53	IREIQTRGA	548	1.7200	14.83
54	LSGTTGLGH	65	1.7000	14.66
55	VHNGIIENF	100	1.7000	14.66
56	LPVIVVMPS	525	1.7000	14.66
57	VTIVIAEEG	557	1.7000	14.66
58	LLQPLLSTI	585	1.7000	14.66
59	VVHNGIIEN	99	1.6000	13.79
60	LFLGRHVGY	479	1.6000	13.79
61	LAICNTNGS	381	1.5200	13.10
62	VGSDVAAFI	196	1.5000	12.93

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	FVGSVLAVL	148	6.3000	54.31
2	FVGSDVAAF	195	6.0000	51.72
3	YRGYDSSGI	25	5.9000	50.86
4	LLSTIPLQV	589	5.3000	45.69
5	FAQSSTVLF	472	5.1200	44.14
6	LAQIAANYL	416	4.9000	42.24
7	VITADGYRI	220	4.6000	39.66
8	VALEGALKL	489	4.2000	36.21
9	YEYFMLKEI	260	4.1000	35.34
10	ICNTNGSQI	383	4.1000	35.34
11	IQTRGAVTI	551	4.1000	35.34
12	FVVACGTAY	307	4.0000	34.48
13	IALVDGGTL	33	3.7000	31.90
14	LEGHFTLVF	159	3.6200	31.21
15	LREIDKVFV	300	3.6000	31.03

16	YAIEHWTRL	323	3.5000	30.17
17	LGRHVGYPV	481	3.4000	29.31
18	IEIPAVSTL	577	3.3000	28.45
19	IAVVHNGII	97	3.2000	27.59
20	VAISQSGET	355	3.0000	25.86
21	LGQDQAVVI	213	2.9000	25.00
22	LVDGGTLTV	35	2.8200	24.31
23	VGRRPAYVV	7	2.8000	24.14
24	VAARRSTPL	177	2.8000	24.14
25	YMHAEGFAA	502	2.8000	24.14
26	VARARGYDV	602	2.8000	24.14
27	YVGRRPAYV	6	2.7000	23.28
28	VVMDALRRM	15	2.7000	23.28
29	LGHFVGGRI	280	2.7000	23.28
30	LVVAISQSG	353	2.7000	23.28
31	VASTKTFLA	409	2.6200	22.59
32	VVVMDALRR	14	2.6000	22.41
33	YRISDFDGN	226	2.6000	22.41
34	IAANYLLGL	419	2.6000	22.41
35	IGVASTKTF	407	2.5200	21.72
36	LAYMHAEGF	500	2.4000	20.69
37	VRPYADHLI	569	2.4000	20.69
38	LRRMEYRGY	20	2.3000	19.83
39	VAEMPSTAL	57	2.3000	19.83
40	LGIGDNEMF	187	2.3000	19.83
41	VLGIGDNEM	186	2.2000	18.97
42	YLLGLALAQ	423	2.2000	18.97
43	FTLVFANAD	163	2.1000	18.10
44	LKHGPIALI	513	2.1000	18.10
45	LSTIPLQVF	590	2.1000	18.10
46	LIEIPAVST	576	2.0000	17.24
47	YDSSGIALV	28	1.9000	16.38
48	VLYTRAGPE	398	1.9000	16.38
49	LRRLEGHFT	156	1.8000	15.52
50	FIEHTREAV	203	1.8000	15.52
51	FRYRDPVLD	341	1.8000	15.52
52	VLDRSTLVV	347	1.7200	14.83

53	IREIQTRGA	548	1.7200	14.83
54	LSGTTGLGH	65	1.7000	14.66
55	VHNGIIENF	100	1.7000	14.66
56	LPVIVVMPS	525	1.7000	14.66
57	VTIVIAEEG	557	1.7000	14.66
58	LLQPLLSTI	585	1.7000	14.66
59	VVHNGIIEN	99	1.6000	13.79
60	LFLGRHVGY	479	1.6000	13.79
61	LAICNTNGS	381	1.5200	13.10
62	VGSDVAAFI	196	1.5000	12.93

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	FMLKEIAEQ	263	6.4000	74.42
2	FRYRDPVLD	341	5.7000	66.28
3	YVGRRPAYV	6	4.7000	54.65
4	LKLKELAYM	495	4.3000	50.00
5	VGGRIVLDE	284	4.2000	48.84
6	LVARVIAAT	454	3.8000	44.19
7	FLGRHVGYP	480	3.3000	38.37
8	YRHGETADD	139	3.2000	37.21
9	VVACGTAYH	308	3.2000	37.21
10	YRGYDSSGI	25	3.1000	36.05
11	VRRRAGRLA	43	2.9000	33.72
12	LLAKYAIEH	319	2.8000	32.56
13	FVGSDVAAF	195	2.4000	27.91
14	FRPFHIDWD	243	2.3000	26.74
15	VLAVLRRLE	152	2.0000	23.26
16	YFMLKEIAE	262	2.0000	23.26
17	YLLGLALAQ	423	2.0000	23.26
18	IVVMPSPKG	528	2.0000	23.26
19	IVIAEEGDE	559	2.0000	23.26
20	FVGGRIVLD	283	1.9000	22.09
21	VLFLGRHVG	478	1.9000	22.09

22	VVMPSPKGS	529	1.9000	22.09
23	VVMDALRRM	15	1.8000	20.93
24	LTVRRRAGR	41	1.8000	20.93
25	VVHNGIIEN	99	1.8000	20.93
26	VVVMDALRR	14	1.7000	19.77
27	LVARAYRHG	134	1.7000	19.77
28	LEGALKLKE	491	1.6000	18.60
29	FVGSVLAVL	148	1.5000	17.44
30	WTRLPVEVE	328	1.5000	17.44
31	LRRMEYRGY	20	1.4000	16.28
32	IVGYVGRRP	3	1.3000	15.12
33	IQTRGAVTI	551	1.3000	15.12
34	LAVLRRLEG	153	1.2000	13.95
35	FAVLRRELE	108	1.1000	12.79
36	VARAYRHGE	135	1.1000	12.79
37	VLDRSTLVV	347	1.1000	12.79
38	VVAISQSGE	354	1.1000	12.79
39	LLGLALAQA	424	1.1000	12.79
40	VGYVGRRPA	4	1.0000	11.63
41	VGRRPAYVV	7	1.0000	11.63
42	VLRRLEGHF	155	1.0000	11.63
43	FTLVFANAD	163	1.0000	11.63
44	YHELEAMPD	445	1.0000	11.63
45	LAHRFAQSS	468	1.0000	11.63
46	VFAASVARA	597	1.0000	11.63
47	IVLDEQRLS	288	0.9000	10.47
48	LPVIVVMPS	525	0.9000	10.47
49	LHAKLLSNI	540	0.9000	10.47
50	VLRRELETA	110	0.8000	9.30
51	LRRLEGHFT	156	0.7000	8.14
52	YEYFMLKEI	260	0.7000	8.14
53	LAICNTNGS	381	0.7000	8.14
54	LVVAISQSG	353	0.6000	6.98
55	LEAVRHAKE	367	0.6000	6.98
56	VLYTRAGPE	398	0.6000	6.98
57	IPAVSTLLQ	579	0.6000	6.98
58	VMDALRRME	16	0.5000	5.81

59	IREIQTRGA	548	0.5000	5.81
60	YHSGLLAKY	315	0.3000	3.49
61	VARVIAATG	455	0.3000	3.49
62	VRPYADHLI	569	0.3000	3.49

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	FMLKEIAEQ	263	5.6000	70.00
2	YVGRRPAYV	6	4.4000	55.00
3	LKLKELAYM	495	3.2000	40.00
4	FRYRDPVLD	341	3.0000	37.50
5	YRGYDSSGI	25	2.9000	36.25
6	VRRRAGRLA	43	2.9000	36.25
7	LVARVIAAT	454	2.9000	36.25
8	FLGRHVGYP	480	2.9000	36.25
9	VVACGTAYH	308	1.9800	24.75
10	VVMPSPKGS	529	1.9000	23.75
11	LTVRRRAGR	41	1.8000	22.50
12	VVVMDALRR	14	1.7000	21.25
13	LLAKYAIEH	319	1.5800	19.75
14	FVGSDVAAF	195	1.5000	18.75
15	VGGRIVLDE	284	1.2000	15.00
16	YLLGLALAQ	423	1.2000	15.00
17	LLGLALAQA	424	1.1000	13.75
18	IQTRGAVTI	551	1.1000	13.75
19	VGYVGRRPA	4	1.0000	12.50
20	LAHRFAQSS	468	1.0000	12.50
21	VFAASVARA	597	1.0000	12.50
22	IVGYVGRRP	3	0.9000	11.25
23	IVLDEQRLS	288	0.9000	11.25
24	LPVIVVMPS	525	0.9000	11.25
25	VLRRELETA	110	0.8000	10.00
26	VLDRSTLVV	347	0.8000	10.00
27	VGRRPAYVV	7	0.7000	8.75

28	VVMDALRRM	15	0.7000	8.75
29	LAICNTNGS	381	0.7000	8.75
30	IVVMPSPKG	528	0.7000	8.75
31	LHAKLLSNI	540	0.7000	8.75
32	VLFLGRHVG	478	0.6000	7.50
33	YRHGETADD	139	0.5000	6.25
34	FVGSVLAVL	148	0.5000	6.25
35	YEYFMLKEI	260	0.5000	6.25
36	IREIQTRGA	548	0.5000	6.25
37	LVARAYRHG	134	0.4000	5.00
38	LRRMEYRGY	20	0.3000	3.75
39	VMPSPKGSA	530	0.2000	2.50
40	VLRRLEGHF	155	0.1000	1.25
41	VFVVACGTA	306	0.1000	1.25
42	VRPYADHLI	569	0.1000	1.25
43	LAVLRRLEG	153	-0.1000	0
44	LQVFAASVA	595	-0.1000	0
45	VVHNGIIEN	99	-0.2000	0
46	LRRLEGHFT	156	-0.2000	0
47	LREIDKVFV	300	-0.2000	0
48	VIVVMPSPK	527	-0.2000	0
49	IPAVSTLLQ	579	-0.2000	0
50	YMHAEGFAA	502	-0.3000	0
51	LKHGPIALI	513	-0.3000	0
52	FRPFHIDWD	243	-0.4000	0
53	YVVVMDALR	13	-0.5000	0
54	LVAARRSTP	176	-0.5000	0
55	IEHWTRLPV	325	-0.7000	0
56	LVVAISQSG	353	-0.7000	0
57	LLSNIREIQ	544	-0.7000	0
58	VAAHLVARA	130	-0.8000	0
59	FVGGRIVLD	283	-0.8000	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	FMLKEIAEQ	263	4.6000	57.50
2	LKLKELAYM	495	4.2000	52.50
3	VRRRAGRLA	43	3.9000	48.75
4	LVARVIAAT	454	3.9000	48.75
5	YVGRRPAYV	6	3.4000	42.50
6	VVACGTAYH	308	2.9800	37.25
7	VVMPSPKGS	529	2.9000	36.25
8	LTVRRRAGR	41	2.8000	35.00
9	VVVMDALRR	14	2.7000	33.75
10	LLAKYAIEH	319	2.5800	32.25
11	VGGRIVLDE	284	2.2000	27.50
12	LLGLALAQA	424	2.1000	26.25
13	IQTRGAVTI	551	2.1000	26.25
14	VGYVGRRPA	4	2.0000	25.00
15	FRYRDPVLD	341	2.0000	25.00
16	LAHRFAQSS	468	2.0000	25.00
17	VFAASVARA	597	2.0000	25.00
18	IVGYVGRRP	3	1.9000	23.75
19	YRGYDSSGI	25	1.9000	23.75
20	IVLDEQRLS	288	1.9000	23.75
21	FLGRHVGYP	480	1.9000	23.75
22	LPVIVVMPS	525	1.9000	23.75
23	VLRRELETA	110	1.8000	22.50
24	VLDRSTLVV	347	1.8000	22.50
25	VGRRPAYVV	7	1.7000	21.25
26	VVMDALRRM	15	1.7000	21.25
27	LAICNTNGS	381	1.7000	21.25
28	IVVMPSPKG	528	1.7000	21.25
29	LHAKLLSNI	540	1.7000	21.25
30	VLFLGRHVG	478	1.6000	20.00
31	IREIQTRGA	548	1.5000	18.75
32	LVARAYRHG	134	1.4000	17.50
33	LRRMEYRGY	20	1.3000	16.25
34	VMPSPKGSA	530	1.2000	15.00
35	VLRRLEGHF	155	1.1000	13.75
36	VFVVACGTA	306	1.1000	13.75

37	VRPYADHLI	569	1.1000	13.75
38	IENFAVLRR	105	1.0000	12.50
39	LYTRAGPEI	399	1.0000	12.50
40	LAVLRRLEG	153	0.9000	11.25
41	LQVFAASVA	595	0.9000	11.25
42	VVHNGIIEN	99	0.8000	10.00
43	LRRLEGHFT	156	0.8000	10.00
44	LREIDKVFV	300	0.8000	10.00
45	VIVVMPSPK	527	0.8000	10.00
46	IPAVSTLLQ	579	0.8000	10.00
47	LKHGPIALI	513	0.7000	8.75
48	LVAARRSTP	176	0.5000	6.25
49	FVGSDVAAF	195	0.5000	6.25
50	IEHWTRLPV	325	0.3000	3.75
51	LVVAISQSG	353	0.3000	3.75
52	LLSNIREIQ	544	0.3000	3.75
53	VAAHLVARA	130	0.2000	2.50
54	YLLGLALAQ	423	0.2000	2.50
55	MEYRGYDSS	23	0.1000	1.25
56	LLGHFVGGR	279	-0.1000	0
57	LANLEEAVA	50	-0.2000	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	FMLKEIAEQ	263	5.4000	62.79
2	LKLKELAYM	495	5.3000	61.63
3	VGGRIVLDE	284	5.2000	60.47
4	LVARVIAAT	454	4.8000	55.81
5	FRYRDPVLD	341	4.7000	54.65
6	VVACGTAYH	308	4.2000	48.84
7	VRRRAGRLA	43	3.9000	45.35
8	LLAKYAIEH	319	3.8000	44.19
9	YVGRRPAYV	6	3.7000	43.02
10	VLAVLRRLE	152	3.0000	34.88

11	IVVMPSPKG	528	3.0000	34.88
12	IVIAEEGDE	559	3.0000	34.88
13	VLFLGRHVG	478	2.9000	33.72
14	VVMPSPKGS	529	2.9000	33.72
15	VVMDALRRM	15	2.8000	32.56
16	LTVRRRAGR	41	2.8000	32.56
17	VVHNGIIEN	99	2.8000	32.56
18	VVVMDALRR	14	2.7000	31.40
19	LVARAYRHG	134	2.7000	31.40
20	LEGALKLKE	491	2.6000	30.23
21	LRRMEYRGY	20	2.4000	27.91
22	IVGYVGRRP	3	2.3000	26.74
23	FLGRHVGYP	480	2.3000	26.74
24	IQTRGAVTI	551	2.3000	26.74
25	YRHGETADD	139	2.2000	25.58
26	LAVLRRLEG	153	2.2000	25.58
27	YRGYDSSGI	25	2.1000	24.42
28	VARAYRHGE	135	2.1000	24.42
29	VLDRSTLVV	347	2.1000	24.42
30	VVAISQSGE	354	2.1000	24.42
31	LLGLALAQA	424	2.1000	24.42
32	VGYVGRRPA	4	2.0000	23.26
33	VGRRPAYVV	7	2.0000	23.26
34	VLRRLEGHF	155	2.0000	23.26
35	LAHRFAQSS	468	2.0000	23.26
36	VFAASVARA	597	2.0000	23.26
37	IVLDEQRLS	288	1.9000	22.09
38	LPVIVVMPS	525	1.9000	22.09
39	LHAKLLSNI	540	1.9000	22.09
40	VLRRELETA	110	1.8000	20.93
41	LRRLEGHFT	156	1.7000	19.77
42	LAICNTNGS	381	1.7000	19.77
43	LVVAISQSG	353	1.6000	18.60
44	LEAVRHAKE	367	1.6000	18.60
45	VLYTRAGPE	398	1.6000	18.60
46	IPAVSTLLQ	579	1.6000	18.60
47	VMDALRRME	16	1.5000	17.44

48	IREIQTRGA	548	1.5000	17.44
49	FVGSDVAAF	195	1.4000	16.28
50	FRPFHIDWD	243	1.3000	15.12
51	VARVIAATG	455	1.3000	15.12
52	VRPYADHLI	569	1.3000	15.12
53	LYTRAGPEI	399	1.2000	13.95
54	VMPSPKGSA	530	1.2000	13.95
55	LREIDKVFV	300	1.1000	12.79
56	VFVVACGTA	306	1.1000	12.79
57	LLSNIREIQ	544	1.1000	12.79
58	IENFAVLRR	105	1.0000	11.63
59	YFMLKEIAE	262	1.0000	11.63
60	YLLGLALAQ	423	1.0000	11.63
61	LVAARRSTP	176	0.9000	10.47
62	LAAAEKGGY	252	0.9000	10.47

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	FMLKEIAEQ	263	5.6000	64.37
2	YRGYDSSGI	25	4.7000	54.02
3	YVGRRPAYV	6	4.4000	50.57
4	FRYRDPVLD	341	4.0000	45.98
5	LKLKELAYM	495	3.2000	36.78
6	LVARVIAAT	454	2.9000	33.33
7	LAICNTNGS	381	2.7000	31.03
8	VRRRAGRLA	43	2.6000	29.89
9	VLRRELETA	110	2.5000	28.74
10	LHAKLLSNI	540	2.5000	28.74
11	LLAKYAIEH	319	2.4600	28.28
12	VVVMDALRR	14	2.3000	26.44
13	FLGRHVGYP	480	2.2000	25.29
14	IQTRGAVTI	551	2.1000	24.14
15	LAHRFAQSS	468	2.0000	22.99
16	VVACGTAYH	308	1.9800	22.76

17	LPVIVVMPS	525	1.9000	21.84
18	LTVRRRAGR	41	1.8000	20.69
19	VGGRIVLDE	284	1.8000	20.69
20	YLLGLALAQ	423	1.8000	20.69
21	LQVFAASVA	595	1.7000	19.54
22	VGRRPAYVV	7	1.6000	18.39
23	VIVVMPSPK	527	1.6000	18.39
24	FVGSDVAAF	195	1.5000	17.24
25	VLDRSTLVV	347	1.4000	16.09
26	VVMPSPKGS	529	1.4000	16.09
27	LVAARRSTP	176	1.3000	14.94
28	FVVACGTAY	307	1.3000	14.94
29	LLGLALAQA	424	1.1000	12.64
30	VLFLGRHVG	478	1.1000	12.64
31	LLSNIREIQ	544	1.0000	11.49
32	VFAASVARA	597	1.0000	11.49
33	IVVMPSPKG	528	0.9000	10.34
34	FRPFHIDWD	243	0.8000	9.20
35	LREIDKVFV	300	0.8000	9.20
36	VGYVGRRPA	4	0.7000	8.05
37	VVHNGIIEN	99	0.6800	7.82
38	IVGYVGRRP	3	0.6000	6.90
39	IENFAVLRR	105	0.6000	6.90
40	VAARRSTPL	177	0.6000	6.90
41	IVLDEQRLS	288	0.6000	6.90
42	VRPYADHLI	569	0.6000	6.90
43	YMHAEGFAA	502	0.5500	6.32
44	YRHGETADD	139	0.5000	5.75
45	FVGSVLAVL	148	0.5000	5.75
46	LAVLRRLEG	153	0.5000	5.75
47	VVMDALRRM	15	0.4000	4.60
48	IPAVSTLLQ	579	0.4000	4.60
49	MEYRGYDSS	23	0.3000	3.45
50	LRRLEGHFT	156	0.3000	3.45
51	FTLVFANAD	163	0.3000	3.45
52	LVVAISQSG	353	0.3000	3.45
53	IEIPAVSTL	577	0.3000	3.45

54	FVGGRIVLD	283	0.2000	2.30
55	LAKYAIEHW	320	0.2000	2.30
56	WTRLPVEVE	328	0.2000	2.30
57	LYTRAGPEI	399	0.2000	2.30
58	IREIQTRGA	548	0.2000	2.30
59	LQPLLSTIP	586	0.2000	2.30
60	LVARAYRHG	134	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	FMLKEIAEQ	263	6.4000	63.37
2	FRYRDPVLD	341	6.2000	61.39
3	VGGRIVLDE	284	6.0000	59.41
4	YVGRRPAYV	6	4.7000	46.53
5	LLAKYAIEH	319	4.4000	43.56
6	LKLKELAYM	495	4.3000	42.57
7	YLLGLALAQ	423	3.8000	37.62
8	LVARVIAAT	454	3.8000	37.62
9	YFMLKEIAE	262	3.6000	35.64
10	VVVMDALRR	14	3.5000	34.65
11	VVHNGIIEN	99	3.4000	33.66
12	FLGRHVGYP	480	3.4000	33.66
13	LEGALKLKE	491	3.4000	33.66
14	YRHGETADD	139	3.2000	31.68
15	VVACGTAYH	308	3.2000	31.68
16	IVVMPSPKG	528	3.1500	31.19
17	YRGYDSSGI	25	3.1000	30.69
18	VRRRAGRLA	43	3.1000	30.69
19	LAVLRRLEG	153	3.0000	29.70
20	VLDRSTLVV	347	2.9000	28.71
21	WTRLPVEVE	328	2.6000	25.74
22	YHELEAMPD	445	2.6000	25.74
23	VLFLGRHVG	478	2.6000	25.74
24	LPVIVVMPS	525	2.5000	24.75

25	VVMPSPKGS	529	2.5000	24.75
26	FVGSDVAAF	195	2.4000	23.76
27	FVGGRIVLD	283	2.4000	23.76
28	IPAVSTLLQ	579	2.4000	23.76
29	FAVLRRELE	108	2.2000	21.78
30	VLAVLRRLE	152	2.2000	21.78
31	IVIAEEGDE	559	2.1000	20.79
32	VVMDALRRM	15	2.0000	19.80
33	FRPFHIDWD	243	2.0000	19.80
34	VLRRELETA	110	1.9000	18.81
35	LVARAYRHG	134	1.9000	18.81
36	LTVRRRAGR	41	1.8000	17.82
37	IENFAVLRR	105	1.8000	17.82
38	VARAYRHGE	135	1.8000	17.82
39	IQTRGAVTI	551	1.8000	17.82
40	VGRRPAYVV	7	1.7000	16.83
41	LRRMEYRGY	20	1.6000	15.84
42	IVGYVGRRP	3	1.5000	14.85
43	FVGSVLAVL	148	1.5000	14.85
44	LRRLEGHFT	156	1.4000	13.86
45	IEHWTRLPV	325	1.4000	13.86
46	LYTRAGPEI	399	1.3500	13.37
47	FTLVFANAD	163	1.3000	12.87
48	YEYFMLKEI	260	1.3000	12.87
49	VGYVGRRPA	4	1.2000	11.88
50	VLDEQRLSD	289	1.2000	11.88
51	LLSNIREIQ	544	1.2000	11.88
52	VLRRLEGHF	155	1.1000	10.89
53	IVLDEQRLS	288	1.1000	10.89
54	VVAISQSGE	354	1.1000	10.89
55	LLGLALAQA	424	1.1000	10.89
56	LAHRFAQSS	468	1.1000	10.89
57	VGYPVALEG	485	1.1000	10.89
58	LAICNTNGS	381	1.0000	9.90
59	VRPYADHLI	569	1.0000	9.90
60	VFAASVARA	597	1.0000	9.90
61	WATHGRPTD	76	0.9500	9.41

62	LHAKLLSNI	540	0.9000	8.91

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	VVVMDALRR	14	3.1000	37.35
2	LPVIVVMPS	525	3.1000	37.35
3	FMLKEIAEQ	263	2.8000	33.73
4	YLLGLALAQ	423	2.3000	27.71
5	LAVLRRLEG	153	2.1000	25.30
6	VVACGTAYH	308	1.9800	23.86
7	FVGSDVAAF	195	1.8000	21.69
8	VVMPSPKGS	529	1.8000	21.69
9	IENFAVLRR	105	1.7000	20.48
10	VLFLGRHVG	478	1.7000	20.48
11	IPAVSTLLQ	579	1.7000	20.48
12	LLGLALAQA	424	1.5000	18.07
13	IVVMPSPKG	528	1.4500	17.47
14	YVGRRPAYV	6	1.4000	16.87
15	VVHNGIIEN	99	1.4000	16.87
16	VGYVGRRPA	4	1.3000	15.66
17	IREIQTRGA	548	1.3000	15.66
18	YEYFMLKEI	260	1.0000	12.05
19	YFMLKEIAE	262	1.0000	12.05
20	IEHWTRLPV	325	1.0000	12.05
21	LAICNTNGS	381	1.0000	12.05
22	VFAASVARA	597	1.0000	12.05
23	LRRLEGHFT	156	0.9000	10.84
24	LREIDKVFV	300	0.9000	10.84
25	LLSTIPLQV	589	0.9000	10.84
26	FVGSVLAVL	148	0.8000	9.64
27	VMPSPKGSA	530	0.6000	7.23
28	FRYRDPVLD	341	0.5000	6.02
29	IVLDEQRLS	288	0.4000	4.82
30	LEGALKLKE	491	0.4000	4.82

31	LKLKELAYM	495	0.4000	4.82
32	LLSNIREIQ	544	0.4000	4.82
33	LLAKYAIEH	319	0.3800	4.58
34	VFVVACGTA	306	0.3000	3.61
35	YHELEAMPD	445	0.3000	3.61
36	VVMDALRRM	15	0.2000	2.41
37	YMHAEGFAA	502	0.2000	2.41
38	MDALRRMEY	17	0.1000	1.20
39	LRRMEYRGY	20	0.1000	1.20
40	VRRRAGRLA	43	0.1000	1.20
41	LVARVIAAT	454	-0.1000	0
42	LKELAYMHA	497	-0.1000	0
43	VIVVMPSPK	527	-0.1000	0
44	YRHGETADD	139	-0.2000	0
45	LQVFAASVA	595	-0.2000	0
46	LVDGGTLTV	35	-0.3000	0
47	FDGNDGLQA	231	-0.3000	0
48	FHIDWDLAA	246	-0.3000	0
49	IAANYLLGL	419	-0.3000	0
50	YVVVMDALR	13	-0.4000	0
51	FAVLRRELE	108	-0.4000	0
52	VAAHLVARA	130	-0.4000	0
53	FVVACGTAY	307	-0.4000	0
54	VLDRSTLVV	347	-0.4000	0
55	IGVASTKTF	407	-0.4000	0
56	FLAQIAANY	415	-0.4000	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	VRRRAGRLA	43	3.6000	42.86
2	IVLDEQRLS	288	3.3000	39.29
3	VVMPSPKGS	529	3.2000	38.10
4	VVMDALRRM	15	3.1000	36.90
5	FMLKEIAEQ	263	3.1000	36.90

6	LAICNTNGS	381	3.1000	36.90
7	VVACGTAYH	308	2.9800	35.48
8	VVVMDALRR	14	2.8000	33.33
9	VAAHLVARA	130	2.7000	32.14
10	LKLKELAYM	495	2.7000	32.14
11	VGYVGRRPA	4	2.6000	30.95
12	LRRMEYRGY	20	2.5000	29.76
13	VLFLGRHVG	478	2.5000	29.76
14	IREIQTRGA	548	2.4000	28.57
15	IENFAVLRR	105	2.0000	23.81
16	LEGHFTLVF	159	2.0000	23.81
17	VFAASVARA	597	2.0000	23.81
18	IVGYVGRRP	3	1.9000	22.62
19	LLGLALAQA	424	1.8000	21.43
20	LVARVIAAT	454	1.8000	21.43
21	IVVMPSPKG	528	1.8000	21.43
22	LLSNIREIQ	544	1.8000	21.43
23	LRRLEGHFT	156	1.7000	20.24
24	IEHWTRLPV	325	1.7000	20.24
25	LQVFAASVA	595	1.6000	19.05
26	LLGHFVGGR	279	1.4000	16.67
27	LLAKYAIEH	319	1.3800	16.43
28	YVGRRPAYV	6	1.3000	15.48
29	LAVLRRLEG	153	1.3000	15.48
30	LPVIVVMPS	525	1.3000	15.48
31	VVHNGIIEN	99	1.2000	14.29
32	VLRRELETA	110	1.1000	13.10
33	LVARAYRHG	134	1.1000	13.10
34	LVVAISQSG	353	1.1000	13.10
35	LGRHVGYPV	481	1.1000	13.10
36	LALAQARGT	427	1.0000	11.90
37	IQTRGAVTI	551	1.0000	11.90
38	LVAARRSTP	176	0.9000	10.71
39	FVGSDVAAF	195	0.9000	10.71
40	LREIDKVFV	300	0.9000	10.71
41	FRYRDPVLD	341	0.9000	10.71
42	VGGRIVLDE	284	0.8000	9.52

43	IGVASTKTF	407	0.8000	9.52
44	LTVRRRAGR	41	0.7000	8.33
45	LAHRFAQSS	468	0.7000	8.33
46	VLAVLRRLE	152	0.6000	7.14
47	YEYFMLKEI	260	0.6000	7.14
48	VRHAKEQKA	370	0.6000	7.14
49	VMPSPKGSA	530	0.6000	7.14
50	LHAKLLSNI	540	0.6000	7.14
51	VGRRPAYVV	7	0.5000	5.95
52	YRGYDSSGI	25	0.5000	5.95
53	VASTKTFLA	409	0.5000	5.95
54	VRPYADHLI	569	0.5000	5.95
55	VLDRSTLVV	347	0.4000	4.76
56	YLLGLALAQ	423	0.4000	4.76
57	IPLQVFAAS	593	0.4000	4.76
58	VMDALRRME	16	0.3000	3.57
59	LETAGVEFA	115	0.3000	3.57
60	VARAYRHGE	135	0.3000	3.57
61	VAELAHRFA	465	0.3000	3.57
62	LEGALKLKE	491	0.3000	3.57

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	VVVMDALRR	14	4.1000	49.40
2	LPVIVVMPS	525	4.1000	49.40
3	LAVLRRLEG	153	3.1000	37.35
4	VVACGTAYH	308	2.9800	35.90
5	VVMPSPKGS	529	2.8000	33.73
6	IENFAVLRR	105	2.7000	32.53
7	VLFLGRHVG	478	2.7000	32.53
8	IPAVSTLLQ	579	2.7000	32.53
9	LLGLALAQA	424	2.5000	30.12
10	IVVMPSPKG	528	2.4500	29.52
11	VVHNGIIEN	99	2.4000	28.92

12	VGYVGRRPA	4	2.3000	27.71
13	IREIQTRGA	548	2.3000	27.71
14	IEHWTRLPV	325	2.0000	24.10
15	LAICNTNGS	381	2.0000	24.10
16	VFAASVARA	597	2.0000	24.10
17	LRRLEGHFT	156	1.9000	22.89
18	LREIDKVFV	300	1.9000	22.89
19	LLSTIPLQV	589	1.9000	22.89
20	FMLKEIAEQ	263	1.8000	21.69
21	VMPSPKGSA	530	1.6000	19.28
22	IVLDEQRLS	288	1.4000	16.87
23	LEGALKLKE	491	1.4000	16.87
24	LKLKELAYM	495	1.4000	16.87
25	LLSNIREIQ	544	1.4000	16.87
26	LLAKYAIEH	319	1.3800	16.63
27	VFVVACGTA	306	1.3000	15.66
28	YLLGLALAQ	423	1.3000	15.66
29	VVMDALRRM	15	1.2000	14.46
30	MDALRRMEY	17	1.1000	13.25
31	LRRMEYRGY	20	1.1000	13.25
32	VRRRAGRLA	43	1.1000	13.25
33	LEGHFTLVF	159	1.0000	12.05
34	VGGRIVLDE	284	1.0000	12.05
35	LVARVIAAT	454	0.9000	10.84
36	LKELAYMHA	497	0.9000	10.84
37	VIVVMPSPK	527	0.9000	10.84
38	FVGSDVAAF	195	0.8000	9.64
39	LQVFAASVA	595	0.8000	9.64
40	LVDGGTLTV	35	0.7000	8.43
41	IAANYLLGL	419	0.7000	8.43
42	VAAHLVARA	130	0.6000	7.23
43	VLDRSTLVV	347	0.6000	7.23
44	IGVASTKTF	407	0.6000	7.23
45	LVAARRSTP	176	0.5000	6.02
46	YVGRRPAYV	6	0.4000	4.82
47	LLGHFVGGR	279	0.4000	4.82
48	LVVAISQSG	353	0.4000	4.82

49	VIAATGPVA	458	0.3500	4.22
50	VLAVLRRLE	152	0.3000	3.61
51	LANLEEAVA	50	0.2000	2.41
52	LEAMPDLVA	448	0.2000	2.41
53	LSGTTGLGH	65	0.1800	2.17
54	VARVIAATG	455	0.1000	1.20
55	VGYPVALEG	485	0.1000	1.20
56	IVIAEEGDE	559	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	VVVMDALRR	14	4.1000	49.40
2	LPVIVVMPS	525	4.1000	49.40
3	LAVLRRLEG	153	3.1000	37.35
4	VVACGTAYH	308	2.9800	35.90
5	VVMPSPKGS	529	2.8000	33.73
6	IENFAVLRR	105	2.7000	32.53
7	VLFLGRHVG	478	2.7000	32.53
8	IPAVSTLLQ	579	2.7000	32.53
9	LLGLALAQA	424	2.5000	30.12
10	IVVMPSPKG	528	2.4500	29.52
11	VVHNGIIEN	99	2.4000	28.92
12	VGYVGRRPA	4	2.3000	27.71
13	IREIQTRGA	548	2.3000	27.71
14	IEHWTRLPV	325	2.0000	24.10
15	LAICNTNGS	381	2.0000	24.10
16	VFAASVARA	597	2.0000	24.10
17	LRRLEGHFT	156	1.9000	22.89
18	LREIDKVFV	300	1.9000	22.89
19	LLSTIPLQV	589	1.9000	22.89
20	FMLKEIAEQ	263	1.8000	21.69
21	VMPSPKGSA	530	1.6000	19.28
22	IVLDEQRLS	288	1.4000	16.87
23	LEGALKLKE	491	1.4000	16.87

24	LKLKELAYM	495	1.4000	16.87
25	LLSNIREIQ	544	1.4000	16.87
26	LLAKYAIEH	319	1.3800	16.63
27	VFVVACGTA	306	1.3000	15.66
28	YLLGLALAQ	423	1.3000	15.66
29	VVMDALRRM	15	1.2000	14.46
30	MDALRRMEY	17	1.1000	13.25
31	LRRMEYRGY	20	1.1000	13.25
32	VRRRAGRLA	43	1.1000	13.25
33	LEGHFTLVF	159	1.0000	12.05
34	VGGRIVLDE	284	1.0000	12.05
35	LVARVIAAT	454	0.9000	10.84
36	LKELAYMHA	497	0.9000	10.84
37	VIVVMPSPK	527	0.9000	10.84
38	FVGSDVAAF	195	0.8000	9.64
39	LQVFAASVA	595	0.8000	9.64
40	LVDGGTLTV	35	0.7000	8.43
41	IAANYLLGL	419	0.7000	8.43
42	VAAHLVARA	130	0.6000	7.23
43	VLDRSTLVV	347	0.6000	7.23
44	IGVASTKTF	407	0.6000	7.23
45	LVAARRSTP	176	0.5000	6.02
46	YVGRRPAYV	6	0.4000	4.82
47	LLGHFVGGR	279	0.4000	4.82
48	LVVAISQSG	353	0.4000	4.82
49	VIAATGPVA	458	0.3500	4.22
50	VLAVLRRLE	152	0.3000	3.61
51	LANLEEAVA	50	0.2000	2.41
52	LEAMPDLVA	448	0.2000	2.41
53	LSGTTGLGH	65	0.1800	2.17
54	VARVIAATG	455	0.1000	1.20
55	VGYPVALEG	485	0.1000	1.20
56	IVIAEEGDE	559	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	IVLDEQRLS	288	4.9000	53.85
2	VVMDALRRM	15	4.7000	51.65
3	LPVIVVMPS	525	3.5000	38.46
4	VMPSPKGSA	530	3.5000	38.46
5	VVACGTAYH	308	2.9800	32.75
6	LAICNTNGS	381	2.9100	31.98
7	LIEDGLPVI	520	2.8000	30.77
8	VVMPSPKGS	529	2.8000	30.77
9	VGSDVAAFI	196	2.7000	29.67
10	LGQDQAVVI	213	2.7000	29.67
11	LLSNIREIQ	544	2.7000	29.67
12	LREIDKVFV	300	2.3000	25.27
13	VVHNGIIEN	99	2.2000	24.18
14	FVGSDVAAF	195	2.2000	24.18
15	YLLGLALAQ	423	2.2000	24.18
16	LKHGPIALI	513	2.2000	24.18
17	IVVMPSPKG	528	2.2000	24.18
18	VFAASVARA	597	2.0000	21.98
19	LVAARRSTP	176	1.8700	20.55
20	VIVVMPSPK	527	1.8700	20.55
21	VVVMDALRR	14	1.8000	19.78
22	LVDGGTLTV	35	1.6000	17.58
23	LLGHFVGGR	279	1.5000	16.48
24	VGYVGRRPA	4	1.4000	15.38
25	FHIDWDLAA	246	1.4000	15.38
26	VFVVACGTA	306	1.4000	15.38
27	LVVAISQSG	353	1.4000	15.38
28	LLGLALAQA	424	1.4000	15.38
29	LFLGRHVGY	479	1.4000	15.38
30	IREIQTRGA	548	1.4000	15.38
31	VHNGIIENF	100	1.3000	14.29
32	FMLKEIAEQ	263	1.3000	14.29
33	VAAHLVARA	130	1.2000	13.19
34	FVGSVLAVL	148	1.2000	13.19
35	VACGTAYHS	309	1.1500	12.64
36	LETAGVEFA	115	1.1000	12.09

37	VIAATGPVA	458	1.1000	12.09
38	YRHGETADD	139	1.0000	10.99
39	LVFANADDP	165	1.0000	10.99
40	FVGGRIVLD	283	1.0000	10.99
41	VAISQSGET	355	1.0000	10.99
42	VLFLGRHVG	478	1.0000	10.99
43	IPAVSTLLQ	579	1.0000	10.99
44	VRHAKEQKA	370	0.9000	9.89
45	LKLKELAYM	495	0.9000	9.89
46	IEIPAVSTL	577	0.8700	9.56
47	LQVFAASVA	595	0.7700	8.46
48	VLRRELETA	110	0.7000	7.69
49	LAVLRRLEG	153	0.7000	7.69
50	LGIGDNEMF	187	0.7000	7.69
51	ITADGYRIS	221	0.7000	7.69
52	VVAISQSGE	354	0.6700	7.36
53	LVLGIGDNE	185	0.6000	6.59
54	LVARVIAAT	454	0.6000	6.59
55	IVIAEEGDE	559	0.6000	6.59
56	LDRSTLVVA	348	0.5000	5.49
57	VASTKTFLA	409	0.5000	5.49
58	LLAKYAIEH	319	0.4800	5.27
59	LAAAEKGGY	252	0.4000	4.40
60	LGLALAQAR	425	0.4000	4.40
61	VRRRAGRLA	43	0.3000	3.30
62	LEGHFTLVF	159	0.3000	3.30

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	FMLKEIAEQ	263	4.1000	48.81
2	VRRRAGRLA	43	2.6000	30.95
3	YVGRRPAYV	6	2.3000	27.38
4	IVLDEQRLS	288	2.3000	27.38
5	VVMPSPKGS	529	2.2000	26.19

6	VVMDALRRM	15	2.1000	25.00
7	LAICNTNGS	381	2.1000	25.00
8	VVACGTAYH	308	1.9800	23.57
9	FVGSDVAAF	195	1.9000	22.62
10	FRYRDPVLD	341	1.9000	22.62
11	VVVMDALRR	14	1.8000	21.43
12	VAAHLVARA	130	1.7000	20.24
13	LKLKELAYM	495	1.7000	20.24
14	VGYVGRRPA	4	1.6000	19.05
15	YEYFMLKEI	260	1.6000	19.05
16	LRRMEYRGY	20	1.5000	17.86
17	YRGYDSSGI	25	1.5000	17.86
18	VLFLGRHVG	478	1.5000	17.86
19	YLLGLALAQ	423	1.4000	16.67
20	IREIQTRGA	548	1.4000	16.67
21	YMHAEGFAA	502	1.2000	14.29
22	IENFAVLRR	105	1.0000	11.90
23	LEGHFTLVF	159	1.0000	11.90
24	VFAASVARA	597	1.0000	11.90
25	IVGYVGRRP	3	0.9000	10.71
26	FVGSVLAVL	148	0.9000	10.71
27	FRPFHIDWD	243	0.8000	9.52
28	LLGLALAQA	424	0.8000	9.52
29	LVARVIAAT	454	0.8000	9.52
30	IVVMPSPKG	528	0.8000	9.52
31	LLSNIREIQ	544	0.8000	9.52
32	LRRLEGHFT	156	0.7000	8.33
33	FIEHTREAV	203	0.7000	8.33
34	IEHWTRLPV	325	0.7000	8.33
35	FLAQIAANY	415	0.6000	7.14
36	LQVFAASVA	595	0.6000	7.14
37	LLGHFVGGR	279	0.4000	4.76
38	LLAKYAIEH	319	0.3800	4.52
39	WATHGRPTD	76	0.3000	3.57
40	LAVLRRLEG	153	0.3000	3.57
41	LPVIVVMPS	525	0.3000	3.57
42	VVHNGIIEN	99	0.2000	2.38

43	VLRRELETA	110	0.1000	1.19
44	LVARAYRHG	134	0.1000	1.19
45	LVVAISQSG	353	0.1000	1.19
46	LGRHVGYPV	481	0.1000	1.19
47	LVAARRSTP	176	-0.1000	0
48	LREIDKVFV	300	-0.1000	0
49	VGGRIVLDE	284	-0.2000	0
50	IGVASTKTF	407	-0.2000	0
51	FLGRHVGYP	480	-0.2000	0
52	LTVRRRAGR	41	-0.3000	0
53	FVGGRIVLD	283	-0.3000	0
54	LAHRFAQSS	468	-0.3000	0
55	VLAVLRRLE	152	-0.4000	0
56	WTRLPVEVE	328	-0.4000	0
57	VRHAKEQKA	370	-0.4000	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	FVGSDVAAF	195	3.8000	43.18
2	VVMDALRRM	15	3.6000	40.91
3	FMLKEIAEQ	263	3.4000	38.64
4	YVGRRPAYV	6	3.3000	37.50
5	VVVMDALRR	14	3.3000	37.50
6	LKLKELAYM	495	3.2000	36.36
7	FRYRDPVLD	341	3.0000	34.09
8	LEGHFTLVF	159	2.9000	32.95
9	VLFLGRHVG	478	2.9000	32.95
10	LRRMEYRGY	20	2.8000	31.82
11	IVLDEQRLS	288	2.7000	30.68
12	VRRRAGRLA	43	2.6000	29.55
13	VVMPSPKGS	529	2.6000	29.55
14	IENFAVLRR	105	2.5000	28.41
15	YEYFMLKEI	260	2.5000	28.41
16	LAICNTNGS	381	2.5000	28.41

17	YRGYDSSGI	25	2.4000	27.27
18	IVVMPSPKG	528	2.2000	25.00
19	IVGYVGRRP	3	1.9000	21.59
20	FRPFHIDWD	243	1.9000	21.59
21	LLGHFVGGR	279	1.9000	21.59
22	FLAQIAANY	415	1.9000	21.59
23	FVGSVLAVL	148	1.8600	21.14
24	VAAHLVARA	130	1.7000	19.32
25	LAVLRRLEG	153	1.7000	19.32
26	FIEHTREAV	203	1.7000	19.32
27	IEHWTRLPV	325	1.7000	19.32
28	IGVASTKTF	407	1.7000	19.32
29	VGYVGRRPA	4	1.6000	18.18
30	LVARAYRHG	134	1.5000	17.05
31	LVVAISQSG	353	1.5000	17.05
32	LVARVIAAT	454	1.5000	17.05
33	WATHGRPTD	76	1.4000	15.91
34	LRRLEGHFT	156	1.4000	15.91
35	VVACGTAYH	308	1.4000	15.91
36	IREIQTRGA	548	1.4000	15.91
37	FVVACGTAY	307	1.3000	14.77
38	LTVRRRAGR	41	1.2000	13.64
39	VGGRIVLDE	284	1.2000	13.64
40	YMHAEGFAA	502	1.2000	13.64
41	YRHGETADD	139	1.1000	12.50
42	LGRHVGYPV	481	1.1000	12.50
43	FAASVARAR	598	1.1000	12.50
44	VVHNGIIEN	99	1.0000	11.36
45	VLAVLRRLE	152	1.0000	11.36
46	WTRLPVEVE	328	1.0000	11.36
47	FAQSSTVLF	472	1.0000	11.36
48	VFAASVARA	597	1.0000	11.36
49	LVAARRSTP	176	0.9000	10.23
50	LREIDKVFV	300	0.9000	10.23
51	IQTRGAVTI	551	0.9000	10.23
52	FVGGRIVLD	283	0.8000	9.09
53	LLGLALAQA	424	0.8000	9.09

54	FLGRHVGYP	480	0.8000	9.09
55	VMDALRRME	16	0.7000	7.95
56	VARAYRHGE	135	0.7000	7.95
57	YLLGLALAQ	423	0.7000	7.95
58	LALAQARGT	427	0.7000	7.95
59	LEGALKLKE	491	0.7000	7.95
60	LPVIVVMPS	525	0.7000	7.95
61	FAVLRRELE	108	0.6000	6.82
62	YTRAGPEIG	400	0.6000	6.82

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	VRRRAGRLA	43	3.6000	42.86
2	IVLDEQRLS	288	3.3000	39.29
3	VVMPSPKGS	529	3.2000	38.10
4	VVMDALRRM	15	3.1000	36.90
5	FMLKEIAEQ	263	3.1000	36.90
6	LAICNTNGS	381	3.1000	36.90
7	VVACGTAYH	308	2.9800	35.48
8	VVVMDALRR	14	2.8000	33.33
9	VAAHLVARA	130	2.7000	32.14
10	LKLKELAYM	495	2.7000	32.14
11	VGYVGRRPA	4	2.6000	30.95
12	LRRMEYRGY	20	2.5000	29.76
13	VLFLGRHVG	478	2.5000	29.76
14	IREIQTRGA	548	2.4000	28.57
15	IENFAVLRR	105	2.0000	23.81
16	LEGHFTLVF	159	2.0000	23.81
17	VFAASVARA	597	2.0000	23.81
18	IVGYVGRRP	3	1.9000	22.62
19	LLGLALAQA	424	1.8000	21.43
20	LVARVIAAT	454	1.8000	21.43
21	IVVMPSPKG	528	1.8000	21.43
22	LLSNIREIQ	544	1.8000	21.43

23	LRRLEGHFT	156	1.7000	20.24
24	IEHWTRLPV	325	1.7000	20.24
25	LQVFAASVA	595	1.6000	19.05
26	LLGHFVGGR	279	1.4000	16.67
27	LLAKYAIEH	319	1.3800	16.43
28	YVGRRPAYV	6	1.3000	15.48
29	LAVLRRLEG	153	1.3000	15.48
30	LPVIVVMPS	525	1.3000	15.48
31	VVHNGIIEN	99	1.2000	14.29
32	VLRRELETA	110	1.1000	13.10
33	LVARAYRHG	134	1.1000	13.10
34	LVVAISQSG	353	1.1000	13.10
35	LGRHVGYPV	481	1.1000	13.10
36	LALAQARGT	427	1.0000	11.90
37	IQTRGAVTI	551	1.0000	11.90
38	LVAARRSTP	176	0.9000	10.71
39	FVGSDVAAF	195	0.9000	10.71
40	LREIDKVFV	300	0.9000	10.71
41	FRYRDPVLD	341	0.9000	10.71
42	VGGRIVLDE	284	0.8000	9.52
43	IGVASTKTF	407	0.8000	9.52
44	LTVRRRAGR	41	0.7000	8.33
45	LAHRFAQSS	468	0.7000	8.33
46	VLAVLRRLE	152	0.6000	7.14
47	YEYFMLKEI	260	0.6000	7.14
48	VRHAKEQKA	370	0.6000	7.14
49	VMPSPKGSA	530	0.6000	7.14
50	LHAKLLSNI	540	0.6000	7.14
51	VGRRPAYVV	7	0.5000	5.95
52	YRGYDSSGI	25	0.5000	5.95
53	VASTKTFLA	409	0.5000	5.95
54	VRPYADHLI	569	0.5000	5.95
55	VLDRSTLVV	347	0.4000	4.76
56	YLLGLALAQ	423	0.4000	4.76
57	IPLQVFAAS	593	0.4000	4.76
58	VMDALRRME	16	0.3000	3.57
59	LETAGVEFA	115	0.3000	3.57

60	VARAYRHGE	135	0.3000	3.57
61	VAELAHRFA	465	0.3000	3.57
62	LEGALKLKE	491	0.3000	3.57

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	VVVMDALRR	14	4.6000	52.87
2	FVGSDVAAF	195	3.7000	42.53
3	LAVLRRLEG	153	3.5000	40.23
4	LPVIVVMPS	525	3.5000	40.23
5	IENFAVLRR	105	3.2000	36.78
6	VLFLGRHVG	478	3.1000	35.63
7	IVVMPSPKG	528	2.8500	32.76
8	YVGRRPAYV	6	2.4000	27.59
9	YFMLKEIAE	262	2.4000	27.59
10	VVHNGIIEN	99	2.2000	25.29
11	VVMPSPKGS	529	2.2000	25.29
12	FMLKEIAEQ	263	2.1000	24.14
13	IEHWTRLPV	325	2.0000	22.99
14	LEGHFTLVF	159	1.9000	21.84
15	YEYFMLKEI	260	1.9000	21.84
16	LREIDKVFV	300	1.9000	21.84
17	LKLKELAYM	495	1.9000	21.84
18	LLSTIPLQV	589	1.9000	21.84
19	LEGALKLKE	491	1.8000	20.69
20	FVGSVLAVL	148	1.7600	20.23
21	VVMDALRRM	15	1.7000	19.54
22	LRRLEGHFT	156	1.6000	18.39
23	FRYRDPVLD	341	1.6000	18.39
24	YLLGLALAQ	423	1.6000	18.39
25	IGVASTKTF	407	1.5000	17.24
26	LLGLALAQA	424	1.5000	17.24
27	MDALRRMEY	17	1.4000	16.09
28	LRRMEYRGY	20	1.4000	16.09

29	VGGRIVLDE	284	1.4000	16.09
30	VVACGTAYH	308	1.4000	16.09
31	WTRLPVEVE	328	1.4000	16.09
32	LAICNTNGS	381	1.4000	16.09
33	YHELEAMPD	445	1.4000	16.09
34	VGYVGRRPA	4	1.3000	14.94
35	IREIQTRGA	548	1.3000	14.94
36	YVVVMDALR	13	1.1000	12.64
37	FAVLRRELE	108	1.0000	11.49
38	FLGRHVGYP	480	1.0000	11.49
39	IPAVSTLLQ	579	1.0000	11.49
40	VFAASVARA	597	1.0000	11.49
41	YRGYDSSGI	25	0.9000	10.34
42	YRHGETADD	139	0.9000	10.34
43	LLGHFVGGR	279	0.9000	10.34
44	FVVACGTAY	307	0.9000	10.34
45	FLAQIAANY	415	0.9000	10.34
46	IVLDEQRLS	288	0.8000	9.20
47	LVVAISQSG	353	0.8000	9.20
48	LVDGGTLTV	35	0.7000	8.05
49	VLAVLRRLE	152	0.7000	8.05
50	IAANYLLGL	419	0.6600	7.59
51	VLDRSTLVV	347	0.6000	6.90
52	LVARVIAAT	454	0.6000	6.90
53	VMPSPKGSA	530	0.6000	6.90
54	LVAARRSTP	176	0.5000	5.75
55	VARVIAATG	455	0.5000	5.75
56	VGYPVALEG	485	0.5000	5.75
57	IVIAEEGDE	559	0.5000	5.75
58	FAQSSTVLF	472	0.4000	4.60
59	LAYMHAEGF	500	0.4000	4.60
60	LTVRRRAGR	41	0.3000	3.45
61	FRPFHIDWD	243	0.3000	3.45
62	VFVVACGTA	306	0.3000	3.45

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	VVMDALRRM	15	4.6000	52.27
2	VVVMDALRR	14	4.3000	48.86
3	LKLKELAYM	495	4.2000	47.73
4	LEGHFTLVF	159	3.9000	44.32
5	VLFLGRHVG	478	3.9000	44.32
6	LRRMEYRGY	20	3.8000	43.18
7	IVLDEQRLS	288	3.7000	42.05
8	VRRRAGRLA	43	3.6000	40.91
9	VVMPSPKGS	529	3.6000	40.91
10	IENFAVLRR	105	3.5000	39.77
11	LAICNTNGS	381	3.5000	39.77
12	IVVMPSPKG	528	3.2000	36.36
13	IVGYVGRRP	3	2.9000	32.95
14	LLGHFVGGR	279	2.9000	32.95
15	FVGSDVAAF	195	2.8000	31.82
16	VAAHLVARA	130	2.7000	30.68
17	LAVLRRLEG	153	2.7000	30.68
18	IEHWTRLPV	325	2.7000	30.68
19	IGVASTKTF	407	2.7000	30.68
20	VGYVGRRPA	4	2.6000	29.55
21	LVARAYRHG	134	2.5000	28.41
22	LVVAISQSG	353	2.5000	28.41
23	LVARVIAAT	454	2.5000	28.41
24	LRRLEGHFT	156	2.4000	27.27
25	FMLKEIAEQ	263	2.4000	27.27
26	VVACGTAYH	308	2.4000	27.27
27	IREIQTRGA	548	2.4000	27.27
28	YVGRRPAYV	6	2.3000	26.14
29	LTVRRRAGR	41	2.2000	25.00
30	VGGRIVLDE	284	2.2000	25.00
31	LGRHVGYPV	481	2.1000	23.86
32	VVHNGIIEN	99	2.0000	22.73
33	VLAVLRRLE	152	2.0000	22.73

34	FRYRDPVLD	341	2.0000	22.73
35	VFAASVARA	597	2.0000	22.73
36	LVAARRSTP	176	1.9000	21.59
37	LREIDKVFV	300	1.9000	21.59
38	IQTRGAVTI	551	1.9000	21.59
39	LLGLALAQA	424	1.8000	20.45
40	VMDALRRME	16	1.7000	19.32
41	VARAYRHGE	135	1.7000	19.32
42	LALAQARGT	427	1.7000	19.32
43	LEGALKLKE	491	1.7000	19.32
44	LPVIVVMPS	525	1.7000	19.32
45	LGLALAQAR	425	1.6000	18.18
46	LQVFAASVA	595	1.6000	18.18
47	VGRRPAYVV	7	1.5000	17.05
48	YEYFMLKEI	260	1.5000	17.05
49	LAYMHAEGF	500	1.5000	17.05
50	LHAKLLSNI	540	1.5000	17.05
51	YRGYDSSGI	25	1.4000	15.91
52	VLDRSTLVV	347	1.4000	15.91
53	VRPYADHLI	569	1.4000	15.91
54	LLSTIPLQV	589	1.3000	14.77
55	VLRRELETA	110	1.1000	12.50
56	LVFANADDP	165	1.1000	12.50
57	LAHRFAQSS	468	1.1000	12.50
58	LKHGPIALI	513	1.1000	12.50
59	LLSNIREIQ	544	1.1000	12.50
60	LSDQELREI	295	1.0000	11.36
61	FRPFHIDWD	243	0.9000	10.23
62	FLAQIAANY	415	0.9000	10.23

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	FVGSDVAAF	195	3.8000	43.18
2	VVMDALRRM	15	3.6000	40.91

3	FMLKEIAEQ	263	3.4000	38.64
4	YVGRRPAYV	6	3.3000	37.50
5	VVVMDALRR	14	3.3000	37.50
6	LKLKELAYM	495	3.2000	36.36
7	FRYRDPVLD	341	3.0000	34.09
8	LEGHFTLVF	159	2.9000	32.95
9	VLFLGRHVG	478	2.9000	32.95
10	LRRMEYRGY	20	2.8000	31.82
11	IVLDEQRLS	288	2.7000	30.68
12	VRRRAGRLA	43	2.6000	29.55
13	VVMPSPKGS	529	2.6000	29.55
14	IENFAVLRR	105	2.5000	28.41
15	YEYFMLKEI	260	2.5000	28.41
16	LAICNTNGS	381	2.5000	28.41
17	YRGYDSSGI	25	2.4000	27.27
18	IVVMPSPKG	528	2.2000	25.00
19	IVGYVGRRP	3	1.9000	21.59
20	FRPFHIDWD	243	1.9000	21.59
21	LLGHFVGGR	279	1.9000	21.59
22	FLAQIAANY	415	1.9000	21.59
23	FVGSVLAVL	148	1.8600	21.14
24	VAAHLVARA	130	1.7000	19.32
25	LAVLRRLEG	153	1.7000	19.32
26	FIEHTREAV	203	1.7000	19.32
27	IEHWTRLPV	325	1.7000	19.32
28	IGVASTKTF	407	1.7000	19.32
29	VGYVGRRPA	4	1.6000	18.18
30	LVARAYRHG	134	1.5000	17.05
31	LVVAISQSG	353	1.5000	17.05
32	LVARVIAAT	454	1.5000	17.05
33	WATHGRPTD	76	1.4000	15.91
34	LRRLEGHFT	156	1.4000	15.91
35	VVACGTAYH	308	1.4000	15.91
36	IREIQTRGA	548	1.4000	15.91
37	FVVACGTAY	307	1.3000	14.77
38	LTVRRRAGR	41	1.2000	13.64
39	VGGRIVLDE	284	1.2000	13.64

40	YMHAEGFAA	502	1.2000	13.64
41	YRHGETADD	139	1.1000	12.50
42	LGRHVGYPV	481	1.1000	12.50
43	FAASVARAR	598	1.1000	12.50
44	VVHNGIIEN	99	1.0000	11.36
45	VLAVLRRLE	152	1.0000	11.36
46	WTRLPVEVE	328	1.0000	11.36
47	FAQSSTVLF	472	1.0000	11.36
48	VFAASVARA	597	1.0000	11.36
49	LVAARRSTP	176	0.9000	10.23
50	LREIDKVFV	300	0.9000	10.23
51	IQTRGAVTI	551	0.9000	10.23
52	FVGGRIVLD	283	0.8000	9.09
53	LLGLALAQA	424	0.8000	9.09
54	FLGRHVGYP	480	0.8000	9.09
55	VMDALRRME	16	0.7000	7.95
56	VARAYRHGE	135	0.7000	7.95
57	YLLGLALAQ	423	0.7000	7.95
58	LALAQARGT	427	0.7000	7.95
59	LEGALKLKE	491	0.7000	7.95
60	LPVIVVMPS	525	0.7000	7.95
61	FAVLRRELE	108	0.6000	6.82
62	YTRAGPEIG	400	0.6000	6.82

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	VVMDALRRM	15	4.2000	46.67
2	VVACGTAYH	308	4.2000	46.67
3	FMLKEIAEQ	263	3.9000	43.33
4	VGGRIVLDE	284	3.8000	42.22
5	VLFLGRHVG	478	3.8000	42.22
6	LKLKELAYM	495	3.8000	42.22
7	LRRMEYRGY	20	3.6000	40.00
8	VRRRAGRLA	43	3.6000	40.00

9	VLAVLRRLE	152	3.6000	40.00
10	FRYRDPVLD	341	3.6000	40.00
11	VMDALRRME	16	3.3000	36.67
12	VARAYRHGE	135	3.3000	36.67
13	IVLDEQRLS	288	3.3000	36.67
14	LEGALKLKE	491	3.3000	36.67
15	VVHNGIIEN	99	3.2000	35.56
16	VVMPSPKGS	529	3.2000	35.56
17	LAICNTNGS	381	3.1000	34.44
18	IVVMPSPKG	528	3.1000	34.44
19	LEGHFTLVF	159	2.9000	32.22
20	VVVMDALRR	14	2.8000	31.11
21	VAAHLVARA	130	2.7000	30.00
22	LVARVIAAT	454	2.7000	30.00
23	VGYVGRRPA	4	2.6000	28.89
24	LAVLRRLEG	153	2.6000	28.89
25	LRRLEGHFT	156	2.6000	28.89
26	LLAKYAIEH	319	2.6000	28.89
27	LLSNIREIQ	544	2.6000	28.89
28	FRPFHIDWD	243	2.5000	27.78
29	LVARAYRHG	134	2.4000	26.67
30	LVVAISQSG	353	2.4000	26.67
31	IREIQTRGA	548	2.4000	26.67
32	IVGYVGRRP	3	2.3000	25.56
33	WATHGRPTD	76	2.0000	22.22
34	IENFAVLRR	105	2.0000	22.22
35	IEHWTRLPV	325	2.0000	22.22
36	IVIAEEGDE	559	2.0000	22.22
37	VFAASVARA	597	2.0000	22.22
38	LALAQARGT	427	1.9000	21.11
39	FVGSDVAAF	195	1.8000	20.00
40	LLGLALAQA	424	1.8000	20.00
41	YRHGETADD	139	1.7000	18.89
42	IGVASTKTF	407	1.7000	18.89
43	YVGRRPAYV	6	1.6000	17.78
44	WTRLPVEVE	328	1.6000	17.78
45	VVAISQSGE	354	1.6000	17.78

46	LQVFAASVA	595	1.6000	17.78
47	LLGHFVGGR	279	1.4000	15.56
48	FVGGRIVLD	283	1.4000	15.56
49	LGRHVGYPV	481	1.4000	15.56
50	LVAARRSTP	176	1.3000	14.44
51	LPVIVVMPS	525	1.3000	14.44
52	FAVLRRELE	108	1.2000	13.33
53	LREIDKVFV	300	1.2000	13.33
54	YLLGLALAQ	423	1.2000	13.33
55	IQTRGAVTI	551	1.2000	13.33
56	VLRRELETA	110	1.1000	12.22
57	IPAVSTLLQ	579	1.1000	12.22
58	YFMLKEIAE	262	1.0000	11.11
59	VLDEQRLSD	289	1.0000	11.11
60	FVGSVLAVL	148	0.9000	10.00
61	LASEFRYRD	337	0.9000	10.00
62	VGRRPAYVV	7	0.8000	8.89

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	VVVMDALRR	14	4.6000	52.87
2	FVGSDVAAF	195	3.7000	42.53
3	LAVLRRLEG	153	3.5000	40.23
4	LPVIVVMPS	525	3.5000	40.23
5	IENFAVLRR	105	3.2000	36.78
6	VLFLGRHVG	478	3.1000	35.63
7	IVVMPSPKG	528	2.8500	32.76
8	YVGRRPAYV	6	2.4000	27.59
9	YFMLKEIAE	262	2.4000	27.59
10	VVHNGIIEN	99	2.2000	25.29
11	VVMPSPKGS	529	2.2000	25.29
12	FMLKEIAEQ	263	2.1000	24.14
13	IEHWTRLPV	325	2.0000	22.99
14	LEGHFTLVF	159	1.9000	21.84

15	YEYFMLKEI	260	1.9000	21.84
16	LREIDKVFV	300	1.9000	21.84
17	LKLKELAYM	495	1.9000	21.84
18	LLSTIPLQV	589	1.9000	21.84
19	LEGALKLKE	491	1.8000	20.69
20	FVGSVLAVL	148	1.7600	20.23
21	VVMDALRRM	15	1.7000	19.54
22	LRRLEGHFT	156	1.6000	18.39
23	FRYRDPVLD	341	1.6000	18.39
24	YLLGLALAQ	423	1.6000	18.39
25	IGVASTKTF	407	1.5000	17.24
26	LLGLALAQA	424	1.5000	17.24
27	MDALRRMEY	17	1.4000	16.09
28	LRRMEYRGY	20	1.4000	16.09
29	VGGRIVLDE	284	1.4000	16.09
30	VVACGTAYH	308	1.4000	16.09
31	WTRLPVEVE	328	1.4000	16.09
32	LAICNTNGS	381	1.4000	16.09
33	YHELEAMPD	445	1.4000	16.09
34	VGYVGRRPA	4	1.3000	14.94
35	IREIQTRGA	548	1.3000	14.94
36	YVVVMDALR	13	1.1000	12.64
37	FAVLRRELE	108	1.0000	11.49
38	FLGRHVGYP	480	1.0000	11.49
39	IPAVSTLLQ	579	1.0000	11.49
40	VFAASVARA	597	1.0000	11.49
41	YRGYDSSGI	25	0.9000	10.34
42	YRHGETADD	139	0.9000	10.34
43	LLGHFVGGR	279	0.9000	10.34
44	FVVACGTAY	307	0.9000	10.34
45	FLAQIAANY	415	0.9000	10.34
46	IVLDEQRLS	288	0.8000	9.20
47	LVVAISQSG	353	0.8000	9.20
48	LVDGGTLTV	35	0.7000	8.05
49	VLAVLRRLE	152	0.7000	8.05
50	IAANYLLGL	419	0.6600	7.59
51	VLDRSTLVV	347	0.6000	6.90

52	LVARVIAAT	454	0.6000	6.90
53	VMPSPKGSA	530	0.6000	6.90
54	LVAARRSTP	176	0.5000	5.75
55	VARVIAATG	455	0.5000	5.75
56	VGYPVALEG	485	0.5000	5.75
57	IVIAEEGDE	559	0.5000	5.75
58	FAQSSTVLF	472	0.4000	4.60
59	LAYMHAEGF	500	0.4000	4.60
60	LTVRRRAGR	41	0.3000	3.45
61	FRPFHIDWD	243	0.3000	3.45
62	VFVVACGTA	306	0.3000	3.45

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	FMLKEIAEQ	263	2.8000	41.18
2	VVACGTAYH	308	1.9800	29.12
3	FVGSDVAAF	195	1.8000	26.47
4	LLGLALAQA	424	1.5000	22.06
5	LPVIVVMPS	525	1.5000	22.06
6	YVGRRPAYV	6	1.4000	20.59
7	VVVMDALRR	14	1.3000	19.12
8	VVMPSPKGS	529	1.2000	17.65
9	VGYVGRRPA	4	1.1000	16.18
10	IREIQTRGA	548	1.1000	16.18
11	VLFLGRHVG	478	1.0000	14.71
12	VFAASVARA	597	1.0000	14.71
13	FVGSVLAVL	148	0.8000	11.76
14	LAICNTNGS	381	0.7000	10.29
15	YLLGLALAQ	423	0.5000	7.35
16	VMPSPKGSA	530	0.5000	7.35
17	YEYFMLKEI	260	0.4000	5.88
18	LREIDKVFV	300	0.4000	5.88
19	LKLKELAYM	495	0.4000	5.88
20	LAVLRRLEG	153	0.3000	4.41

21	IVVMPSPKG	528	0.3000	4.41
22	LRRLEGHFT	156	0.2000	2.94
23	IVLDEQRLS	288	0.2000	2.94
24	VFVVACGTA	306	0.2000	2.94
25	LRRMEYRGY	20	-0.1000	0
26	VRRRAGRLA	43	-0.1000	0
27	IENFAVLRR	105	-0.1000	0
28	LVARVIAAT	454	-0.1000	0
29	FLGRHVGYP	480	-0.1000	0
30	VIVVMPSPK	527	-0.1000	0
31	IPAVSTLLQ	579	-0.1000	0
32	VVHNGIIEN	99	-0.2000	0
33	YRHGETADD	139	-0.2000	0
34	LQVFAASVA	595	-0.2000	0
35	YMHAEGFAA	502	-0.3000	0
36	YVVVMDALR	13	-0.4000	0
37	VAAHLVARA	130	-0.4000	0
38	FLAQIAANY	415	-0.4000	0
39	LVAARRSTP	176	-0.5000	0
40	FRPFHIDWD	243	-0.5000	0
41	YFMLKEIAE	262	-0.6000	0
42	LLGHFVGGR	279	-0.7000	0
43	LVVAISQSG	353	-0.7000	0
44	LLSNIREIQ	544	-0.7000	0
45	LANLEEAVA	50	-0.8000	0
46	IEHWTRLPV	325	-0.8000	0
47	VLAVLRRLE	152	-0.9000	0
48	VARVIAATG	455	-0.9000	0
49	LLSTIPLQV	589	-0.9000	0
50	IGVASTKTF	407	-1.0000	0
51	LKHGPIALI	513	-1.0000	0
52	IVIAEEGDE	559	-1.0000	0
53	WTRLPVEVE	328	-1.1000	0
54	LTVRRRAGR	41	-1.2000	0
55	LAAAEKGGY	252	-1.2000	0
56	VRHAKEQKA	370	-1.2000	0
57	LLAKYAIEH	319	-1.2200	0

58	VVAISQSGE	354	-1.3000	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	VVVMDALRR	14	4.1000	49.40
2	LPVIVVMPS	525	4.1000	49.40
3	LAVLRRLEG	153	3.1000	37.35
4	VVACGTAYH	308	2.9800	35.90
5	VVMPSPKGS	529	2.8000	33.73
6	IENFAVLRR	105	2.7000	32.53
7	VLFLGRHVG	478	2.7000	32.53
8	IPAVSTLLQ	579	2.7000	32.53
9	LLGLALAQA	424	2.5000	30.12
10	IVVMPSPKG	528	2.4500	29.52
11	VVHNGIIEN	99	2.4000	28.92
12	VGYVGRRPA	4	2.3000	27.71
13	IREIQTRGA	548	2.3000	27.71
14	IEHWTRLPV	325	2.0000	24.10
15	LAICNTNGS	381	2.0000	24.10
16	VFAASVARA	597	2.0000	24.10
17	LRRLEGHFT	156	1.9000	22.89
18	LREIDKVFV	300	1.9000	22.89
19	LLSTIPLQV	589	1.9000	22.89
20	FMLKEIAEQ	263	1.8000	21.69
21	VMPSPKGSA	530	1.6000	19.28
22	IVLDEQRLS	288	1.4000	16.87
23	LEGALKLKE	491	1.4000	16.87
24	LKLKELAYM	495	1.4000	16.87
25	LLSNIREIQ	544	1.4000	16.87
26	LLAKYAIEH	319	1.3800	16.63
27	VFVVACGTA	306	1.3000	15.66
28	YLLGLALAQ	423	1.3000	15.66
29	VVMDALRRM	15	1.2000	14.46
30	MDALRRMEY	17	1.1000	13.25

31	LRRMEYRGY	20	1.1000	13.25
32	VRRRAGRLA	43	1.1000	13.25
33	LEGHFTLVF	159	1.0000	12.05
34	VGGRIVLDE	284	1.0000	12.05
35	LVARVIAAT	454	0.9000	10.84
36	LKELAYMHA	497	0.9000	10.84
37	VIVVMPSPK	527	0.9000	10.84
38	FVGSDVAAF	195	0.8000	9.64
39	LQVFAASVA	595	0.8000	9.64
40	LVDGGTLTV	35	0.7000	8.43
41	IAANYLLGL	419	0.7000	8.43
42	VAAHLVARA	130	0.6000	7.23
43	VLDRSTLVV	347	0.6000	7.23
44	IGVASTKTF	407	0.6000	7.23
45	LVAARRSTP	176	0.5000	6.02
46	YVGRRPAYV	6	0.4000	4.82
47	LLGHFVGGR	279	0.4000	4.82
48	LVVAISQSG	353	0.4000	4.82
49	VIAATGPVA	458	0.3500	4.22
50	VLAVLRRLE	152	0.3000	3.61
51	LANLEEAVA	50	0.2000	2.41
52	LEAMPDLVA	448	0.2000	2.41
53	LSGTTGLGH	65	0.1800	2.17
54	VARVIAATG	455	0.1000	1.20
55	VGYPVALEG	485	0.1000	1.20
56	IVIAEEGDE	559	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	YFMLKEIAE	262	4.0000	44.94
2	FMLKEIAEQ	263	3.6000	40.45
3	VVHNGIIEN	99	3.4000	38.20
4	LAVLRRLEG	153	3.4000	38.20
5	LEGALKLKE	491	3.4000	38.20

6	VVACGTAYH	308	3.2000	35.96
7	FRYRDPVLD	341	3.2000	35.96
8	VVVMDALRR	14	3.1000	34.83
9	YLLGLALAQ	423	3.1000	34.83
10	LPVIVVMPS	525	3.1000	34.83
11	VGGRIVLDE	284	3.0000	33.71
12	WTRLPVEVE	328	3.0000	33.71
13	YHELEAMPD	445	3.0000	33.71
14	VLFLGRHVG	478	3.0000	33.71
15	IVVMPSPKG	528	2.7500	30.90
16	FVGSDVAAF	195	2.7000	30.34
17	FAVLRRELE	108	2.6000	29.21
18	YRHGETADD	139	2.5000	28.09
19	IPAVSTLLQ	579	2.5000	28.09
20	VLAVLRRLE	152	2.3000	25.84
21	IVIAEEGDE	559	2.1000	23.60
22	FRPFHIDWD	243	1.9000	21.35
23	VARAYRHGE	135	1.8000	20.22
24	FVGSVLAVL	148	1.8000	20.22
25	LRRLEGHFT	156	1.8000	20.22
26	VVMPSPKGS	529	1.8000	20.22
27	YVGRRPAYV	6	1.7000	19.10
28	IENFAVLRR	105	1.7000	19.10
29	FVGGRIVLD	283	1.7000	19.10
30	VVAISQSGE	354	1.7000	19.10
31	LLAKYAIEH	319	1.6000	17.98
32	LLGLALAQA	424	1.5000	16.85
33	LKLKELAYM	495	1.5000	16.85
34	FTLVFANAD	163	1.4000	15.73
35	WATHGRPTD	76	1.3500	15.17
36	VGYVGRRPA	4	1.3000	14.61
37	VVMDALRRM	15	1.3000	14.61
38	IEHWTRLPV	325	1.3000	14.61
39	IREIQTRGA	548	1.3000	14.61
40	MDALRRMEY	17	1.2000	13.48
41	LRRMEYRGY	20	1.2000	13.48
42	YEYFMLKEI	260	1.2000	13.48

43	LREIDKVFV	300	1.2000	13.48
44	LLSNIREIQ	544	1.2000	13.48
45	LLSTIPLQV	589	1.2000	13.48
46	VLYTRAGPE	398	1.1000	12.36
47	LAICNTNGS	381	1.0000	11.24
48	VFAASVARA	597	1.0000	11.24
49	LEGHFTLVF	159	0.9000	10.11
50	LVARVIAAT	454	0.8000	8.99
51	VMDALRRME	16	0.7000	7.87
52	FVVACGTAY	307	0.7000	7.87
53	LVVAISQSG	353	0.7000	7.87
54	LEAVRHAKE	367	0.7000	7.87
55	FLAQIAANY	415	0.7000	7.87
56	IAANYLLGL	419	0.7000	7.87
57	VMPSPKGSA	530	0.6000	6.74
58	VLDEQRLSD	289	0.5000	5.62
59	IGVASTKTF	407	0.5000	5.62
60	LSGTTGLGH	65	0.4000	4.49
61	IVLDEQRLS	288	0.4000	4.49
62	VARVIAATG	455	0.4000	4.49

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	VRRRAGRLA	43	3.6000	42.86
2	IVLDEQRLS	288	3.3000	39.29
3	VVMPSPKGS	529	3.2000	38.10
4	VVMDALRRM	15	3.1000	36.90
5	FMLKEIAEQ	263	3.1000	36.90
6	LAICNTNGS	381	3.1000	36.90
7	VVACGTAYH	308	2.9800	35.48
8	VVVMDALRR	14	2.8000	33.33
9	VAAHLVARA	130	2.7000	32.14
10	LKLKELAYM	495	2.7000	32.14
11	VGYVGRRPA	4	2.6000	30.95

12	LRRMEYRGY	20	2.5000	29.76
13	VLFLGRHVG	478	2.5000	29.76
14	IREIQTRGA	548	2.4000	28.57
15	IENFAVLRR	105	2.0000	23.81
16	LEGHFTLVF	159	2.0000	23.81
17	VFAASVARA	597	2.0000	23.81
18	IVGYVGRRP	3	1.9000	22.62
19	LLGLALAQA	424	1.8000	21.43
20	LVARVIAAT	454	1.8000	21.43
21	IVVMPSPKG	528	1.8000	21.43
22	LLSNIREIQ	544	1.8000	21.43
23	LRRLEGHFT	156	1.7000	20.24
24	IEHWTRLPV	325	1.7000	20.24
25	LQVFAASVA	595	1.6000	19.05
26	LLGHFVGGR	279	1.4000	16.67
27	LLAKYAIEH	319	1.3800	16.43
28	YVGRRPAYV	6	1.3000	15.48
29	LAVLRRLEG	153	1.3000	15.48
30	LPVIVVMPS	525	1.3000	15.48
31	VVHNGIIEN	99	1.2000	14.29
32	VLRRELETA	110	1.1000	13.10
33	LVARAYRHG	134	1.1000	13.10
34	LVVAISQSG	353	1.1000	13.10
35	LGRHVGYPV	481	1.1000	13.10
36	LALAQARGT	427	1.0000	11.90
37	IQTRGAVTI	551	1.0000	11.90
38	LVAARRSTP	176	0.9000	10.71
39	FVGSDVAAF	195	0.9000	10.71
40	LREIDKVFV	300	0.9000	10.71
41	FRYRDPVLD	341	0.9000	10.71
42	VGGRIVLDE	284	0.8000	9.52
43	IGVASTKTF	407	0.8000	9.52
44	LTVRRRAGR	41	0.7000	8.33
45	LAHRFAQSS	468	0.7000	8.33
46	VLAVLRRLE	152	0.6000	7.14
47	YEYFMLKEI	260	0.6000	7.14
48	VRHAKEQKA	370	0.6000	7.14

49	VMPSPKGSA	530	0.6000	7.14
50	LHAKLLSNI	540	0.6000	7.14
51	VGRRPAYVV	7	0.5000	5.95
52	YRGYDSSGI	25	0.5000	5.95
53	VASTKTFLA	409	0.5000	5.95
54	VRPYADHLI	569	0.5000	5.95
55	VLDRSTLVV	347	0.4000	4.76
56	YLLGLALAQ	423	0.4000	4.76
57	IPLQVFAAS	593	0.4000	4.76
58	VMDALRRME	16	0.3000	3.57
59	LETAGVEFA	115	0.3000	3.57
60	VARAYRHGE	135	0.3000	3.57
61	VAELAHRFA	465	0.3000	3.57
62	LEGALKLKE	491	0.3000	3.57

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	FMLKEIAEQ	263	4.1000	48.81
2	VRRRAGRLA	43	2.6000	30.95
3	YVGRRPAYV	6	2.3000	27.38
4	IVLDEQRLS	288	2.3000	27.38
5	VVMPSPKGS	529	2.2000	26.19
6	VVMDALRRM	15	2.1000	25.00
7	LAICNTNGS	381	2.1000	25.00
8	VVACGTAYH	308	1.9800	23.57
9	FVGSDVAAF	195	1.9000	22.62
10	FRYRDPVLD	341	1.9000	22.62
11	VVVMDALRR	14	1.8000	21.43
12	VAAHLVARA	130	1.7000	20.24
13	LKLKELAYM	495	1.7000	20.24
14	VGYVGRRPA	4	1.6000	19.05
15	YEYFMLKEI	260	1.6000	19.05
16	LRRMEYRGY	20	1.5000	17.86
17	YRGYDSSGI	25	1.5000	17.86

18	VLFLGRHVG	478	1.5000	17.86
19	YLLGLALAQ	423	1.4000	16.67
20	IREIQTRGA	548	1.4000	16.67
21	YMHAEGFAA	502	1.2000	14.29
22	IENFAVLRR	105	1.0000	11.90
23	LEGHFTLVF	159	1.0000	11.90
24	VFAASVARA	597	1.0000	11.90
25	IVGYVGRRP	3	0.9000	10.71
26	FVGSVLAVL	148	0.9000	10.71
27	FRPFHIDWD	243	0.8000	9.52
28	LLGLALAQA	424	0.8000	9.52
29	LVARVIAAT	454	0.8000	9.52
30	IVVMPSPKG	528	0.8000	9.52
31	LLSNIREIQ	544	0.8000	9.52
32	LRRLEGHFT	156	0.7000	8.33
33	FIEHTREAV	203	0.7000	8.33
34	IEHWTRLPV	325	0.7000	8.33
35	FLAQIAANY	415	0.6000	7.14
36	LQVFAASVA	595	0.6000	7.14
37	LLGHFVGGR	279	0.4000	4.76
38	LLAKYAIEH	319	0.3800	4.52
39	WATHGRPTD	76	0.3000	3.57
40	LAVLRRLEG	153	0.3000	3.57
41	LPVIVVMPS	525	0.3000	3.57
42	VVHNGIIEN	99	0.2000	2.38
43	VLRRELETA	110	0.1000	1.19
44	LVARAYRHG	134	0.1000	1.19
45	LVVAISQSG	353	0.1000	1.19
46	LGRHVGYPV	481	0.1000	1.19
47	LVAARRSTP	176	-0.1000	0
48	LREIDKVFV	300	-0.1000	0
49	VGGRIVLDE	284	-0.2000	0
50	IGVASTKTF	407	-0.2000	0
51	FLGRHVGYP	480	-0.2000	0
52	LTVRRRAGR	41	-0.3000	0
53	FVGGRIVLD	283	-0.3000	0
54	LAHRFAQSS	468	-0.3000	0

55	VLAVLRRLE	152	-0.4000	0
56	WTRLPVEVE	328	-0.4000	0
57	VRHAKEQKA	370	-0.4000	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	VVMDALRRM	15	4.6000	52.27
2	VVVMDALRR	14	4.3000	48.86
3	LKLKELAYM	495	4.2000	47.73
4	LEGHFTLVF	159	3.9000	44.32
5	VLFLGRHVG	478	3.9000	44.32
6	LRRMEYRGY	20	3.8000	43.18
7	IVLDEQRLS	288	3.7000	42.05
8	VRRRAGRLA	43	3.6000	40.91
9	VVMPSPKGS	529	3.6000	40.91
10	IENFAVLRR	105	3.5000	39.77
11	LAICNTNGS	381	3.5000	39.77
12	IVVMPSPKG	528	3.2000	36.36
13	IVGYVGRRP	3	2.9000	32.95
14	LLGHFVGGR	279	2.9000	32.95
15	FVGSDVAAF	195	2.8000	31.82
16	VAAHLVARA	130	2.7000	30.68
17	LAVLRRLEG	153	2.7000	30.68
18	IEHWTRLPV	325	2.7000	30.68
19	IGVASTKTF	407	2.7000	30.68
20	VGYVGRRPA	4	2.6000	29.55
21	LVARAYRHG	134	2.5000	28.41
22	LVVAISQSG	353	2.5000	28.41
23	LVARVIAAT	454	2.5000	28.41
24	LRRLEGHFT	156	2.4000	27.27
25	FMLKEIAEQ	263	2.4000	27.27
26	VVACGTAYH	308	2.4000	27.27
27	IREIQTRGA	548	2.4000	27.27
28	YVGRRPAYV	6	2.3000	26.14

29	LTVRRRAGR	41	2.2000	25.00
30	VGGRIVLDE	284	2.2000	25.00
31	LGRHVGYPV	481	2.1000	23.86
32	VVHNGIIEN	99	2.0000	22.73
33	VLAVLRRLE	152	2.0000	22.73
34	FRYRDPVLD	341	2.0000	22.73
35	VFAASVARA	597	2.0000	22.73
36	LVAARRSTP	176	1.9000	21.59
37	LREIDKVFV	300	1.9000	21.59
38	IQTRGAVTI	551	1.9000	21.59
39	LLGLALAQA	424	1.8000	20.45
40	VMDALRRME	16	1.7000	19.32
41	VARAYRHGE	135	1.7000	19.32
42	LALAQARGT	427	1.7000	19.32
43	LEGALKLKE	491	1.7000	19.32
44	LPVIVVMPS	525	1.7000	19.32
45	LGLALAQAR	425	1.6000	18.18
46	LQVFAASVA	595	1.6000	18.18
47	VGRRPAYVV	7	1.5000	17.05
48	YEYFMLKEI	260	1.5000	17.05
49	LAYMHAEGF	500	1.5000	17.05
50	LHAKLLSNI	540	1.5000	17.05
51	YRGYDSSGI	25	1.4000	15.91
52	VLDRSTLVV	347	1.4000	15.91
53	VRPYADHLI	569	1.4000	15.91
54	LLSTIPLQV	589	1.3000	14.77
55	VLRRELETA	110	1.1000	12.50
56	LVFANADDP	165	1.1000	12.50
57	LAHRFAQSS	468	1.1000	12.50
58	LKHGPIALI	513	1.1000	12.50
59	LLSNIREIQ	544	1.1000	12.50
60	LSDQELREI	295	1.0000	11.36
61	FRPFHIDWD	243	0.9000	10.23
62	FLAQIAANY	415	0.9000	10.23

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	VVMDALRRM	15	4.6000	52.27
2	VVVMDALRR	14	4.3000	48.86
3	LKLKELAYM	495	4.2000	47.73
4	LEGHFTLVF	159	3.9000	44.32
5	VLFLGRHVG	478	3.9000	44.32
6	LRRMEYRGY	20	3.8000	43.18
7	IVLDEQRLS	288	3.7000	42.05
8	VRRRAGRLA	43	3.6000	40.91
9	VVMPSPKGS	529	3.6000	40.91
10	IENFAVLRR	105	3.5000	39.77
11	LAICNTNGS	381	3.5000	39.77
12	IVVMPSPKG	528	3.2000	36.36
13	IVGYVGRRP	3	2.9000	32.95
14	LLGHFVGGR	279	2.9000	32.95
15	FVGSDVAAF	195	2.8000	31.82
16	VAAHLVARA	130	2.7000	30.68
17	LAVLRRLEG	153	2.7000	30.68
18	IEHWTRLPV	325	2.7000	30.68
19	IGVASTKTF	407	2.7000	30.68
20	VGYVGRRPA	4	2.6000	29.55
21	LVARAYRHG	134	2.5000	28.41
22	LVVAISQSG	353	2.5000	28.41
23	LVARVIAAT	454	2.5000	28.41
24	LRRLEGHFT	156	2.4000	27.27
25	FMLKEIAEQ	263	2.4000	27.27
26	VVACGTAYH	308	2.4000	27.27
27	IREIQTRGA	548	2.4000	27.27
28	YVGRRPAYV	6	2.3000	26.14
29	LTVRRRAGR	41	2.2000	25.00
30	VGGRIVLDE	284	2.2000	25.00
31	LGRHVGYPV	481	2.1000	23.86
32	VVHNGIIEN	99	2.0000	22.73
33	VLAVLRRLE	152	2.0000	22.73

34	FRYRDPVLD	341	2.0000	22.73
35	VFAASVARA	597	2.0000	22.73
36	LVAARRSTP	176	1.9000	21.59
37	LREIDKVFV	300	1.9000	21.59
38	IQTRGAVTI	551	1.9000	21.59
39	LLGLALAQA	424	1.8000	20.45
40	VMDALRRME	16	1.7000	19.32
41	VARAYRHGE	135	1.7000	19.32
42	LALAQARGT	427	1.7000	19.32
43	LEGALKLKE	491	1.7000	19.32
44	LPVIVVMPS	525	1.7000	19.32
45	LGLALAQAR	425	1.6000	18.18
46	LQVFAASVA	595	1.6000	18.18
47	VGRRPAYVV	7	1.5000	17.05
48	YEYFMLKEI	260	1.5000	17.05
49	LAYMHAEGF	500	1.5000	17.05
50	LHAKLLSNI	540	1.5000	17.05
51	YRGYDSSGI	25	1.4000	15.91
52	VLDRSTLVV	347	1.4000	15.91
53	VRPYADHLI	569	1.4000	15.91
54	LLSTIPLQV	589	1.3000	14.77
55	VLRRELETA	110	1.1000	12.50
56	LVFANADDP	165	1.1000	12.50
57	LAHRFAQSS	468	1.1000	12.50
58	LKHGPIALI	513	1.1000	12.50
59	LLSNIREIQ	544	1.1000	12.50
60	LSDQELREI	295	1.0000	11.36
61	FRPFHIDWD	243	0.9000	10.23
62	FLAQIAANY	415	0.9000	10.23

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	VRPYADHLI	569	5.9000	60.20
2	YRGYDSSGI	25	5.5000	56.12

3	VVVMDALRR	14	4.5000	45.92
4	LQVFAASVA	595	4.4000	44.90
5	LRRLEGHFT	156	4.3000	43.88
6	LGHFVGGRI	280	4.3000	43.88
7	IEHWTRLPV	325	3.9000	39.80
8	LGRHVGYPV	481	3.8000	38.78
9	IVGYVGRRP	3	3.7000	37.76
10	IVVMPSPKG	528	3.7000	37.76
11	IENFAVLRR	105	3.6000	36.73
12	VRRRAGRLA	43	3.1000	31.63
13	LAVLRRLEG	153	3.1000	31.63
14	VLFLGRHVG	478	3.1000	31.63
15	VITADGYRI	220	3.0000	30.61
16	LVDGGTLTV	35	2.9600	30.20
17	LRRMEYRGY	20	2.9000	29.59
18	YEYFMLKEI	260	2.9000	29.59
19	LLSTIPLQV	589	2.9000	29.59
20	VVMDALRRM	15	2.8800	29.39
21	LEGHFTLVF	159	2.8600	29.18
22	VALEGALKL	489	2.8000	28.57
23	LYTRAGPEI	399	2.6000	26.53
24	LEAMPDLVA	448	2.6000	26.53
25	LKELAYMHA	497	2.5000	25.51
26	VVHNGIIEN	99	2.4500	25.00
27	VGRRPAYVV	7	2.4000	24.49
28	FHIDWDLAA	246	2.4000	24.49
29	IAANYLLGL	419	2.4000	24.49
30	VVMPSPKGS	529	2.4000	24.49
31	IQTRGAVTI	551	2.4000	24.49
32	LVAARRSTP	176	2.3000	23.47
33	IALVDGGTL	33	2.2000	22.45
34	YMHAEGFAA	502	2.2000	22.45
35	VARARGYDV	602	2.2000	22.45
36	VLGIGDNEM	186	2.1800	22.24
37	LVARVIAAT	454	2.1500	21.94
38	IAVVHNGII	97	2.1000	21.43
39	LVVAISQSG	353	2.1000	21.43

40	VGYPVALEG	485	2.1000	21.43
41	VLDRSTLVV	347	2.0600	21.02
42	LKHGPIALI	513	2.0500	20.92
43	VGYVGRRPA	4	2.0000	20.41
44	VVITADGYR	219	1.9000	19.39
45	LREIDKVFV	300	1.9000	19.39
46	LLGLALAQA	424	1.9000	19.39
47	VIAATGPVA	458	1.9000	19.39
48	LLQPLLSTI	585	1.9000	19.39
49	LAICNTNGS	381	1.8600	18.98
50	LAQIAANYL	416	1.8000	18.37
51	IEIPAVSTL	577	1.8000	18.37
52	FVGSVLAVL	148	1.7000	17.35
53	VLAICNTNG	380	1.7000	17.35
54	ICNTNGSQI	383	1.7000	17.35
55	LPVIVVMPS	525	1.7000	17.35
56	LQPLLSTIP	586	1.7000	17.35
57	LKLKELAYM	495	1.6800	17.14
58	YVGRRPAYV	6	1.6000	16.33
59	LGIGDNEMF	187	1.6000	16.33
60	VAISQSGET	355	1.6000	16.33
61	VAARRSTPL	177	1.5000	15.31
62	VFVVACGTA	306	1.5000	15.31

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	YRGYDSSGI	25	6.5000	66.33
2	VRPYADHLI	569	4.9000	50.00
3	YEYFMLKEI	260	3.9000	39.80
4	VVVMDALRR	14	3.5000	35.71
5	FHIDWDLAA	246	3.4000	34.69
6	LQVFAASVA	595	3.4000	34.69
7	LRRLEGHFT	156	3.3000	33.67
8	LGHFVGGRI	280	3.3000	33.67

9	YMHAEGFAA	502	3.2000	32.65
10	IEHWTRLPV	325	2.9000	29.59
11	LGRHVGYPV	481	2.8000	28.57
12	IVGYVGRRP	3	2.7000	27.55
13	FVGSVLAVL	148	2.7000	27.55
14	IVVMPSPKG	528	2.7000	27.55
15	YVGRRPAYV	6	2.6000	26.53
16	IENFAVLRR	105	2.6000	26.53
17	FVVACGTAY	307	2.4000	24.49
18	FRPFHIDWD	243	2.3500	23.98
19	YLLGLALAQ	423	2.3000	23.47
20	VRRRAGRLA	43	2.1000	21.43
21	LAVLRRLEG	153	2.1000	21.43
22	VLFLGRHVG	478	2.1000	21.43
23	VITADGYRI	220	2.0000	20.41
24	LVDGGTLTV	35	1.9600	20.00
25	LRRMEYRGY	20	1.9000	19.39
26	LLSTIPLQV	589	1.9000	19.39
27	VVMDALRRM	15	1.8800	19.18
28	LEGHFTLVF	159	1.8600	18.98
29	VALEGALKL	489	1.8000	18.37
30	FIEHTREAV	203	1.6000	16.33
31	LYTRAGPEI	399	1.6000	16.33
32	LEAMPDLVA	448	1.6000	16.33
33	LKELAYMHA	497	1.5000	15.31
34	VVHNGIIEN	99	1.4500	14.80
35	VGRRPAYVV	7	1.4000	14.29
36	YVVVMDALR	13	1.4000	14.29
37	FRYRDPVLD	341	1.4000	14.29
38	IAANYLLGL	419	1.4000	14.29
39	VVMPSPKGS	529	1.4000	14.29
40	IQTRGAVTI	551	1.4000	14.29
41	LVAARRSTP	176	1.3000	13.27
42	FVGSDVAAF	195	1.3000	13.27
43	YFMLKEIAE	262	1.3000	13.27
44	IALVDGGTL	33	1.2000	12.24
45	YRISDFDGN	226	1.2000	12.24

46	YAIEHWTRL	323	1.2000	12.24
47	VARARGYDV	602	1.2000	12.24
48	VLGIGDNEM	186	1.1800	12.04
49	LVARVIAAT	454	1.1500	11.73
50	IAVVHNGII	97	1.1000	11.22
51	FDGNDGLQA	231	1.1000	11.22
52	LVVAISQSG	353	1.1000	11.22
53	VGYPVALEG	485	1.1000	11.22
54	VLDRSTLVV	347	1.0600	10.82
55	LKHGPIALI	513	1.0500	10.71
56	VGYVGRRPA	4	1.0000	10.20
57	VVITADGYR	219	0.9000	9.18
58	LREIDKVFV	300	0.9000	9.18
59	LLGLALAQA	424	0.9000	9.18
60	VIAATGPVA	458	0.9000	9.18
61	LLQPLLSTI	585	0.9000	9.18
62	LAICNTNGS	381	0.8600	8.78

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	VRPYADHLI	569	5.9000	60.20
2	YRGYDSSGI	25	5.5000	56.12
3	VVVMDALRR	14	4.5000	45.92
4	LQVFAASVA	595	4.4000	44.90
5	LRRLEGHFT	156	4.3000	43.88
6	LGHFVGGRI	280	4.3000	43.88
7	IEHWTRLPV	325	3.9000	39.80
8	LGRHVGYPV	481	3.8000	38.78
9	IVGYVGRRP	3	3.7000	37.76
10	IVVMPSPKG	528	3.7000	37.76
11	IENFAVLRR	105	3.6000	36.73
12	VRRRAGRLA	43	3.1000	31.63
13	LAVLRRLEG	153	3.1000	31.63
14	VLFLGRHVG	478	3.1000	31.63

15	VITADGYRI	220	3.0000	30.61
16	LVDGGTLTV	35	2.9600	30.20
17	LRRMEYRGY	20	2.9000	29.59
18	YEYFMLKEI	260	2.9000	29.59
19	LLSTIPLQV	589	2.9000	29.59
20	VVMDALRRM	15	2.8800	29.39
21	LEGHFTLVF	159	2.8600	29.18
22	VALEGALKL	489	2.8000	28.57
23	LYTRAGPEI	399	2.6000	26.53
24	LEAMPDLVA	448	2.6000	26.53
25	LKELAYMHA	497	2.5000	25.51
26	VVHNGIIEN	99	2.4500	25.00
27	VGRRPAYVV	7	2.4000	24.49
28	FHIDWDLAA	246	2.4000	24.49
29	IAANYLLGL	419	2.4000	24.49
30	VVMPSPKGS	529	2.4000	24.49
31	IQTRGAVTI	551	2.4000	24.49
32	LVAARRSTP	176	2.3000	23.47
33	IALVDGGTL	33	2.2000	22.45
34	YMHAEGFAA	502	2.2000	22.45
35	VARARGYDV	602	2.2000	22.45
36	VLGIGDNEM	186	2.1800	22.24
37	LVARVIAAT	454	2.1500	21.94
38	IAVVHNGII	97	2.1000	21.43
39	LVVAISQSG	353	2.1000	21.43
40	VGYPVALEG	485	2.1000	21.43
41	VLDRSTLVV	347	2.0600	21.02
42	LKHGPIALI	513	2.0500	20.92
43	VGYVGRRPA	4	2.0000	20.41
44	VVITADGYR	219	1.9000	19.39
45	LREIDKVFV	300	1.9000	19.39
46	LLGLALAQA	424	1.9000	19.39
47	VIAATGPVA	458	1.9000	19.39
48	LLQPLLSTI	585	1.9000	19.39
49	LAICNTNGS	381	1.8600	18.98
50	LAQIAANYL	416	1.8000	18.37
51	IEIPAVSTL	577	1.8000	18.37

52	FVGSVLAVL	148	1.7000	17.35
53	VLAICNTNG	380	1.7000	17.35
54	ICNTNGSQI	383	1.7000	17.35
55	LPVIVVMPS	525	1.7000	17.35
56	LQPLLSTIP	586	1.7000	17.35
57	LKLKELAYM	495	1.6800	17.14
58	YVGRRPAYV	6	1.6000	16.33
59	LGIGDNEMF	187	1.6000	16.33
60	VAISQSGET	355	1.6000	16.33
61	VAARRSTPL	177	1.5000	15.31
62	VFVVACGTA	306	1.5000	15.31

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	VVVMDALRR	14	6.4000	65.31
2	LRRMEYRGY	20	5.2000	53.06
3	VIVVMPSPK	527	4.4000	44.90
4	YVVVMDALR	13	4.2000	42.86
5	VVITADGYR	219	4.0000	40.82
6	FVVACGTAY	307	3.9000	39.80
7	LGLALAQAR	425	3.7000	37.76
8	FAASVARAR	598	3.3000	33.67
9	LRRLEGHFT	156	3.2000	32.65
10	VGSVLAVLR	149	3.0000	30.61
11	VVMPSPKGS	529	2.8000	28.57
12	IALVDGGTL	33	2.7000	27.55
13	IVVMPSPKG	528	2.6000	26.53
14	YMHAEGFAA	502	2.5000	25.51
15	YRGYDSSGI	25	2.3000	23.47
16	VITADGYRI	220	2.2000	22.45
17	LVVAISQSG	353	2.2000	22.45
18	FVGSVLAVL	148	2.1000	21.43
19	LAQIAANYL	416	2.1000	21.43
20	VFVVACGTA	306	2.0000	20.41

21	VCGIVGYVG	0	1.8000	18.37
22	LAYMHAEGF	500	1.8000	18.37
23	IREIQTRGA	548	1.8000	18.37
24	FVGSDVAAF	195	1.7000	17.35
25	YLLGLALAQ	423	1.7000	17.35
26	VLFLGRHVG	478	1.7000	17.35
27	FLAQIAANY	415	1.6000	16.33
28	VGYVGRRPA	4	1.4000	14.29
29	VVMDALRRM	15	1.4000	14.29
30	YEYFMLKEI	260	1.4000	14.29
31	YFMLKEIAE	262	1.4000	14.29
32	VVACGTAYH	308	1.3000	13.27
33	IGVASTKTF	407	1.3000	13.27
34	VRPYADHLI	569	1.3000	13.27
35	VRRRAGRLA	43	1.2000	12.24
36	VARVIAATG	455	1.2000	12.24
37	IAVVHNGII	97	1.1000	11.22
38	FTLVFANAD	163	1.1000	11.22
39	VLYTRAGPE	398	1.1000	11.22
40	LALAQARGT	427	1.1000	11.22
41	VTIVIAEEG	557	1.1000	11.22
42	LLSTIPLQV	589	1.1000	11.22
43	IVGYVGRRP	3	0.9000	9.18
44	VELASEFRY	335	0.9000	9.18
45	LAICNTNGS	381	0.9000	9.18
46	LSTIPLQVF	590	0.9000	9.18
47	IENFAVLRR	105	0.8000	8.16
48	IVLDEQRLS	288	0.8000	8.16
49	VLAICNTNG	380	0.7000	7.14
50	YVGRRPAYV	6	0.6000	6.12
51	VAEMPSTAL	57	0.6000	6.12
52	LLGHFVGGR	279	0.6000	6.12
53	LGHFVGGRI	280	0.6000	6.12
54	VALEGALKL	489	0.6000	6.12
55	IVIAEEGDE	559	0.6000	6.12
56	LSGTTGLGH	65	0.5000	5.10
57	VLAVLRRLE	152	0.5000	5.10

58	VLGIGDNEM	186	0.5000	5.10
59	LLAKYAIEH	319	0.5000	5.10
60	ICNTNGSQI	383	0.5000	5.10
61	YTRAGPEIG	400	0.4000	4.08
62	VARARGYDV	602	0.4000	4.08

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	VVVMDALRR	14	6.4000	65.31
2	LRRMEYRGY	20	5.2000	53.06
3	VIVVMPSPK	527	4.4000	44.90
4	YVVVMDALR	13	4.2000	42.86
5	VVITADGYR	219	4.0000	40.82
6	FVVACGTAY	307	3.9000	39.80
7	LGLALAQAR	425	3.7000	37.76
8	FAASVARAR	598	3.3000	33.67
9	LRRLEGHFT	156	3.2000	32.65
10	VGSVLAVLR	149	3.0000	30.61
11	VVMPSPKGS	529	2.8000	28.57
12	IALVDGGTL	33	2.7000	27.55
13	IVVMPSPKG	528	2.6000	26.53
14	YMHAEGFAA	502	2.5000	25.51
15	YRGYDSSGI	25	2.3000	23.47
16	VITADGYRI	220	2.2000	22.45
17	LVVAISQSG	353	2.2000	22.45
18	FVGSVLAVL	148	2.1000	21.43
19	LAQIAANYL	416	2.1000	21.43
20	VFVVACGTA	306	2.0000	20.41
21	VCGIVGYVG	0	1.8000	18.37
22	LAYMHAEGF	500	1.8000	18.37
23	IREIQTRGA	548	1.8000	18.37
24	FVGSDVAAF	195	1.7000	17.35
25	YLLGLALAQ	423	1.7000	17.35
26	VLFLGRHVG	478	1.7000	17.35

27	FLAQIAANY	415	1.6000	16.33
28	VGYVGRRPA	4	1.4000	14.29
29	VVMDALRRM	15	1.4000	14.29
30	YEYFMLKEI	260	1.4000	14.29
31	YFMLKEIAE	262	1.4000	14.29
32	VVACGTAYH	308	1.3000	13.27
33	IGVASTKTF	407	1.3000	13.27
34	VRPYADHLI	569	1.3000	13.27
35	VRRRAGRLA	43	1.2000	12.24
36	VARVIAATG	455	1.2000	12.24
37	IAVVHNGII	97	1.1000	11.22
38	FTLVFANAD	163	1.1000	11.22
39	VLYTRAGPE	398	1.1000	11.22
40	LALAQARGT	427	1.1000	11.22
41	VTIVIAEEG	557	1.1000	11.22
42	LLSTIPLQV	589	1.1000	11.22
43	IVGYVGRRP	3	0.9000	9.18
44	VELASEFRY	335	0.9000	9.18
45	LAICNTNGS	381	0.9000	9.18
46	LSTIPLQVF	590	0.9000	9.18
47	IENFAVLRR	105	0.8000	8.16
48	IVLDEQRLS	288	0.8000	8.16
49	VLAICNTNG	380	0.7000	7.14
50	YVGRRPAYV	6	0.6000	6.12
51	VAEMPSTAL	57	0.6000	6.12
52	LLGHFVGGR	279	0.6000	6.12
53	LGHFVGGRI	280	0.6000	6.12
54	VALEGALKL	489	0.6000	6.12
55	IVIAEEGDE	559	0.6000	6.12
56	LSGTTGLGH	65	0.5000	5.10
57	VLAVLRRLE	152	0.5000	5.10
58	VLGIGDNEM	186	0.5000	5.10
59	LLAKYAIEH	319	0.5000	5.10
60	ICNTNGSQI	383	0.5000	5.10
61	YTRAGPEIG	400	0.4000	4.08
62	VARARGYDV	602	0.4000	4.08