MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Sat Feb 20 23:49:32 2010
Length of input sequence	644 amino acids
Number of nanomers from input sequence	636
Number of nanomers with obligatory P1 anchor residue	184
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	64

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	YLPIDPRDV	409	1.9900	33.17
2	WRFEYSPES	210	1.7700	29.50
3	LQIEFSQVI	452	1.6000	26.67
4	LVRMGYKEI	101	1.1000	18.33
5	WNPQRASSM	32	1.0800	18.00
6	WGVGIAPSI	618	1.0700	17.83
7	IIFNLPATV	246	1.0400	17.33
8	VGIAPSITT	620	0.8000	13.33
9	VKPAGPPRV	19	0.5700	9.50

10	VVSAVNRAA	634	0.2900	4.83
11	FRANRAEVQ	180	0.0400	0.67
12	FQACSGAPR	154	-0.1000	0
13	YVEASVTIA	569	-0.1100	0
14	IVHFYNSTS	164	-0.2200	0
15	LVTLGLNLF	323	-0.3000	0
16	VHFYNSTSI	165	-0.3100	0
17	VRPLERIRQ	491	-0.4000	0
18	VIRVNSQSG	424	-0.4500	0
19	FVHALADVG	537	-0.5000	0
20	FNLPATVEM	248	-0.5200	0
21	IFNLPATVE	247	-0.6100	0
22	LRAVVSAVN	631	-0.6500	0
23	MLWQVPYLP	403	-0.7000	0
24	YCNQLPVHE	353	-0.8000	0
25	VTIASPAQP	574	-0.8000	0
26	VTIASPAQP	593	-0.8000	0
27	FVREIIEQG	123	-0.9000	0
28	FYNSTSILQ	167	-0.9000	0
29	ILSLHPHND	280	-0.9000	0
30	VFRANRAEV	179	-1.0000	0
31	LGFAAGADR	298	-1.0000	0
32	LTQCRPELI	142	-1.1000	0
33	VLTQCRPEL	141	-1.1300	0
34	VNSQSGKGG	427	-1.2000	0
35	IQVLTQCRP	139	-1.3000	0
36	VEYCNQLPV	351	-1.3000	0
37	VTIQVLTQC	137	-1.3100	0
38	YEAVIRVNS	421	-1.3500	0
39	VEMTTPNVY	254	-1.5000	0
40	YAKQVCDAV	226	-1.6000	0
41	LAPVRPLER	488	-1.6500	0
42	VREIIEQGA	124	-1.7000	0
43	LVYTAFSGS	369	-1.7000	0

44	YIMKTDHGL	438	-1.7000	0
45	VHALADVGF	538	-1.7000	0
46	IEVGFPSAS	109	-1.8000	0
47	IEWMSRNLA	266	-1.8000	0
48	VTLGLNLFS	324	-1.8000	0
49	MKTDHGLSL	440	-1.8000	0
50	LRDGNQALI	78	-1.9000	0
51	IRVNSQSGK	425	-1.9600	0
52	VKINGVETE	517	-1.9600	0
53	VGFPSASQT	111	-2.0000	0
54	LQRRVVFRA	174	-2.0000	0
55	LANRESVIL	273	-2.0000	0
56	FDLLVRMGY	98	-2.0100	0
57	YTAFSGSHQ	371	-2.0200	0
58	IVKPAGPPR	18	-2.0300	0
59	FSNIDEIRR	341	-2.1000	0
60	LWQVPYLPI	404	-2.1500	0
61	INGVETEIS	519	-2.1500	0
62	IRRTVEYCN	347	-2.2000	0
63	VAVLDYYEH	548	-2.2000	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	LQIEFSQVI	452	2.6000	43.33
2	LVRMGYKEI	101	2.1000	35.00
3	IIFNLPATV	246	2.0400	34.00
4	VGIAPSITT	620	1.8000	30.00
5	VKPAGPPRV	19	1.5700	26.17
6	VVSAVNRAA	634	1.2900	21.50
7	YLPIDPRDV	409	0.9900	16.50
8	IVHFYNSTS	164	0.7800	13.00
9	WRFEYSPES	210	0.7700	12.83

10	LVTLGLNLF	323	0.7000	11.67
11	VHFYNSTSI	165	0.6900	11.50
12	VRPLERIRQ	491	0.6000	10.00
13	VIRVNSQSG	424	0.5500	9.17
14	IFNLPATVE	247	0.3900	6.50
15	LRAVVSAVN	631	0.3500	5.83
16	MLWQVPYLP	403	0.3000	5.00
17	VTIASPAQP	574	0.2000	3.33
18	VTIASPAQP	593	0.2000	3.33
19	ILSLHPHND	280	0.1000	1.67
20	WNPQRASSM	32	0.0800	1.33
21	WGVGIAPSI	618	0.0700	1.17
22	FRANRAEVQ	180	0.0400	0.67
23	LTQCRPELI	142	-0.1000	0
24	FQACSGAPR	154	-0.1000	0
25	VLTQCRPEL	141	-0.1300	0
26	VNSQSGKGG	427	-0.2000	0
27	IQVLTQCRP	139	-0.3000	0
28	VEYCNQLPV	351	-0.3000	0
29	VTIQVLTQC	137	-0.3100	0
30	VEMTTPNVY	254	-0.5000	0
31	FVHALADVG	537	-0.5000	0
32	FNLPATVEM	248	-0.5200	0
33	LAPVRPLER	488	-0.6500	0
34	VREIIEQGA	124	-0.7000	0
35	LVYTAFSGS	369	-0.7000	0
36	VHALADVGF	538	-0.7000	0
37	IEVGFPSAS	109	-0.8000	0
38	IEWMSRNLA	266	-0.8000	0
39	VTLGLNLFS	324	-0.8000	0
40	MKTDHGLSL	440	-0.8000	0
41	LRDGNQALI	78	-0.9000	0
42	FVREIIEQG	123	-0.9000	0
43	FYNSTSILQ	167	-0.9000	0

44	IRVNSQSGK	425	-0.9600	0
45	VKINGVETE	517	-0.9600	0
46	VGFPSASQT	111	-1.0000	0
47	LQRRVVFRA	174	-1.0000	0
48	LANRESVIL	273	-1.0000	0
49	IVKPAGPPR	18	-1.0300	0
50	YVEASVTIA	569	-1.1100	0
51	LWQVPYLPI	404	-1.1500	0
52	INGVETEIS	519	-1.1500	0
53	IRRTVEYCN	347	-1.2000	0
54	VAVLDYYEH	548	-1.2000	0
55	VTTSESPDA	0	-1.2300	0
56	IIEQGAIPD	127	-1.3000	0
57	MSRNLANRE	269	-1.3600	0
58	VNRYRPFAE	42	-1.4000	0
59	MFDLLVRMG	97	-1.4100	0
60	VQAIATDGA	187	-1.5000	0
61	VCDAVGEVI	230	-1.5000	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	VRMGYKEIE	102	4.9000	51.58
2	VYADSIEWM	261	4.8000	50.53
3	LPIDPRDVG	410	4.1000	43.16
4	VRPLERIRQ	491	3.7000	38.95
5	VKINGVETE	517	3.5000	36.84
6	VGFDVAVLD	544	3.2000	33.68
7	YGGDLVYTA	365	3.1500	33.16
8	LVTLGLNLF	323	3.1100	32.74
9	VEASVTIAS	570	3.1000	32.63
10	IEFSQVIQK	454	3.0000	31.58
11	VKPAGPPRV	19	2.9000	30.53

12	IIFNLPATV	246	2.9000	30.53
13	MKTDHGLSL	440	2.8600	30.11
14	IRLRNRTWP	55	2.8000	29.47
15	VFRANRAEV	179	2.8000	29.47
16	VILSLHPHN	279	2.8000	29.47
17	IAPSITTAS	622	2.8000	29.47
18	IEVGFPSAS	109	2.7700	29.16
19	WRFEYSPES	210	2.7000	28.42
20	INGVETEIS	519	2.7000	28.42
21	VLTQCRPEL	141	2.6600	28.00
22	LQRRVVFRA	174	2.6000	27.37
23	IRVNSQSGK	425	2.4700	26.00
24	VTLGLNLFS	324	2.2000	23.16
25	LQIEFSQVI	452	2.1000	22.11
26	IPDDVTIQV	133	2.0000	21.05
27	VIRVNSQSG	424	2.0000	21.05
28	VAYIMKTDH	436	2.0000	21.05
29	ILQRRVVFR	173	1.9000	20.00
30	VQAIATDGA	187	1.9000	20.00
31	FNLPATVEM	248	1.9000	20.00
32	VWGVGIAPS	617	1.9000	20.00
33	IVHFYNSTS	164	1.8700	19.68
34	WGVGIAPSI	618	1.8000	18.95
35	VGIAPSITT	620	1.8000	18.95
36	VEQAAKYPG	199	1.7500	18.42
37	LRDGNQALI	78	1.7000	17.89
38	FVREIIEQG	123	1.7000	17.89
39	VTIASPAQP	574	1.7000	17.89
40	VTIASPAQP	593	1.7000	17.89
41	LVYTAFSGS	369	1.6700	17.58
42	IVKPAGPPR	18	1.6000	16.84
43	VTIQVLTQC	137	1.6000	16.84
44	LRNRTWPDR	57	1.5000	15.79
45	MSPARKRRM	89	1.5000	15.79

46	LSLPRRLQI	446	1.5000	15.79
47	LAPVRPLER	488	1.5000	15.79
48	LRAVVSAVN	631	1.5000	15.79
49	IEQGAIPDD	128	1.4000	14.74
50	IATDGARKC	190	1.4000	14.74
51	MKLDADAAD	389	1.4000	14.74
52	YEAVIRVNS	421	1.4000	14.74
53	VTTSESPDA	0	1.3000	13.68
54	LNLFSRGVD	328	1.3000	13.68
55	WNPQRASSM	32	1.2700	13.37
56	VEMTTPNVY	254	1.2100	12.74
57	VNRYRPFAE	42	1.2000	12.63
58	MGYKEIEVG	104	1.2000	12.63
59	FYNSTSILQ	167	1.2000	12.63
60	IMKTDHGLS	439	1.2000	12.63
61	VSAVNRAAR	635	1.2000	12.63
62	MLWQVPYLP	403	1.1500	12.11
63	FDLLVRMGY	98	1.1000	11.58
64	LVRMGYKEI	101	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	YGGDLVYTA	365	4.1500	45.60
2	VRPLERIRQ	491	3.4000	37.36
3	WRFEYSPES	210	3.3000	36.26
4	FYNSTSILQ	167	2.9000	31.87
5	FRANRAEVQ	180	2.7000	29.67
6	VRMGYKEIE	102	2.5000	27.47
7	VYADSIEWM	261	2.3000	25.27
8	YEAVIRVNS	421	2.0000	21.98
9	YVEASVTIA	569	2.0000	21.98
10	IEFSQVIQK	454	1.9000	20.88

11	WGVGIAPSI	618	1.9000	20.88
12	LPIDPRDVG	410	1.7000	18.68
13	VEASVTIAS	570	1.7000	18.68
14	LQRRVVFRA	174	1.6000	17.58
15	VAYIMKTDH	436	1.5800	17.36
16	FNLPATVEM	248	1.4000	15.38
17	IAPSITTAS	622	1.4000	15.38
18	IEVGFPSAS	109	1.3700	15.05
19	IRVNSQSGK	425	1.3700	15.05
20	FVREIIEQG	123	1.3000	14.29
21	INGVETEIS	519	1.3000	14.29
22	VKINGVETE	517	1.1000	12.09
23	VGFDVAVLD	544	1.1000	12.09
24	VILSLHPHN	279	1.0000	10.99
25	FGNGERTGN	312	1.0000	10.99
26	VKPAGPPRV	19	0.9000	9.89
27	VQAIATDGA	187	0.9000	9.89
28	IIFNLPATV	246	0.9000	9.89
29	MKTDHGLSL	440	0.9000	9.89
30	IRLRNRTWP	55	0.8000	8.79
31	FDLLVRMGY	98	0.8000	8.79
32	VFRANRAEV	179	0.8000	8.79
33	VTLGLNLFS	324	0.8000	8.79
34	WNPQRASSM	32	0.7700	8.46
35	VLTQCRPEL	141	0.7000	7.69
36	YLPIDPRDV	409	0.7000	7.69
37	FVHALADVG	537	0.7000	7.69
38	VTIQVLTQC	137	0.6000	6.59
39	VWGVGIAPS	617	0.5000	5.49
40	IVHFYNSTS	164	0.4700	5.16
41	YKEIEVGFP	106	0.4000	4.40
42	IATDGARKC	190	0.4000	4.40
43	VTTSESPDA	0	0.3000	3.30
44	LVYTAFSGS	369	0.2700	2.97

45	LVTLGLNLF	323	0.2100	2.31
46	LQIEFSQVI	452	0.2000	2.20
47	FGAHTIVKP	13	0.1000	1.10
48	LFSRGVDPQ	330	0.1000	1.10
49	VGIAPSITT	620	0.1000	1.10
50	IEWMSRNLA	266	0.0100	0.11
51	VYTAFSGSH	370	-0.0200	0
52	YNSTSILQR	168	-0.1000	0
53	WQVPYLPID	405	-0.1000	0
54	LRDGNQALI	78	-0.2000	0
55	IMKTDHGLS	439	-0.2000	0
56	VVSAVNRAA	634	-0.2000	0
57	VTIASPAQP	574	-0.3000	0
58	VTIASPAQP	593	-0.3000	0
59	LRAVVSAVN	631	-0.3000	0
60	VIRVNSQSG	424	-0.4000	0
61	LSLPRRLQI	446	-0.4000	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	VRPLERIRQ	491	4.0800	46.36
2	VRMGYKEIE	102	3.9000	44.32
3	VYADSIEWM	261	3.7000	42.05
4	LPIDPRDVG	410	3.0000	34.09
5	INGVETEIS	519	2.7000	30.68
6	VAYIMKTDH	436	2.5800	29.32
7	IEFSQVIQK	454	2.5800	29.32
8	VKINGVETE	517	2.5000	28.41
9	MKTDHGLSL	440	2.4000	27.27
10	IAPSITTAS	622	2.4000	27.27
11	VEASVTIAS	570	2.3800	27.05
12	VTLGLNLFS	324	2.3000	26.14

13	VQAIATDGA	187	2.2000	25.00
14	IEVGFPSAS	109	2.1000	23.86
15	FRANRAEVQ	180	2.1000	23.86
16	IRVNSQSGK	425	2.1000	23.86
17	YGGDLVYTA	365	2.0000	22.73
18	VGFDVAVLD	544	1.9800	22.50
19	IIFNLPATV	246	1.9000	21.59
20	LVTLGLNLF	323	1.9000	21.59
21	IRLRNRTWP	55	1.8000	20.45
22	VFRANRAEV	179	1.8000	20.45
23	IEWMSRNLA	266	1.7000	19.32
24	VTIQVLTQC	137	1.6000	18.18
25	FYNSTSILQ	167	1.5800	17.95
26	VWGVGIAPS	617	1.5000	17.05
27	LFSRGVDPQ	330	1.4000	15.91
28	LQIEFSQVI	452	1.3000	14.77
29	IVHFYNSTS	164	1.2000	13.64
30	LQRRVVFRA	174	1.1000	12.50
31	IATDGARKC	190	1.1000	12.50
32	LSLPRRLQI	446	1.1000	12.50
33	LVYTAFSGS	369	1.0000	11.36
34	YVEASVTIA	569	1.0000	11.36
35	WRFEYSPES	210	0.9000	10.23
36	YEAVIRVNS	421	0.8800	10.00
37	LRDGNQALI	78	0.8000	9.09
38	LVRMGYKEI	101	0.8000	9.09
39	VGIAPSITT	620	0.7800	8.86
40	FVREIIEQG	123	0.7000	7.95
41	VIRVNSQSG	424	0.7000	7.95
42	VTIASPAQP	574	0.7000	7.95
43	VTIASPAQP	593	0.7000	7.95
44	LRAVVSAVN	631	0.7000	7.95
45	IPDDVTIQV	133	0.6800	7.73
46	VEMTTPNVY	254	0.6000	6.82

47	VILSLHPHN	279	0.6000	6.82
48	VEYCNQLPV	351	0.6000	6.82
49	VKPAGPPRV	19	0.5000	5.68
50	LAPVRPLER	488	0.5000	5.68
51	VVSAVNRAA	634	0.5000	5.68
52	LTQCRPELI	142	0.4000	4.55
53	VLTQCRPEL	141	0.3000	3.41
54	IDFSNIDEI	339	0.3000	3.41
55	MKLDADAAD	389	0.3000	3.41
56	ILQRRVVFR	173	0.2800	3.18
57	FNLPATVEM	248	0.2800	3.18
58	MGYKEIEVG	104	0.2000	2.27
59	IERTFQACS	150	0.2000	2.27
60	LSLHPHNDR	281	0.2000	2.27
61	VREIIEQGA	124	0.1000	1.14
62	IQVLTQCRP	139	0.1000	1.14
63	VHFYNSTSI	165	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	VRPLERIRQ	491	4.0800	46.36
2	VRMGYKEIE	102	3.9000	44.32
3	VYADSIEWM	261	3.7000	42.05
4	LPIDPRDVG	410	3.0000	34.09
5	INGVETEIS	519	2.7000	30.68
6	VAYIMKTDH	436	2.5800	29.32
7	IEFSQVIQK	454	2.5800	29.32
8	VKINGVETE	517	2.5000	28.41
9	MKTDHGLSL	440	2.4000	27.27
10	IAPSITTAS	622	2.4000	27.27
11	VEASVTIAS	570	2.3800	27.05
12	VTLGLNLFS	324	2.3000	26.14

13	VQAIATDGA	187	2.2000	25.00
14	IEVGFPSAS	109	2.1000	23.86
15	FRANRAEVQ	180	2.1000	23.86
16	IRVNSQSGK	425	2.1000	23.86
17	YGGDLVYTA	365	2.0000	22.73
18	VGFDVAVLD	544	1.9800	22.50
19	IIFNLPATV	246	1.9000	21.59
20	LVTLGLNLF	323	1.9000	21.59
21	IRLRNRTWP	55	1.8000	20.45
22	VFRANRAEV	179	1.8000	20.45
23	IEWMSRNLA	266	1.7000	19.32
24	VTIQVLTQC	137	1.6000	18.18
25	FYNSTSILQ	167	1.5800	17.95
26	VWGVGIAPS	617	1.5000	17.05
27	LFSRGVDPQ	330	1.4000	15.91
28	LQIEFSQVI	452	1.3000	14.77
29	IVHFYNSTS	164	1.2000	13.64
30	LQRRVVFRA	174	1.1000	12.50
31	IATDGARKC	190	1.1000	12.50
32	LSLPRRLQI	446	1.1000	12.50
33	LVYTAFSGS	369	1.0000	11.36
34	YVEASVTIA	569	1.0000	11.36
35	WRFEYSPES	210	0.9000	10.23
36	YEAVIRVNS	421	0.8800	10.00
37	LRDGNQALI	78	0.8000	9.09
38	LVRMGYKEI	101	0.8000	9.09
39	VGIAPSITT	620	0.7800	8.86
40	FVREIIEQG	123	0.7000	7.95
41	VIRVNSQSG	424	0.7000	7.95
42	VTIASPAQP	574	0.7000	7.95
43	VTIASPAQP	593	0.7000	7.95
44	LRAVVSAVN	631	0.7000	7.95
45	IPDDVTIQV	133	0.6800	7.73
46	VEMTTPNVY	254	0.6000	6.82

47	VILSLHPHN	279	0.6000	6.82
48	VEYCNQLPV	351	0.6000	6.82
49	VKPAGPPRV	19	0.5000	5.68
50	LAPVRPLER	488	0.5000	5.68
51	VVSAVNRAA	634	0.5000	5.68
52	LTQCRPELI	142	0.4000	4.55
53	VLTQCRPEL	141	0.3000	3.41
54	IDFSNIDEI	339	0.3000	3.41
55	MKLDADAAD	389	0.3000	3.41
56	ILQRRVVFR	173	0.2800	3.18
57	FNLPATVEM	248	0.2800	3.18
58	MGYKEIEVG	104	0.2000	2.27
59	IERTFQACS	150	0.2000	2.27
60	LSLHPHNDR	281	0.2000	2.27
61	VREIIEQGA	124	0.1000	1.14
62	IQVLTQCRP	139	0.1000	1.14
63	VHFYNSTSI	165	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	VRPLERIRQ	491	4.0800	46.36
2	VRMGYKEIE	102	3.9000	44.32
3	VYADSIEWM	261	3.7000	42.05
4	LPIDPRDVG	410	3.0000	34.09
5	INGVETEIS	519	2.7000	30.68
6	VAYIMKTDH	436	2.5800	29.32
7	IEFSQVIQK	454	2.5800	29.32
8	VKINGVETE	517	2.5000	28.41
9	MKTDHGLSL	440	2.4000	27.27
10	IAPSITTAS	622	2.4000	27.27
11	VEASVTIAS	570	2.3800	27.05
12	VTLGLNLFS	324	2.3000	26.14

13	VQAIATDGA	187	2.2000	25.00
14	IEVGFPSAS	109	2.1000	23.86
15	FRANRAEVQ	180	2.1000	23.86
16	IRVNSQSGK	425	2.1000	23.86
17	YGGDLVYTA	365	2.0000	22.73
18	VGFDVAVLD	544	1.9800	22.50
19	IIFNLPATV	246	1.9000	21.59
20	LVTLGLNLF	323	1.9000	21.59
21	IRLRNRTWP	55	1.8000	20.45
22	VFRANRAEV	179	1.8000	20.45
23	IEWMSRNLA	266	1.7000	19.32
24	VTIQVLTQC	137	1.6000	18.18
25	FYNSTSILQ	167	1.5800	17.95
26	VWGVGIAPS	617	1.5000	17.05
27	LFSRGVDPQ	330	1.4000	15.91
28	LQIEFSQVI	452	1.3000	14.77
29	IVHFYNSTS	164	1.2000	13.64
30	LQRRVVFRA	174	1.1000	12.50
31	IATDGARKC	190	1.1000	12.50
32	LSLPRRLQI	446	1.1000	12.50
33	LVYTAFSGS	369	1.0000	11.36
34	YVEASVTIA	569	1.0000	11.36
35	WRFEYSPES	210	0.9000	10.23
36	YEAVIRVNS	421	0.8800	10.00
37	LRDGNQALI	78	0.8000	9.09
38	LVRMGYKEI	101	0.8000	9.09
39	VGIAPSITT	620	0.7800	8.86
40	FVREIIEQG	123	0.7000	7.95
41	VIRVNSQSG	424	0.7000	7.95
42	VTIASPAQP	574	0.7000	7.95
43	VTIASPAQP	593	0.7000	7.95
44	LRAVVSAVN	631	0.7000	7.95
45	IPDDVTIQV	133	0.6800	7.73
46	VEMTTPNVY	254	0.6000	6.82

47	VILSLHPHN	279	0.6000	6.82
48	VEYCNQLPV	351	0.6000	6.82
49	VKPAGPPRV	19	0.5000	5.68
50	LAPVRPLER	488	0.5000	5.68
51	VVSAVNRAA	634	0.5000	5.68
52	LTQCRPELI	142	0.4000	4.55
53	VLTQCRPEL	141	0.3000	3.41
54	IDFSNIDEI	339	0.3000	3.41
55	MKLDADAAD	389	0.3000	3.41
56	ILQRRVVFR	173	0.2800	3.18
57	FNLPATVEM	248	0.2800	3.18
58	MGYKEIEVG	104	0.2000	2.27
59	IERTFQACS	150	0.2000	2.27
60	LSLHPHNDR	281	0.2000	2.27
61	VREIIEQGA	124	0.1000	1.14
62	IQVLTQCRP	139	0.1000	1.14
63	VHFYNSTSI	165	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	YGGDLVYTA	365	4.1500	43.68
2	VRMGYKEIE	102	3.9000	41.05
3	VYADSIEWM	261	3.8000	40.00
4	WRFEYSPES	210	3.7000	38.95
5	LPIDPRDVG	410	3.1000	32.63
6	FNLPATVEM	248	2.9000	30.53
7	WGVGIAPSI	618	2.8000	29.47
8	FVREIIEQG	123	2.7000	28.42
9	VRPLERIRQ	491	2.7000	28.42
10	VKINGVETE	517	2.5000	26.32
11	YEAVIRVNS	421	2.4000	25.26
12	WNPQRASSM	32	2.2700	23.89

13	FYNSTSILQ	167	2.2000	23.16
14	VGFDVAVLD	544	2.2000	23.16
15	LVTLGLNLF	323	2.1100	22.21
16	FDLLVRMGY	98	2.1000	22.11
17	FVHALADVG	537	2.1000	22.11
18	VEASVTIAS	570	2.1000	22.11
19	FRANRAEVQ	180	2.0000	21.05
20	IEFSQVIQK	454	2.0000	21.05
21	YVEASVTIA	569	2.0000	21.05
22	VKPAGPPRV	19	1.9000	20.00
23	IIFNLPATV	246	1.9000	20.00
24	MKTDHGLSL	440	1.8600	19.58
25	IRLRNRTWP	55	1.8000	18.95
26	VFRANRAEV	179	1.8000	18.95
27	VILSLHPHN	279	1.8000	18.95
28	FGNGERTGN	312	1.8000	18.95
29	IAPSITTAS	622	1.8000	18.95
30	IEVGFPSAS	109	1.7700	18.63
31	YLPIDPRDV	409	1.7000	17.89
32	INGVETEIS	519	1.7000	17.89
33	VLTQCRPEL	141	1.6600	17.47
34	LQRRVVFRA	174	1.6000	16.84
35	IRVNSQSGK	425	1.4700	15.47
36	YKEIEVGFP	106	1.4000	14.74
37	YNSTSILQR	168	1.4000	14.74
38	YLAPVRPLE	487	1.4000	14.74
39	VTLGLNLFS	324	1.2000	12.63
40	FGAHTIVKP	13	1.1000	11.58
41	LQIEFSQVI	452	1.1000	11.58
42	IPDDVTIQV	133	1.0000	10.53
43	FQACSGAPR	154	1.0000	10.53
44	WMSRNLANR	268	1.0000	10.53
45	WQVPYLPID	405	1.0000	10.53
46	VIRVNSQSG	424	1.0000	10.53

47	VAYIMKTDH	436	1.0000	10.53
48	ILQRRVVFR	173	0.9000	9.47
49	VQAIATDGA	187	0.9000	9.47
50	YCNQLPVHE	353	0.9000	9.47
51	VWGVGIAPS	617	0.9000	9.47
52	IVHFYNSTS	164	0.8700	9.16
53	VGIAPSITT	620	0.8000	8.42
54	VEQAAKYPG	199	0.7500	7.89
55	LRDGNQALI	78	0.7000	7.37
56	VTIASPAQP	574	0.7000	7.37
57	VTIASPAQP	593	0.7000	7.37
58	LVYTAFSGS	369	0.6700	7.05
59	IVKPAGPPR	18	0.6000	6.32
60	VTIQVLTQC	137	0.6000	6.32
61	LRNRTWPDR	57	0.5000	5.26
62	MSPARKRRM	89	0.5000	5.26
63	LSLPRRLQI	446	0.5000	5.26
64	LAPVRPLER	488	0.5000	5.26

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VRPLERIRQ	491	4.0800	46.36
2	VRMGYKEIE	102	3.9000	44.32
3	VYADSIEWM	261	3.7000	42.05
4	LPIDPRDVG	410	3.0000	34.09
5	INGVETEIS	519	2.7000	30.68
6	VAYIMKTDH	436	2.5800	29.32
7	IEFSQVIQK	454	2.5800	29.32
8	VKINGVETE	517	2.5000	28.41
9	MKTDHGLSL	440	2.4000	27.27
10	IAPSITTAS	622	2.4000	27.27
11	VEASVTIAS	570	2.3800	27.05

12	VTLGLNLFS	324	2.3000	26.14
13	VQAIATDGA	187	2.2000	25.00
14	IEVGFPSAS	109	2.1000	23.86
15	FRANRAEVQ	180	2.1000	23.86
16	IRVNSQSGK	425	2.1000	23.86
17	YGGDLVYTA	365	2.0000	22.73
18	VGFDVAVLD	544	1.9800	22.50
19	IIFNLPATV	246	1.9000	21.59
20	LVTLGLNLF	323	1.9000	21.59
21	IRLRNRTWP	55	1.8000	20.45
22	VFRANRAEV	179	1.8000	20.45
23	IEWMSRNLA	266	1.7000	19.32
24	VTIQVLTQC	137	1.6000	18.18
25	FYNSTSILQ	167	1.5800	17.95
26	VWGVGIAPS	617	1.5000	17.05
27	LFSRGVDPQ	330	1.4000	15.91
28	LQIEFSQVI	452	1.3000	14.77
29	IVHFYNSTS	164	1.2000	13.64
30	LQRRVVFRA	174	1.1000	12.50
31	IATDGARKC	190	1.1000	12.50
32	LSLPRRLQI	446	1.1000	12.50
33	LVYTAFSGS	369	1.0000	11.36
34	YVEASVTIA	569	1.0000	11.36
35	WRFEYSPES	210	0.9000	10.23
36	YEAVIRVNS	421	0.8800	10.00
37	LRDGNQALI	78	0.8000	9.09
38	LVRMGYKEI	101	0.8000	9.09
39	VGIAPSITT	620	0.7800	8.86
40	FVREIIEQG	123	0.7000	7.95
41	VIRVNSQSG	424	0.7000	7.95
42	VTIASPAQP	574	0.7000	7.95
43	VTIASPAQP	593	0.7000	7.95
44	LRAVVSAVN	631	0.7000	7.95
45	IPDDVTIQV	133	0.6800	7.73

46	VEMTTPNVY	254	0.6000	6.82
47	VILSLHPHN	279	0.6000	6.82
48	VEYCNQLPV	351	0.6000	6.82
49	VKPAGPPRV	19	0.5000	5.68
50	LAPVRPLER	488	0.5000	5.68
51	VVSAVNRAA	634	0.5000	5.68
52	LTQCRPELI	142	0.4000	4.55
53	VLTQCRPEL	141	0.3000	3.41
54	IDFSNIDEI	339	0.3000	3.41
55	MKLDADAAD	389	0.3000	3.41
56	ILQRRVVFR	173	0.2800	3.18
57	FNLPATVEM	248	0.2800	3.18
58	MGYKEIEVG	104	0.2000	2.27
59	IERTFQACS	150	0.2000	2.27
60	LSLHPHNDR	281	0.2000	2.27
61	VREIIEQGA	124	0.1000	1.14
62	IQVLTQCRP	139	0.1000	1.14
63	VHFYNSTSI	165	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	WRFEYSPES	210	5.5000	63.95
2	LQIEFSQVI	452	3.9000	45.35
3	FRANRAEVQ	180	3.8000	44.19
4	FYNSTSILQ	167	3.7800	43.95
5	FVREIIEQG	123	3.4000	39.53
6	VQAIATDGA	187	2.6000	30.23
7	IAPSITTAS	622	2.6000	30.23
8	VEASVTIAS	570	2.5800	30.00
9	IVHFYNSTS	164	2.2000	25.58
10	LVYTAFSGS	369	2.0000	23.26
11	VKINGVETE	517	1.9000	22.09

12	INGVETEIS	519	1.9000	22.09
13	YGGDLVYTA	365	1.8000	20.93
14	FNLPATVEM	248	1.7800	20.70
15	YVEASVTIA	569	1.7000	19.77
16	VVSAVNRAA	634	1.4000	16.28
17	IEFSQVIQK	454	1.3800	16.05
18	WNPQRASSM	32	1.3000	15.12
19	YNSTSILQR	168	1.3000	15.12
20	IIFNLPATV	246	1.1000	12.79
21	VTLGLNLFS	324	1.1000	12.79
22	VYADSIEWM	261	1.0000	11.63
23	FVHALADVG	537	1.0000	11.63
24	VGIAPSITT	620	0.8800	10.23
25	VEMTTPNVY	254	0.8000	9.30
26	LVRMGYKEI	101	0.6000	6.98
27	IRVNSQSGK	425	0.6000	6.98
28	VRPLERIRQ	491	0.4800	5.58
29	LVTLGLNLF	323	0.4000	4.65
30	FGAHTIVKP	13	0.2800	3.26
31	YLPIDPRDV	409	0.2000	2.33
32	VTTSESPDA	0	0.1000	1.16
33	VTIQVLTQC	137	0.1000	1.16
34	VGFDVAVLD	544	0.0800	0.93
35	VIRVNSQSG	424	-0.1000	0
36	LRAVVSAVN	631	-0.1000	0
37	IPDDVTIQV	133	-0.1200	0
38	YAKQVCDAV	226	-0.2000	0
39	IERTFQACS	150	-0.3000	0
40	MKLDADAAD	389	-0.3000	0
41	MKTDHGLSL	440	-0.3000	0
42	YCNQLPVHE	353	-0.3200	0
43	VYTAFSGSH	370	-0.3200	0
44	VHFYNSTSI	165	-0.4000	0
45	YEHAMSAGD	554	-0.4000	0

46	IRQHVDAAD	497	-0.5000	0
47	IFNLPATVE	247	-0.7000	0
48	ILSLHPHND	280	-0.7000	0
49	VETEISGSG	522	-0.7000	0
50	IATDGARKC	190	-0.8000	0
51	MSRNLANRE	269	-0.8000	0
52	LFSRGVDPQ	330	-0.8000	0
53	VTIASPAQP	574	-0.8000	0
54	VTIASPAQP	593	-0.8000	0
55	LGLNLFSRG	326	-0.9000	0
56	VKPAGPPRV	19	-1.0000	0
57	YKEIEVGFP	106	-1.0000	0
58	LSLHPHNDR	281	-1.0000	0
59	LTQCRPELI	142	-1.1000	0
60	LQRRVVFRA	174	-1.1000	0
61	IMKTDHGLS	439	-1.2000	0
62	VWGVGIAPS	617	-1.2000	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	VVSAVNRAA	634	5.3000	55.21
2	VVFRANRAE	178	5.2000	54.17
3	LQRRVVFRA	174	4.3000	44.79
4	IVHFYNSTS	164	4.2000	43.75
5	VTLGLNLFS	324	3.3000	34.38
6	VGIAPSITT	620	2.3000	23.96
7	VIRVNSQSG	424	2.2000	22.92
8	LQIEFSQVI	452	2.2000	22.92
9	VEASVTIAS	570	2.2000	22.92
10	ILQRRVVFR	173	2.1000	21.88
11	VHFYNSTSI	165	2.0000	20.83
12	IAPSITTAS	622	2.0000	20.83

13	VTSKTVWGV	612	1.9000	19.79
14	VIDRAPLWC	66	1.8000	18.75
15	LANRESVIL	273	1.7000	17.71
16	LHPHNDRGT	283	1.7000	17.71
17	INGVETEIS	519	1.7000	17.71
18	LVRMGYKEI	101	1.6000	16.67
19	LVYTAFSGS	369	1.6000	16.67
20	FYNSTSILQ	167	1.4000	14.58
21	YLPIDPRDV	409	1.3800	14.37
22	LFSRGVDPQ	330	1.3000	13.54
23	FNLPATVEM	248	1.2000	12.50
24	LRAVVSAVN	631	1.1000	11.46
25	VQAIATDGA	187	1.0800	11.25
26	IEFSQVIQK	454	1.0000	10.42
27	LIERTFQAC	149	0.9000	9.38
28	YVEASVTIA	569	0.9000	9.38
29	IIFNLPATV	246	0.8000	8.33
30	LRNRTWPDR	57	0.7000	7.29
31	IRLRNRTWP	55	0.6000	6.25
32	VEMTTPNVY	254	0.6000	6.25
33	IRQHVDAAD	497	0.6000	6.25
34	MFDLLVRMG	97	0.5000	5.21
35	VHERHPYGG	359	0.5000	5.21
36	VRPLERIRQ	491	0.5000	5.21
37	WRFEYSPES	210	0.4000	4.17
38	VSPKEMWDA	474	0.4000	4.17
39	LLVRMGYKE	100	0.2000	2.08
40	IEVGFPSAS	109	0.2000	2.08
41	MLWQVPYLP	403	0.2000	2.08
42	VKINGVETE	517	0.2000	2.08
43	VTIASPAQP	574	0.2000	2.08
44	VTIASPAQP	593	0.2000	2.08
45	VTIQVLTQC	137	0.1000	1.04
46	FRANRAEVQ	180	0.1000	1.04

47	LSLHPHNDR	281	0.1000	1.04
48	IRVNSQSGK	425	0.1000	1.04
49	VEPIRLRNR	52	0.0800	0.83
50	VNRYRPFAE	42	-0.1000	0
51	ITTASLRAV	626	-0.1000	0
52	VYTAFSGSH	370	-0.1200	0
53	VDLRDGNQA	76	-0.2000	0
54	VREIIEQGA	124	-0.2200	0
55	VKPAGPPRV	19	-0.3000	0
56	IDRAPLWCA	67	-0.3000	0
57	VEYCNQLPV	351	-0.3000	0
58	LAPVRPLER	488	-0.4000	0
59	FGAHTIVKP	13	-0.5000	0
60	IERTFQACS	150	-0.5000	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	IVHFYNSTS	164	5.8000	65.91
2	INGVETEIS	519	3.4000	38.64
3	VQAIATDGA	187	3.0000	34.09
4	VVSAVNRAA	634	2.7000	30.68
5	IAPSITTAS	622	2.6000	29.55
6	VHFYNSTSI	165	2.3000	26.14
7	LRAVVSAVN	631	2.3000	26.14
8	LVYTAFSGS	369	2.1000	23.86
9	VIRVNSQSG	424	2.1000	23.86
10	LQIEFSQVI	452	2.1000	23.86
11	VEASVTIAS	570	2.0800	23.64
12	VGIAPSITT	620	1.8800	21.36
13	LVTLGLNLF	323	1.7000	19.32
14	VRPLERIRQ	491	1.6800	19.09
15	WRFEYSPES	210	1.6000	18.18

16	LVRMGYKEI	101	1.5000	17.05
17	FYNSTSILQ	167	1.2800	14.55
18	YVEASVTIA	569	1.2000	13.64
19	VWGVGIAPS	617	1.2000	13.64
20	IFNLPATVE	247	1.0000	11.36
21	FNLPATVEM	248	0.9000	10.23
22	VTLGLNLFS	324	0.9000	10.23
23	IEFSQVIQK	454	0.8800	10.00
24	VTIQVLTQC	137	0.8000	9.09
25	VYTAFSGSH	370	0.7800	8.86
26	IRVNSQSGK	425	0.7000	7.95
27	IDPMSPARK	86	0.5000	5.68
28	IIFNLPATV	246	0.5000	5.68
29	VKINGVETE	517	0.4000	4.55
30	LQRRVVFRA	174	0.3500	3.98
31	FRANRAEVQ	180	0.3000	3.41
32	VEMTTPNVY	254	0.3000	3.41
33	WNPQRASSM	32	0.2000	2.27
34	IEWMSRNLA	266	0.2000	2.27
35	VTIASPAQP	574	0.2000	2.27
36	VTIASPAQP	593	0.2000	2.27
37	ILSLHPHND	280	0.1000	1.14
38	LAPVRPLER	488	0.1000	1.14
39	VAYIMKTDH	436	-0.0200	0
40	IQVLTQCRP	139	-0.1000	0
41	VAVLDYYEH	548	-0.1200	0
42	YLPIDPRDV	409	-0.2000	0
43	VKPAGPPRV	19	-0.3000	0
44	LAAFVHALA	534	-0.4000	0
45	VHALADVGF	538	-0.4000	0
46	MFDLLVRMG	97	-0.5000	0
47	VREIIEQGA	124	-0.5000	0
48	YTAFSGSHQ	371	-0.5000	0
49	MLWQVPYLP	403	-0.5000	0

50	VGQPSWNPQ	27	-0.6000	0
51	IEVGFPSAS	109	-0.6000	0
52	VNRYRPFAE	42	-0.6500	0
53	VTTSESPDA	0	-0.7000	0
54	VGFPSASQT	111	-0.7000	0
55	YGGDLVYTA	365	-0.7000	0
56	VVFRANRAE	178	-0.8000	0
57	LGLNLFSRG	326	-0.8000	0
58	IERTFQACS	150	-0.9000	0
59	FVHALADVG	537	-0.9000	0
60	LTQCRPELI	142	-1.0000	0
61	VEYCNQLPV	351	-1.0000	0
62	VPYLPIDPR	407	-1.0000	0
63	FVREIIEQG	123	-1.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IVHFYNSTS	164	4.8000	51.06
2	LRAVVSAVN	631	3.3000	35.11
3	FYNSTSILQ	167	3.0800	32.77
4	IFNLPATVE	247	3.0000	31.91
5	FNLPATVEM	248	3.0000	31.91
6	WRFEYSPES	210	2.6000	27.66
7	VIRVNSQSG	424	2.4000	25.53
8	VKINGVETE	517	2.4000	25.53
9	INGVETEIS	519	2.4000	25.53
10	WNPQRASSM	32	2.3000	24.47
11	YEHAMSAGD	554	2.3000	24.47
12	YVEASVTIA	569	2.2000	23.40
13	FRANRAEVQ	180	2.1000	22.34
14	VQAIATDGA	187	2.0000	21.28
15	ILSLHPHND	280	1.8000	19.15

16	VGIAPSITT	620	1.7800	18.94
17	YRPFAEEVE	45	1.7000	18.09
18	YCNQLPVHE	353	1.7000	18.09
19	VVSAVNRAA	634	1.7000	18.09
20	LVTLGLNLF	323	1.6000	17.02
21	IAPSITTAS	622	1.6000	17.02
22	VHFYNSTSI	165	1.5000	15.96
23	VRPLERIRQ	491	1.4800	15.74
24	FVHALADVG	537	1.4000	14.89
25	VNRYRPFAE	42	1.3500	14.36
26	YTAFSGSHQ	371	1.3000	13.83
27	LQIEFSQVI	452	1.3000	13.83
28	FVREIIEQG	123	1.2000	12.77
29	VVFRANRAE	178	1.2000	12.77
30	LVYTAFSGS	369	1.1000	11.70
31	YLPIDPRDV	409	1.1000	11.70
32	VEASVTIAS	570	1.0800	11.49
33	VYTAFSGSH	370	1.0000	10.64
34	LVRMGYKEI	101	0.7000	7.45
35	MSRNLANRE	269	0.7000	7.45
36	VEMTTPNVY	254	0.4000	4.26
37	YGGDLVYTA	365	0.3000	3.19
38	VAYIMKTDH	436	0.2000	2.13
39	VWGVGIAPS	617	0.2000	2.13
40	IRQHVDAAD	497	0.1000	1.06
41	VGFDVAVLD	544	0.1000	1.06
42	VAVLDYYEH	548	0.1000	1.06
43	IIEQGAIPD	127	-0.0200	0
44	VTLGLNLFS	324	-0.1000	0
45	MKLDADAAD	389	-0.1000	0
46	MFDLLVRMG	97	-0.2000	0
47	YKEIEVGFP	106	-0.2000	0
48	VTIQVLTQC	137	-0.2000	0
49	IIFNLPATV	246	-0.2000	0

50	VTIASPAQP	574	-0.4000	0
51	VTIASPAQP	593	-0.4000	0
52	LGLNLFSRG	326	-0.5000	0
53	YIMKTDHGL	438	-0.5000	0
54	VHALADVGF	538	-0.5000	0
55	MTTPNVYAD	256	-0.6000	0
56	LQRRVVFRA	174	-0.6500	0
57	IQVLTQCRP	139	-0.7000	0
58	YNSTSILQR	168	-0.7000	0
59	LEYAKQVCD	224	-0.7000	0
60	WQVPYLPID	405	-0.7000	0
61	VGQPSWNPQ	27	-0.8000	0
62	VGFPSASQT	111	-0.8000	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	IVHFYNSTS	164	4.8000	54.55
2	WRFEYSPES	210	2.6000	29.55
3	INGVETEIS	519	2.4000	27.27
4	FYNSTSILQ	167	2.2800	25.91
5	YVEASVTIA	569	2.2000	25.00
6	VQAIATDGA	187	2.0000	22.73
7	FNLPATVEM	248	1.9000	21.59
8	VVSAVNRAA	634	1.7000	19.32
9	IAPSITTAS	622	1.6000	18.18
10	VHFYNSTSI	165	1.3000	14.77
11	FRANRAEVQ	180	1.3000	14.77
12	LRAVVSAVN	631	1.3000	14.77
13	WNPQRASSM	32	1.2000	13.64
14	LVYTAFSGS	369	1.1000	12.50
15	VIRVNSQSG	424	1.1000	12.50
16	LQIEFSQVI	452	1.1000	12.50

17	VEASVTIAS	570	1.0800	12.27
18	VGIAPSITT	620	0.8800	10.00
19	YLPIDPRDV	409	0.8000	9.09
20	LVTLGLNLF	323	0.7000	7.95
21	VRPLERIRQ	491	0.6800	7.73
22	LVRMGYKEI	101	0.5000	5.68
23	YTAFSGSHQ	371	0.5000	5.68
24	YGGDLVYTA	365	0.3000	3.41
25	VWGVGIAPS	617	0.2000	2.27
26	FVHALADVG	537	0.1000	1.14
27	FVREIIEQG	123	-0.1000	0
28	VTLGLNLFS	324	-0.1000	0
29	IEFSQVIQK	454	-0.1200	0
30	VTIQVLTQC	137	-0.2000	0
31	VYTAFSGSH	370	-0.2200	0
32	IRVNSQSGK	425	-0.3000	0
33	YEHAMSAGD	554	-0.4000	0
34	IDPMSPARK	86	-0.5000	0
35	IIFNLPATV	246	-0.5000	0
36	YKEIEVGFP	106	-0.6000	0
37	VKINGVETE	517	-0.6000	0
38	LQRRVVFRA	174	-0.6500	0
39	YNSTSILQR	168	-0.7000	0
40	VEMTTPNVY	254	-0.7000	0
41	IEWMSRNLA	266	-0.8000	0
42	VTIASPAQP	574	-0.8000	0
43	VTIASPAQP	593	-0.8000	0
44	ILSLHPHND	280	-0.9000	0
45	LAPVRPLER	488	-0.9000	0
46	VAYIMKTDH	436	-1.0200	0
47	IQVLTQCRP	139	-1.1000	0
48	VAVLDYYEH	548	-1.1200	0
49	YEAVIRVNS	421	-1.2000	0
50	VKPAGPPRV	19	-1.3000	0

51	YRPFAEEVE	45	-1.3000	0
52	FQACSGAPR	154	-1.3000	0
53	YCNQLPVHE	353	-1.3000	0
54	LAAFVHALA	534	-1.4000	0
55	VHALADVGF	538	-1.4000	0
56	MFDLLVRMG	97	-1.5000	0
57	VREIIEQGA	124	-1.5000	0
58	MLWQVPYLP	403	-1.5000	0
59	YIMKTDHGL	438	-1.5000	0
60	VGQPSWNPQ	27	-1.6000	0
61	IEVGFPSAS	109	-1.6000	0
62	VNRYRPFAE	42	-1.6500	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	IVHFYNSTS	164	5.8000	61.70
2	LRAVVSAVN	631	4.3000	45.74
3	IFNLPATVE	247	4.0000	42.55
4	VIRVNSQSG	424	3.4000	36.17
5	VKINGVETE	517	3.4000	36.17
6	INGVETEIS	519	3.4000	36.17
7	VQAIATDGA	187	3.0000	31.91
8	ILSLHPHND	280	2.8000	29.79
9	VGIAPSITT	620	2.7800	29.57
10	VVSAVNRAA	634	2.7000	28.72
11	LVTLGLNLF	323	2.6000	27.66
12	IAPSITTAS	622	2.6000	27.66
13	VHFYNSTSI	165	2.5000	26.60
14	VRPLERIRQ	491	2.4800	26.38
15	VNRYRPFAE	42	2.3500	25.00
16	LQIEFSQVI	452	2.3000	24.47
17	VVFRANRAE	178	2.2000	23.40

18	LVYTAFSGS	369	2.1000	22.34
19	FYNSTSILQ	167	2.0800	22.13
20	VEASVTIAS	570	2.0800	22.13
21	FNLPATVEM	248	2.0000	21.28
22	VYTAFSGSH	370	2.0000	21.28
23	LVRMGYKEI	101	1.7000	18.09
24	MSRNLANRE	269	1.7000	18.09
25	WRFEYSPES	210	1.6000	17.02
26	VEMTTPNVY	254	1.4000	14.89
27	WNPQRASSM	32	1.3000	13.83
28	YEHAMSAGD	554	1.3000	13.83
29	VAYIMKTDH	436	1.2000	12.77
30	YVEASVTIA	569	1.2000	12.77
31	VWGVGIAPS	617	1.2000	12.77
32	FRANRAEVQ	180	1.1000	11.70
33	IRQHVDAAD	497	1.1000	11.70
34	VGFDVAVLD	544	1.1000	11.70
35	VAVLDYYEH	548	1.1000	11.70
36	LERIRQHVD	494	1.0000	10.64
37	IIEQGAIPD	127	0.9800	10.43
38	VTLGLNLFS	324	0.9000	9.57
39	MKLDADAAD	389	0.9000	9.57
40	MFDLLVRMG	97	0.8000	8.51
41	VTIQVLTQC	137	0.8000	8.51
42	IIFNLPATV	246	0.8000	8.51
43	YRPFAEEVE	45	0.7000	7.45
44	YCNQLPVHE	353	0.7000	7.45
45	VTIASPAQP	574	0.6000	6.38
46	VTIASPAQP	593	0.6000	6.38
47	LGLNLFSRG	326	0.5000	5.32
48	VHALADVGF	538	0.5000	5.32
49	MTTPNVYAD	256	0.4000	4.26
50	FVHALADVG	537	0.4000	4.26
51	LQRRVVFRA	174	0.3500	3.72

52	IQVLTQCRP	139	0.3000	3.19
53	LEYAKQVCD	224	0.3000	3.19
54	YTAFSGSHQ	371	0.3000	3.19
55	VGQPSWNPQ	27	0.2000	2.13
56	VGFPSASQT	111	0.2000	2.13
57	FVREIIEQG	123	0.2000	2.13
58	IEWMSRNLA	266	0.2000	2.13
59	LNLFSRGVD	328	0.2000	2.13
60	IEFSQVIQK	454	0.1800	1.91
61	LWCAVDLRD	72	0.1000	1.06
62	YLPIDPRDV	409	0.1000	1.06
63	LAPVRPLER	488	0.1000	1.06

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	WRFEYSPES	210	5.9000	65.56
2	FVREIIEQG	123	4.8000	53.33
3	LQIEFSQVI	452	4.8000	53.33
4	VKINGVETE	517	3.3000	36.67
5	FNLPATVEM	248	3.2800	36.44
6	FRANRAEVQ	180	3.1000	34.44
7	FYNSTSILQ	167	3.0800	34.22
8	IAPSITTAS	622	3.0000	33.33
9	VEASVTIAS	570	2.9800	33.11
10	WNPQRASSM	32	2.8000	31.11
11	YNSTSILQR	168	2.8000	31.11
12	IVHFYNSTS	164	2.6000	28.89
13	VQAIATDGA	187	2.6000	28.89
14	VYADSIEWM	261	2.5000	27.78
15	LVYTAFSGS	369	2.4000	26.67
16	FVHALADVG	537	2.4000	26.67
17	LVTLGLNLF	323	2.3000	25.56

18	INGVETEIS	519	2.3000	25.56
19	IIFNLPATV	246	2.1000	23.33
20	VEMTTPNVY	254	2.1000	23.33
21	YGGDLVYTA	365	1.8000	20.00
22	YVEASVTIA	569	1.7000	18.89
23	VGIAPSITT	620	1.5800	17.56
24	LVRMGYKEI	101	1.5000	16.67
25	VTLGLNLFS	324	1.5000	16.67
26	IEFSQVIQK	454	1.4800	16.44
27	VVSAVNRAA	634	1.4000	15.56
28	VIRVNSQSG	424	1.3000	14.44
29	FGAHTIVKP	13	1.2800	14.22
30	YLPIDPRDV	409	1.2000	13.33
31	VGFDVAVLD	544	1.1800	13.11
32	YCNQLPVHE	353	1.0800	12.00
33	IPDDVTIQV	133	0.8800	9.78
34	YAKQVCDAV	226	0.8000	8.89
35	MKLDADAAD	389	0.8000	8.89
36	IFNLPATVE	247	0.7000	7.78
37	IRVNSQSGK	425	0.7000	7.78
38	VETEISGSG	522	0.7000	7.78
39	YEHAMSAGD	554	0.7000	7.78
40	LRAVVSAVN	631	0.7000	7.78
41	MKTDHGLSL	440	0.6600	7.33
42	MSRNLANRE	269	0.6000	6.67
43	IRQHVDAAD	497	0.6000	6.67
44	VHFYNSTSI	165	0.5000	5.56
45	LSLHPHNDR	281	0.5000	5.56
46	LGLNLFSRG	326	0.5000	5.56
47	VHALADVGF	538	0.4800	5.33
48	ILSLHPHND	280	0.4000	4.44
49	FQACSGAPR	154	0.2000	2.22
50	VPYLPIDPR	407	0.2000	2.22
51	VTIASPAQP	574	0.2000	2.22

52	VTIASPAQP	593	0.2000	2.22
53	VTTSESPDA	0	0.1000	1.11
54	VTIQVLTQC	137	0.1000	1.11
55	IERTFQACS	150	0.1000	1.11
56	YYEHAMSAG	553	-0.1000	0
57	LTQCRPELI	142	-0.2000	0
58	VVFRANRAE	178	-0.2000	0
59	VRPLERIRQ	491	-0.2200	0
60	IQVLTQCRP	139	-0.3000	0

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	IVHFYNSTS	164	5.8000	65.91
2	INGVETEIS	519	3.4000	38.64
3	VQAIATDGA	187	3.0000	34.09
4	VVSAVNRAA	634	2.7000	30.68
5	IAPSITTAS	622	2.6000	29.55
6	VHFYNSTSI	165	2.3000	26.14
7	LRAVVSAVN	631	2.3000	26.14
8	LVYTAFSGS	369	2.1000	23.86
9	VIRVNSQSG	424	2.1000	23.86
10	LQIEFSQVI	452	2.1000	23.86
11	VEASVTIAS	570	2.0800	23.64
12	VGIAPSITT	620	1.8800	21.36
13	LVTLGLNLF	323	1.7000	19.32
14	VRPLERIRQ	491	1.6800	19.09
15	WRFEYSPES	210	1.6000	18.18
16	LVRMGYKEI	101	1.5000	17.05
17	FYNSTSILQ	167	1.2800	14.55
18	YVEASVTIA	569	1.2000	13.64
19	VWGVGIAPS	617	1.2000	13.64
20	IFNLPATVE	247	1.0000	11.36

21	FNLPATVEM	248	0.9000	10.23
22	VTLGLNLFS	324	0.9000	10.23
23	IEFSQVIQK	454	0.8800	10.00
24	VTIQVLTQC	137	0.8000	9.09
25	VYTAFSGSH	370	0.7800	8.86
26	IRVNSQSGK	425	0.7000	7.95
27	IDPMSPARK	86	0.5000	5.68
28	IIFNLPATV	246	0.5000	5.68
29	VKINGVETE	517	0.4000	4.55
30	LQRRVVFRA	174	0.3500	3.98
31	FRANRAEVQ	180	0.3000	3.41
32	VEMTTPNVY	254	0.3000	3.41
33	WNPQRASSM	32	0.2000	2.27
34	IEWMSRNLA	266	0.2000	2.27
35	VTIASPAQP	574	0.2000	2.27
36	VTIASPAQP	593	0.2000	2.27
37	ILSLHPHND	280	0.1000	1.14
38	LAPVRPLER	488	0.1000	1.14
39	VAYIMKTDH	436	-0.0200	0
40	IQVLTQCRP	139	-0.1000	0
41	VAVLDYYEH	548	-0.1200	0
42	YLPIDPRDV	409	-0.2000	0
43	VKPAGPPRV	19	-0.3000	0
44	LAAFVHALA	534	-0.4000	0
45	VHALADVGF	538	-0.4000	0
46	MFDLLVRMG	97	-0.5000	0
47	VREIIEQGA	124	-0.5000	0
48	YTAFSGSHQ	371	-0.5000	0
49	MLWQVPYLP	403	-0.5000	0
50	VGQPSWNPQ	27	-0.6000	0
51	IEVGFPSAS	109	-0.6000	0
52	VNRYRPFAE	42	-0.6500	0
53	VTTSESPDA	0	-0.7000	0
54	VGFPSASQT	111	-0.7000	0

55	YGGDLVYTA	365	-0.7000	0
56	VVFRANRAE	178	-0.8000	0
57	LGLNLFSRG	326	-0.8000	0
58	IERTFQACS	150	-0.9000	0
59	FVHALADVG	537	-0.9000	0
60	LTQCRPELI	142	-1.0000	0
61	VEYCNQLPV	351	-1.0000	0
62	VPYLPIDPR	407	-1.0000	0
63	FVREIIEQG	123	-1.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	WRFEYSPES	210	5.5000	63.95
2	LQIEFSQVI	452	3.9000	45.35
3	FRANRAEVQ	180	3.8000	44.19
4	FYNSTSILQ	167	3.7800	43.95
5	FVREIIEQG	123	3.4000	39.53
6	VQAIATDGA	187	2.6000	30.23
7	IAPSITTAS	622	2.6000	30.23
8	VEASVTIAS	570	2.5800	30.00
9	IVHFYNSTS	164	2.2000	25.58
10	LVYTAFSGS	369	2.0000	23.26
11	VKINGVETE	517	1.9000	22.09
12	INGVETEIS	519	1.9000	22.09
13	YGGDLVYTA	365	1.8000	20.93
14	FNLPATVEM	248	1.7800	20.70
15	YVEASVTIA	569	1.7000	19.77
16	VVSAVNRAA	634	1.4000	16.28
17	IEFSQVIQK	454	1.3800	16.05
18	WNPQRASSM	32	1.3000	15.12
19	YNSTSILQR	168	1.3000	15.12
20	IIFNLPATV	246	1.1000	12.79

21	VTLGLNLFS	324	1.1000	12.79
22	VYADSIEWM	261	1.0000	11.63
23	FVHALADVG	537	1.0000	11.63
24	VGIAPSITT	620	0.8800	10.23
25	VEMTTPNVY	254	0.8000	9.30
26	LVRMGYKEI	101	0.6000	6.98
27	IRVNSQSGK	425	0.6000	6.98
28	VRPLERIRQ	491	0.4800	5.58
29	LVTLGLNLF	323	0.4000	4.65
30	FGAHTIVKP	13	0.2800	3.26
31	YLPIDPRDV	409	0.2000	2.33
32	VTTSESPDA	0	0.1000	1.16
33	VTIQVLTQC	137	0.1000	1.16
34	VGFDVAVLD	544	0.0800	0.93
35	VIRVNSQSG	424	-0.1000	0
36	LRAVVSAVN	631	-0.1000	0
37	IPDDVTIQV	133	-0.1200	0
38	YAKQVCDAV	226	-0.2000	0
39	IERTFQACS	150	-0.3000	0
40	MKLDADAAD	389	-0.3000	0
41	MKTDHGLSL	440	-0.3000	0
42	YCNQLPVHE	353	-0.3200	0
43	VYTAFSGSH	370	-0.3200	0
44	VHFYNSTSI	165	-0.4000	0
45	YEHAMSAGD	554	-0.4000	0
46	IRQHVDAAD	497	-0.5000	0
47	IFNLPATVE	247	-0.7000	0
48	ILSLHPHND	280	-0.7000	0
49	VETEISGSG	522	-0.7000	0
50	IATDGARKC	190	-0.8000	0
51	MSRNLANRE	269	-0.8000	0
52	LFSRGVDPQ	330	-0.8000	0
53	VTIASPAQP	574	-0.8000	0
54	VTIASPAQP	593	-0.8000	0

55	LGLNLFSRG	326	-0.9000	0
56	VKPAGPPRV	19	-1.0000	0
57	YKEIEVGFP	106	-1.0000	0
58	LSLHPHNDR	281	-1.0000	0
59	LTQCRPELI	142	-1.1000	0
60	LQRRVVFRA	174	-1.1000	0
61	IMKTDHGLS	439	-1.2000	0
62	VWGVGIAPS	617	-1.2000	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	LQIEFSQVI	452	5.4000	46.55
2	FYNSTSILQ	167	5.0000	43.10
3	VHFYNSTSI	165	4.6000	39.66
4	YLPIDPRDV	409	4.6000	39.66
5	LWQVPYLPI	404	4.4000	37.93
6	VGIAPSITT	620	4.4000	37.93
7	LVRMGYKEI	101	4.3000	37.07
8	FNLPATVEM	248	4.1200	35.52
9	LANRESVIL	273	4.0000	34.48
10	VEMTTPNVY	254	3.9000	33.62
11	MKTDHGLSL	440	3.5000	30.17
12	YNSTSILQR	168	3.3000	28.45
13	ISGSGNGPL	526	3.2000	27.59
14	WGVGIAPSI	618	3.1000	26.72
15	VEYCNQLPV	351	3.0000	25.86
16	YIMKTDHGL	438	3.0000	25.86
17	LSLPRRLQI	446	3.0000	25.86
18	LVTLGLNLF	323	2.9000	25.00
19	LTQCRPELI	142	2.8000	24.14
20	VIRVNSQSG	424	2.8000	24.14
21	IEFSQVIQK	454	2.8000	24.14

22	VEASVTIAS	570	2.6200	22.59
23	LVYTAFSGS	369	2.6000	22.41
24	VGRTYEAVI	417	2.5000	21.55
25	FSGSHQDAI	374	2.4000	20.69
26	IAPTPERPI	238	2.3000	19.83
27	LRAVVSAVN	631	2.2000	18.97
28	WNPQRASSM	32	2.0000	17.24
29	LQRRVVFRA	174	2.0000	17.24
30	IRRTVEYCN	347	2.0000	17.24
31	YVEASVTIA	569	1.9000	16.38
32	VKPAGPPRV	19	1.7000	14.66
33	WRFEYSPES	210	1.7000	14.66
34	FPSASQTDF	113	1.6000	13.79
35	YTGTELEYA	219	1.6000	13.79
36	IDFSNIDEI	339	1.6000	13.79
37	LPRRLQIEF	448	1.5000	12.93
38	INGVETEIS	519	1.4200	12.24
39	VFRANRAEV	179	1.4000	12.07
40	VCDAVGEVI	230	1.4000	12.07
41	VTSKTVWGV	612	1.4000	12.07
42	VVSAVNRAA	634	1.4000	12.07
43	IAPSITTAS	622	1.3200	11.38
44	IIFNLPATV	246	1.3000	11.21
45	FVREIIEQG	123	1.2000	10.34
46	YEAVIRVNS	421	1.2000	10.34
47	VKINGVETE	517	1.2000	10.34
48	FGAHTIVKP	13	1.1000	9.48
49	LRDGNQALI	78	1.1000	9.48
50	FRANRAEVQ	180	1.1000	9.48
51	VILSLHPHN	279	1.1000	9.48
52	LAPVRPLER	488	1.1000	9.48
53	VRPLERIRQ	491	1.1000	9.48
54	ITATVKING	513	1.1000	9.48
55	VRMGYKEIE	102	1.0000	8.62

56	IVHFYNSTS	164	1.0000	8.62
57	VTTSESPDA	0	0.9000	7.76
58	VNRYRPFAE	42	0.9000	7.76
59	YGGDLVYTA	365	0.9000	7.76
60	YRPFAEEVE	45	0.8000	6.90
61	ITTASLRAV	626	0.8000	6.90
62	FDLLVRMGY	98	0.7000	6.03
63	FEYSPESYT	212	0.7000	6.03
64	VYADSIEWM	261	0.7000	6.03

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	LQIEFSQVI	452	5.4000	46.55
2	FYNSTSILQ	167	5.0000	43.10
3	VHFYNSTSI	165	4.6000	39.66
4	YLPIDPRDV	409	4.6000	39.66
5	LWQVPYLPI	404	4.4000	37.93
6	VGIAPSITT	620	4.4000	37.93
7	LVRMGYKEI	101	4.3000	37.07
8	FNLPATVEM	248	4.1200	35.52
9	LANRESVIL	273	4.0000	34.48
10	VEMTTPNVY	254	3.9000	33.62
11	MKTDHGLSL	440	3.5000	30.17
12	YNSTSILQR	168	3.3000	28.45
13	ISGSGNGPL	526	3.2000	27.59
14	WGVGIAPSI	618	3.1000	26.72
15	VEYCNQLPV	351	3.0000	25.86
16	YIMKTDHGL	438	3.0000	25.86
17	LSLPRRLQI	446	3.0000	25.86
18	LVTLGLNLF	323	2.9000	25.00
19	LTQCRPELI	142	2.8000	24.14
20	VIRVNSQSG	424	2.8000	24.14

21	IEFSQVIQK	454	2.8000	24.14
22	VEASVTIAS	570	2.6200	22.59
23	LVYTAFSGS	369	2.6000	22.41
24	VGRTYEAVI	417	2.5000	21.55
25	FSGSHQDAI	374	2.4000	20.69
26	IAPTPERPI	238	2.3000	19.83
27	LRAVVSAVN	631	2.2000	18.97
28	WNPQRASSM	32	2.0000	17.24
29	LQRRVVFRA	174	2.0000	17.24
30	IRRTVEYCN	347	2.0000	17.24
31	YVEASVTIA	569	1.9000	16.38
32	VKPAGPPRV	19	1.7000	14.66
33	WRFEYSPES	210	1.7000	14.66
34	FPSASQTDF	113	1.6000	13.79
35	YTGTELEYA	219	1.6000	13.79
36	IDFSNIDEI	339	1.6000	13.79
37	LPRRLQIEF	448	1.5000	12.93
38	INGVETEIS	519	1.4200	12.24
39	VFRANRAEV	179	1.4000	12.07
40	VCDAVGEVI	230	1.4000	12.07
41	VTSKTVWGV	612	1.4000	12.07
42	VVSAVNRAA	634	1.4000	12.07
43	IAPSITTAS	622	1.3200	11.38
44	IIFNLPATV	246	1.3000	11.21
45	FVREIIEQG	123	1.2000	10.34
46	YEAVIRVNS	421	1.2000	10.34
47	VKINGVETE	517	1.2000	10.34
48	FGAHTIVKP	13	1.1000	9.48
49	LRDGNQALI	78	1.1000	9.48
50	FRANRAEVQ	180	1.1000	9.48
51	VILSLHPHN	279	1.1000	9.48
52	LAPVRPLER	488	1.1000	9.48
53	VRPLERIRQ	491	1.1000	9.48
54	ITATVKING	513	1.1000	9.48

55	VRMGYKEIE	102	1.0000	8.62
56	IVHFYNSTS	164	1.0000	8.62
57	VTTSESPDA	0	0.9000	7.76
58	VNRYRPFAE	42	0.9000	7.76
59	YGGDLVYTA	365	0.9000	7.76
60	YRPFAEEVE	45	0.8000	6.90
61	ITTASLRAV	626	0.8000	6.90
62	FDLLVRMGY	98	0.7000	6.03
63	FEYSPESYT	212	0.7000	6.03
64	VYADSIEWM	261	0.7000	6.03

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	VVFRANRAE	178	4.3000	50.00
2	VRPLERIRQ	491	3.7000	43.02
3	VNRYRPFAE	42	3.6000	41.86
4	LQRRVVFRA	174	3.5000	40.70
5	WMSRNLANR	268	2.8000	32.56
6	LNLFSRGVD	328	2.8000	32.56
7	LFSRGVDPQ	330	2.4000	27.91
8	LLVRMGYKE	100	2.3000	26.74
9	IRLRNRTWP	55	2.2000	25.58
10	LRAVVSAVN	631	2.0000	23.26
11	VRMGYKEIE	102	1.8000	20.93
12	VKINGVETE	517	1.7000	19.77
13	ILSLHPHND	280	1.5000	17.44
14	YIMKTDHGL	438	1.5000	17.44
15	ILQRRVVFR	173	1.4000	16.28
16	WRFEYSPES	210	1.4000	16.28
17	VIDRAPLWC	66	1.3000	15.12
18	LDYYEHAMS	551	1.3000	15.12
19	FDLLVRMGY	98	1.2000	13.95

20	MGYKEIEVG	104	1.2000	13.95
21	FNLPATVEM	248	1.2000	13.95
22	YEHAMSAGD	554	1.2000	13.95
23	VFRANRAEV	179	1.1000	12.79
24	FRANRAEVQ	180	1.1000	12.79
25	YLPIDPRDV	409	1.1000	12.79
26	YLAPVRPLE	487	1.1000	12.79
27	VTSKTVWGV	612	1.1000	12.79
28	IIFNLPATV	246	1.0000	11.63
29	YEAVIRVNS	421	1.0000	11.63
30	LVRMGYKEI	101	0.9000	10.47
31	FYNSTSILQ	167	0.8000	9.30
32	VWGVGIAPS	617	0.8000	9.30
33	WQVPYLPID	405	0.7000	8.14
34	IDPRDVGRT	412	0.7000	8.14
35	IVHFYNSTS	164	0.6000	6.98
36	LANRESVIL	273	0.6000	6.98
37	VCLVTLGLN	321	0.6000	6.98
38	LVTLGLNLF	323	0.6000	6.98
39	VHERHPYGG	359	0.6000	6.98
40	VYTAFSGSH	370	0.6000	6.98
41	YRPFAEEVE	45	0.5000	5.81
42	LRNRTWPDR	57	0.4000	4.65
43	MSPARKRRM	89	0.4000	4.65
44	FVREIIEQG	123	0.4000	4.65
45	VAYIMKTDH	436	0.3000	3.49
46	LPRRLQIEF	448	0.3000	3.49
47	WCAVDLRDG	73	0.2000	2.33
48	IQVLTQCRP	139	0.2000	2.33
49	VHFYNSTSI	165	0.2000	2.33
50	IEWMSRNLA	266	0.2000	2.33
51	YCNQLPVHE	353	0.2000	2.33
52	FVHALADVG	537	0.2000	2.33
53	MFDLLVRMG	97	0.1000	1.16

54	VIRVNSQSG	424	0.1000	1.16
55	VTIASPAQP	574	0.1000	1.16
56	VTIASPAQP	593	0.1000	1.16
57	VVSAVNRAA	634	0.1000	1.16
58	IFNLPATVE	247	-0.1000	0
59	LERIRQHVD	494	-0.1000	0
60	YGGDLVYTA	365	-0.2000	0
61	YTAFSGSHQ	371	-0.2000	0
62	VGIAPSITT	620	-0.2000	0

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	LQRRVVFRA	174	3.5000	43.75
2	VRPLERIRQ	491	2.9000	36.25
3	WMSRNLANR	268	2.8000	35.00
4	IRLRNRTWP	55	1.8000	22.50
5	LFSRGVDPQ	330	1.6000	20.00
6	ILQRRVVFR	173	1.4000	17.50
7	WRFEYSPES	210	1.4000	17.50
8	VIDRAPLWC	66	1.3000	16.25
9	VVFRANRAE	178	1.3000	16.25
10	LDYYEHAMS	551	1.3000	16.25
11	YEAVIRVNS	421	1.0000	12.50
12	VFRANRAEV	179	0.8000	10.00
13	YLPIDPRDV	409	0.8000	10.00
14	VTSKTVWGV	612	0.8000	10.00
15	VWGVGIAPS	617	0.8000	10.00
16	LVRMGYKEI	101	0.7000	8.75
17	IIFNLPATV	246	0.7000	8.75
18	VNRYRPFAE	42	0.6000	7.50
19	IVHFYNSTS	164	0.6000	7.50
20	YIMKTDHGL	438	0.5000	6.25

21	LRNRTWPDR	57	0.4000	5.00
22	FRANRAEVQ	180	0.3000	3.75
23	IEWMSRNLA	266	0.2000	2.50
24	FDLLVRMGY	98	0.1000	1.25
25	FNLPATVEM	248	0.1000	1.25
26	LNLFSRGVD	328	0.1000	1.25
27	VVSAVNRAA	634	0.1000	1.25
28	MGYKEIEVG	104	-0.1000	0
29	IQVLTQCRP	139	-0.2000	0
30	YGGDLVYTA	365	-0.2000	0
31	IDPRDVGRT	412	-0.2000	0
32	IRVNSQSGK	425	-0.2000	0
33	LVTLGLNLF	323	-0.3000	0
34	YVEASVTIA	569	-0.3000	0
35	VTIASPAQP	574	-0.3000	0
36	VTIASPAQP	593	-0.3000	0
37	IDPMSPARK	86	-0.4000	0
38	YKEIEVGFP	106	-0.4000	0
39	LANRESVIL	273	-0.4000	0
40	FQACSGAPR	154	-0.5000	0
41	YNSTSILQR	168	-0.6000	0
42	LPRRLQIEF	448	-0.6000	0
43	INGVETEIS	519	-0.6000	0
44	LAAFVHALA	534	-0.6000	0
45	VYTAFSGSH	370	-0.6200	0
46	MSPARKRRM	89	-0.7000	0
47	LLVRMGYKE	100	-0.7000	0
48	VHERHPYGG	359	-0.7000	0
49	IERTFQACS	150	-0.8000	0
50	IMKTDHGLS	439	-0.8000	0
51	VSPKEMWDA	474	-0.8000	0
52	FVREIIEQG	123	-0.9000	0
53	LSLPRRLQI	446	-0.9000	0
54	LQIEFSQVI	452	-0.9000	0

55	VAYIMKTDH	436	-0.9200	0
56	VKPAGPPRV	19	-1.0000	0
57	VDLRDGNQA	76	-1.0000	0
58	YTAFSGSHQ	371	-1.0000	0
59	IEFSQVIQK	454	-1.0000	0
60	VSAVNRAAR	635	-1.0000	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	LQRRVVFRA	174	4.5000	56.25
2	VRPLERIRQ	491	3.9000	48.75
3	IRLRNRTWP	55	2.8000	35.00
4	LFSRGVDPQ	330	2.6000	32.50
5	ILQRRVVFR	173	2.4000	30.00
6	VIDRAPLWC	66	2.3000	28.75
7	VVFRANRAE	178	2.3000	28.75
8	LDYYEHAMS	551	2.3000	28.75
9	VFRANRAEV	179	1.8000	22.50
10	WMSRNLANR	268	1.8000	22.50
11	VTSKTVWGV	612	1.8000	22.50
12	VWGVGIAPS	617	1.8000	22.50
13	LVRMGYKEI	101	1.7000	21.25
14	IIFNLPATV	246	1.7000	21.25
15	VNRYRPFAE	42	1.6000	20.00
16	IVHFYNSTS	164	1.6000	20.00
17	LRNRTWPDR	57	1.4000	17.50
18	IEWMSRNLA	266	1.2000	15.00
19	LNLFSRGVD	328	1.1000	13.75
20	VVSAVNRAA	634	1.1000	13.75
21	VHFYNSTSI	165	1.0000	12.50
22	LRAVVSAVN	631	1.0000	12.50
23	MGYKEIEVG	104	0.9000	11.25

24	IQVLTQCRP	139	0.8000	10.00
25	IDPRDVGRT	412	0.8000	10.00
26	IRVNSQSGK	425	0.8000	10.00
27	LVTLGLNLF	323	0.7000	8.75
28	VTIASPAQP	574	0.7000	8.75
29	VTIASPAQP	593	0.7000	8.75
30	IDPMSPARK	86	0.6000	7.50
31	LANRESVIL	273	0.6000	7.50
32	WRFEYSPES	210	0.4000	5.00
33	LPRRLQIEF	448	0.4000	5.00
34	INGVETEIS	519	0.4000	5.00
35	LAAFVHALA	534	0.4000	5.00
36	VYTAFSGSH	370	0.3800	4.75
37	MSPARKRRM	89	0.3000	3.75
38	LLVRMGYKE	100	0.3000	3.75
39	VHERHPYGG	359	0.3000	3.75
40	IERTFQACS	150	0.2000	2.50
41	IMKTDHGLS	439	0.2000	2.50
42	VSPKEMWDA	474	0.2000	2.50
43	LSLPRRLQI	446	0.1000	1.25
44	LQIEFSQVI	452	0.1000	1.25
45	VAYIMKTDH	436	0.0800	1.00
46	VQAIATDGA	187	-0.1000	0
47	LVYTAFSGS	369	-0.1000	0
48	VGIAPSITT	620	-0.1000	0
49	MFDLLVRMG	97	-0.2000	0
50	VRMGYKEIE	102	-0.2000	0
51	ILSLHPHND	280	-0.2000	0
52	VTLGLNLFS	324	-0.2000	0
53	YLPIDPRDV	409	-0.2000	0
54	VIRVNSQSG	424	-0.2000	0
55	VIQKIAEGT	459	-0.2000	0
56	LAPVRPLER	488	-0.2000	0
57	VEASVTIAS	570	-0.2000	0

58	VAAAELGFA	293	-0.3000	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	VVFRANRAE	178	5.3000	61.63
2	VRPLERIRQ	491	4.7000	54.65
3	VNRYRPFAE	42	4.6000	53.49
4	LQRRVVFRA	174	4.5000	52.33
5	LNLFSRGVD	328	3.8000	44.19
6	LFSRGVDPQ	330	3.4000	39.53
7	LLVRMGYKE	100	3.3000	38.37
8	IRLRNRTWP	55	3.2000	37.21
9	LRAVVSAVN	631	3.0000	34.88
10	VRMGYKEIE	102	2.8000	32.56
11	VKINGVETE	517	2.7000	31.40
12	ILSLHPHND	280	2.5000	29.07
13	ILQRRVVFR	173	2.4000	27.91
14	VIDRAPLWC	66	2.3000	26.74
15	LDYYEHAMS	551	2.3000	26.74
16	MGYKEIEVG	104	2.2000	25.58
17	VFRANRAEV	179	2.1000	24.42
18	VTSKTVWGV	612	2.1000	24.42
19	IIFNLPATV	246	2.0000	23.26
20	LVRMGYKEI	101	1.9000	22.09
21	WMSRNLANR	268	1.8000	20.93
22	VWGVGIAPS	617	1.8000	20.93
23	IDPRDVGRT	412	1.7000	19.77
24	IVHFYNSTS	164	1.6000	18.60
25	LANRESVIL	273	1.6000	18.60
26	VCLVTLGLN	321	1.6000	18.60
27	LVTLGLNLF	323	1.6000	18.60
28	VHERHPYGG	359	1.6000	18.60

29	VYTAFSGSH	370	1.6000	18.60
30	LRNRTWPDR	57	1.4000	16.28
31	MSPARKRRM	89	1.4000	16.28
32	VAYIMKTDH	436	1.3000	15.12
33	LPRRLQIEF	448	1.3000	15.12
34	IQVLTQCRP	139	1.2000	13.95
35	VHFYNSTSI	165	1.2000	13.95
36	IEWMSRNLA	266	1.2000	13.95
37	MFDLLVRMG	97	1.1000	12.79
38	VIRVNSQSG	424	1.1000	12.79
39	VTIASPAQP	574	1.1000	12.79
40	VTIASPAQP	593	1.1000	12.79
41	VVSAVNRAA	634	1.1000	12.79
42	IFNLPATVE	247	0.9000	10.47
43	LERIRQHVD	494	0.9000	10.47
44	VGIAPSITT	620	0.8000	9.30
45	VIQKIAEGT	459	0.7000	8.14
46	VEQAAKYPG	199	0.6000	6.98
47	LEYAKQVCD	224	0.5000	5.81
48	YIMKTDHGL	438	0.5000	5.81
49	WRFEYSPES	210	0.4000	4.65
50	MSRNLANRE	269	0.4000	4.65
51	VILSLHPHN	279	0.4000	4.65
52	INGVETEIS	519	0.4000	4.65
53	LAAFVHALA	534	0.4000	4.65
54	VKPAGPPRV	19	0.3000	3.49
55	LSLPRRLQI	446	0.3000	3.49
56	LQIEFSQVI	452	0.3000	3.49
57	VLDYYEHAM	550	0.3000	3.49
58	FDLLVRMGY	98	0.2000	2.33
59	IERTFQACS	150	0.2000	2.33
60	FNLPATVEM	248	0.2000	2.33
61	IMKTDHGLS	439	0.2000	2.33
62	VSPKEMWDA	474	0.2000	2.33

63	VGFDVAVLD	544	0.2000	2.33
64	YEHAMSAGD	554	0.2000	2.33

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	IRLRNRTWP	55	4.6000	52.87
2	LQRRVVFRA	174	4.3500	50.00
3	VRPLERIRQ	491	3.7800	43.45
4	VHFYNSTSI	165	2.8000	32.18
5	WMSRNLANR	268	2.8000	32.18
6	LFSRGVDPQ	330	2.8000	32.18
7	YVEASVTIA	569	2.5000	28.74
8	IVHFYNSTS	164	2.4000	27.59
9	ILQRRVVFR	173	2.4000	27.59
10	IEWMSRNLA	266	2.2000	25.29
11	FRANRAEVQ	180	2.0000	22.99
12	YEAVIRVNS	421	2.0000	22.99
13	VIDRAPLWC	66	1.9000	21.84
14	VAYIMKTDH	436	1.8800	21.61
15	LVTLGLNLF	323	1.7000	19.54
16	MGYKEIEVG	104	1.6000	18.39
17	WRFEYSPES	210	1.6000	18.39
18	IRVNSQSGK	425	1.6000	18.39
19	VNRYRPFAE	42	1.4500	16.67
20	LDYYEHAMS	551	1.3000	14.94
21	VTSKTVWGV	612	1.3000	14.94
22	FDLLVRMGY	98	1.1000	12.64
23	FNLPATVEM	248	1.1000	12.64
24	INGVETEIS	519	1.1000	12.64
25	VDLRDGNQA	76	1.0000	11.49
26	VVFRANRAE	178	1.0000	11.49
27	YIMKTDHGL	438	1.0000	11.49

28	FYNSTSILQ	167	0.8800	10.11
29	FVREIIEQG	123	0.8000	9.20
30	VFRANRAEV	179	0.8000	9.20
31	YTAFSGSHQ	371	0.8000	9.20
32	VWGVGIAPS	617	0.8000	9.20
33	IIFNLPATV	246	0.7000	8.05
34	YGGDLVYTA	365	0.7000	8.05
35	LVYTAFSGS	369	0.7000	8.05
36	LRNRTWPDR	57	0.6000	6.90
37	LANRESVIL	273	0.6000	6.90
38	VRMGYKEIE	102	0.5000	5.75
39	YLPIDPRDV	409	0.5000	5.75
40	VIQKIAEGT	459	0.5000	5.75
41	VKINGVETE	517	0.4000	4.60
42	IEVGFPSAS	109	0.3000	3.45
43	LPRRLQIEF	448	0.2800	3.22
44	WNPQRASSM	32	0.2000	2.30
45	LLVRMGYKE	100	0.2000	2.30
46	LVRMGYKEI	101	0.2000	2.30
47	VHERHPYGG	359	0.2000	2.30
48	IAPSITTAS	622	0.2000	2.30
49	VTIQVLTQC	137	0.1000	1.15
50	VQAIATDGA	187	0.1000	1.15
51	LQIEFSQVI	452	0.1000	1.15
52	FVHALADVG	537	0.1000	1.15
53	IEFSQVIQK	454	-0.1200	0
54	IQVLTQCRP	139	-0.2000	0
55	VIRVNSQSG	424	-0.2000	0
56	VVSAVNRAA	634	-0.2000	0
57	VGIAPSITT	620	-0.2200	0
58	IFNLPATVE	247	-0.3000	0
59	VEMTTPNVY	254	-0.3000	0

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	VRPLERIRQ	491	5.3000	52.48
2	VVFRANRAE	178	4.5000	44.55
3	VNRYRPFAE	42	4.1000	40.59
4	LQRRVVFRA	174	4.0000	39.60
5	IRLRNRTWP	55	3.3000	32.67
6	VIDRAPLWC	66	3.1000	30.69
7	LLVRMGYKE	100	3.0000	29.70
8	VRMGYKEIE	102	2.9000	28.71
9	LNLFSRGVD	328	2.9000	28.71
10	FDLLVRMGY	98	2.8000	27.72
11	WMSRNLANR	268	2.8000	27.72
12	VKINGVETE	517	2.8000	27.72
13	WRFEYSPES	210	2.5500	25.25
14	FYNSTSILQ	167	2.4000	23.76
15	MGYKEIEVG	104	2.3000	22.77
16	YLAPVRPLE	487	2.2500	22.28
17	FRANRAEVQ	180	2.2000	21.78
18	ILSLHPHND	280	2.2000	21.78
19	YIMKTDHGL	438	2.2000	21.78
20	LFSRGVDPQ	330	2.1000	20.79
21	LRAVVSAVN	631	2.0000	19.80
22	ILQRRVVFR	173	1.9000	18.81
23	LPRRLQIEF	448	1.9000	18.81
24	VTSKTVWGV	612	1.9000	18.81
25	WQVPYLPID	405	1.8500	18.32
26	FNLPATVEM	248	1.7000	16.83
27	YRPFAEEVE	45	1.6000	15.84
28	LRNRTWPDR	57	1.5500	15.35
29	LVRMGYKEI	101	1.5000	14.85
30	FVREIIEQG	123	1.5000	14.85
31	YEAVIRVNS	421	1.5000	14.85

32	VAYIMKTDH	436	1.4000	13.86
33	VGIAPSITT	620	1.4000	13.86
34	VHFYNSTSI	165	1.3000	12.87
35	VHERHPYGG	359	1.3000	12.87
36	YLPIDPRDV	409	1.3000	12.87
37	LDYYEHAMS	551	1.3000	12.87
38	YNSTSILQR	168	1.2000	11.88
39	YEHAMSAGD	554	1.2000	11.88
40	VFRANRAEV	179	1.1000	10.89
41	LANRESVIL	273	1.1000	10.89
42	LSLPRRLQI	446	1.1000	10.89
43	IIFNLPATV	246	1.0000	9.90
44	IFNLPATVE	247	1.0000	9.90
45	LVTLGLNLF	323	0.9000	8.91
46	IDPRDVGRT	412	0.8000	7.92
47	VIQKIAEGT	459	0.8000	7.92
48	YVEASVTIA	569	0.8000	7.92
49	VWGVGIAPS	617	0.8000	7.92
50	VCLVTLGLN	321	0.7000	6.93
51	VEYCNQLPV	351	0.7000	6.93
52	YCNQLPVHE	353	0.7000	6.93
53	VYTAFSGSH	370	0.7000	6.93
54	MSPARKRRM	89	0.6000	5.94
55	IVHFYNSTS	164	0.6000	5.94
56	VTLGLNLFS	324	0.6000	5.94
57	LAPVRPLER	488	0.6000	5.94
58	LERIRQHVD	494	0.6000	5.94
59	VILSLHPHN	279	0.5500	5.45
60	FDFVREIIE	121	0.5000	4.95
61	IEWMSRNLA	266	0.5000	4.95
62	YGGDLVYTA	365	0.5000	4.95
63	INGVETEIS	519	0.5000	4.95
64	VKPAGPPRV	19	0.4500	4.46

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	VRPLERIRQ	491	4.9000	59.04
2	FDLLVRMGY	98	2.1000	25.30
3	FYNSTSILQ	167	1.9000	22.89
4	WRFEYSPES	210	1.8500	22.29
5	YNSTSILQR	168	1.6000	19.28
6	YLPIDPRDV	409	1.6000	19.28
7	YEAVIRVNS	421	1.6000	19.28
8	FRANRAEVQ	180	1.4000	16.87
9	LQRRVVFRA	174	1.0000	12.05
10	LVRMGYKEI	101	0.9000	10.84
11	IEFSQVIQK	454	0.9000	10.84
12	VWGVGIAPS	617	0.9000	10.84
13	VFRANRAEV	179	0.8000	9.64
14	YVEASVTIA	569	0.8000	9.64
15	VAYIMKTDH	436	0.7800	9.40
16	IIFNLPATV	246	0.7000	8.43
17	LAPVRPLER	488	0.7000	8.43
18	VEASVTIAS	570	0.7000	8.43
19	INGVETEIS	519	0.6000	7.23
20	IVHFYNSTS	164	0.5000	6.02
21	VGIAPSITT	620	0.5000	6.02
22	LVTLGLNLF	323	0.4000	4.82
23	VEYCNQLPV	351	0.4000	4.82
24	YKEIEVGFP	106	0.3000	3.61
25	VVSAVNRAA	634	0.3000	3.61
26	IQVLTQCRP	139	0.2000	2.41
27	LSLPRRLQI	446	0.2000	2.41
28	VKPAGPPRV	19	0.1500	1.81
29	VIDRAPLWC	66	0.1000	1.20
30	IEWMSRNLA	266	0.1000	1.20

31	LNLFSRGVD	328	0.1000	1.20
32	LRAVVSAVN	631	0.1000	1.20
33	IRLRNRTWP	55	-0.1000	0
34	FNLPATVEM	248	-0.1000	0
35	ILSLHPHND	280	-0.1000	0
36	VTLGLNLFS	324	-0.1000	0
37	WMSRNLANR	268	-0.2000	0
38	YGGDLVYTA	365	-0.2000	0
39	IRVNSQSGK	425	-0.2000	0
40	VKINGVETE	517	-0.2000	0
41	IMKTDHGLS	439	-0.3000	0
42	VTIASPAQP	574	-0.3000	0
43	VTIASPAQP	593	-0.3000	0
44	IERTFQACS	150	-0.4000	0
45	FSQVIQKIA	456	-0.4000	0
46	VLTQCRPEL	141	-0.4500	0
47	MSPARKRRM	89	-0.5000	0
48	FVREIIEQG	123	-0.5000	0
49	FQACSGAPR	154	-0.5000	0
50	FSNIDEIRR	341	-0.5000	0
51	ITATVKING	513	-0.5000	0
52	VYTAFSGSH	370	-0.5200	0
53	MFDLLVRMG	97	-0.6000	0
54	LVYTAFSGS	369	-0.7000	0
55	IQKIAEGTA	460	-0.7000	0
56	LAAFVHALA	534	-0.7000	0
57	WCAVDLRDG	73	-0.8000	0
58	IDPMSPARK	86	-0.8000	0
59	VRMGYKEIE	102	-0.8000	0
60	VQAIATDGA	187	-0.8000	0
61	VEPIRLRNR	52	-0.9000	0
62	LWQVPYLPI	404	-0.9000	0
63	VSAVNRAAR	635	-0.9000	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	LQRRVVFRA	174	3.9000	46.43
2	VRPLERIRQ	491	3.9000	46.43
3	VVSAVNRAA	634	2.9000	34.52
4	IVHFYNSTS	164	2.3000	27.38
5	IRLRNRTWP	55	2.2000	26.19
6	MSPARKRRM	89	2.1000	25.00
7	VVFRANRAE	178	2.0000	23.81
8	IEWMSRNLA	266	2.0000	23.81
9	LVRMGYKEI	101	1.9000	22.62
10	VTSKTVWGV	612	1.9000	22.62
11	VFRANRAEV	179	1.8000	21.43
12	IIFNLPATV	246	1.8000	21.43
13	LVTLGLNLF	323	1.8000	21.43
14	LPVHERHPY	357	1.8000	21.43
15	VTIQVLTQC	137	1.4000	16.67
16	LFSRGVDPQ	330	1.4000	16.67
17	VNRYRPFAE	42	1.3000	15.48
18	MFDLLVRMG	97	1.3000	15.48
19	ILQRRVVFR	173	1.3000	15.48
20	IRVNSQSGK	425	1.3000	15.48
21	LSLHPHNDR	281	1.2000	14.29
22	VKINGVETE	517	1.2000	14.29
23	VLTQCRPEL	141	1.1000	13.10
24	WRFEYSPES	210	1.0000	11.90
25	VIDRAPLWC	66	0.9000	10.71
26	MGYKEIEVG	104	0.8000	9.52
27	FRANRAEVQ	180	0.8000	9.52
28	LQIEFSQVI	452	0.8000	9.52
29	VKPAGPPRV	19	0.7000	8.33
30	VRMGYKEIE	102	0.7000	8.33

31	VHFYNSTSI	165	0.7000	8.33
32	ILSLHPHND	280	0.7000	8.33
33	YLPIDPRDV	409	0.7000	8.33
34	IEFSQVIQK	454	0.7000	8.33
35	LAAFVHALA	534	0.7000	8.33
36	VTIASPAQP	574	0.7000	8.33
37	VTIASPAQP	593	0.7000	8.33
38	ITTASLRAV	626	0.7000	8.33
39	VAYIMKTDH	436	0.6800	8.10
40	MLWQVPYLP	403	0.6000	7.14
41	INGVETEIS	519	0.6000	7.14
42	VWGVGIAPS	617	0.6000	7.14
43	IQVLTQCRP	139	0.5000	5.95
44	LDYYEHAMS	551	0.5000	5.95
45	VEASVTIAS	570	0.5000	5.95
46	LNLFSRGVD	328	0.4000	4.76
47	FGAHTIVKP	13	0.3000	3.57
48	VEYCNQLPV	351	0.3000	3.57
49	LSLPRRLQI	446	0.3000	3.57
50	VSPKEMWDA	474	0.3000	3.57
51	IAPSITTAS	622	0.3000	3.57
52	VEPIRLRNR	52	0.2000	2.38
53	VEQAAKYPG	199	0.2000	2.38
54	LHPHNDRGT	283	0.2000	2.38
55	LVYTAFSGS	369	0.2000	2.38
56	YVEASVTIA	569	0.2000	2.38
57	VGIAPSITT	620	0.2000	2.38
58	IERTFQACS	150	0.1000	1.19

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VRPLERIRQ	491	5.9000	71.08

2	LQRRVVFRA	174	2.0000	24.10
3	LVRMGYKEI	101	1.9000	22.89
4	IEFSQVIQK	454	1.9000	22.89
5	VWGVGIAPS	617	1.9000	22.89
6	VFRANRAEV	179	1.8000	21.69
7	VAYIMKTDH	436	1.7800	21.45
8	IIFNLPATV	246	1.7000	20.48
9	LAPVRPLER	488	1.7000	20.48
10	VEASVTIAS	570	1.7000	20.48
11	INGVETEIS	519	1.6000	19.28
12	IVHFYNSTS	164	1.5000	18.07
13	VGIAPSITT	620	1.5000	18.07
14	LVTLGLNLF	323	1.4000	16.87
15	VEYCNQLPV	351	1.4000	16.87
16	VVSAVNRAA	634	1.3000	15.66
17	IQVLTQCRP	139	1.2000	14.46
18	LSLPRRLQI	446	1.2000	14.46
19	VKPAGPPRV	19	1.1500	13.86
20	VIDRAPLWC	66	1.1000	13.25
21	FDLLVRMGY	98	1.1000	13.25
22	IEWMSRNLA	266	1.1000	13.25
23	LNLFSRGVD	328	1.1000	13.25
24	LRAVVSAVN	631	1.1000	13.25
25	IRLRNRTWP	55	0.9000	10.84
26	FYNSTSILQ	167	0.9000	10.84
27	ILSLHPHND	280	0.9000	10.84
28	VTLGLNLFS	324	0.9000	10.84
29	WRFEYSPES	210	0.8500	10.24
30	IRVNSQSGK	425	0.8000	9.64
31	VKINGVETE	517	0.8000	9.64
32	IMKTDHGLS	439	0.7000	8.43
33	VTIASPAQP	574	0.7000	8.43
34	VTIASPAQP	593	0.7000	8.43
35	IERTFQACS	150	0.6000	7.23

36	YNSTSILQR	168	0.6000	7.23
37	YLPIDPRDV	409	0.6000	7.23
38	YEAVIRVNS	421	0.6000	7.23
39	VLTQCRPEL	141	0.5500	6.63
40	MSPARKRRM	89	0.5000	6.02
41	ITATVKING	513	0.5000	6.02
42	VYTAFSGSH	370	0.4800	5.78
43	MFDLLVRMG	97	0.4000	4.82
44	FRANRAEVQ	180	0.4000	4.82
45	LVYTAFSGS	369	0.3000	3.61
46	IQKIAEGTA	460	0.3000	3.61
47	LAAFVHALA	534	0.3000	3.61
48	IDPMSPARK	86	0.2000	2.41
49	VRMGYKEIE	102	0.2000	2.41
50	VQAIATDGA	187	0.2000	2.41
51	VEPIRLRNR	52	0.1000	1.20
52	LWQVPYLPI	404	0.1000	1.20
53	VSAVNRAAR	635	0.1000	1.20
54	ILQRRVVFR	173	-0.1000	0
55	VAVLDYYEH	548	-0.1200	0
56	VILSLHPHN	279	-0.1500	0
57	VAAAELGFA	293	-0.2000	0
58	VCLVTLGLN	321	-0.2000	0
59	YVEASVTIA	569	-0.2000	0
60	VTSKTVWGV	612	-0.2000	0

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	VRPLERIRQ	491	5.9000	71.08
2	LQRRVVFRA	174	2.0000	24.10
3	LVRMGYKEI	101	1.9000	22.89
4	IEFSQVIQK	454	1.9000	22.89

5	VWGVGIAPS	617	1.9000	22.89
6	VFRANRAEV	179	1.8000	21.69
7	VAYIMKTDH	436	1.7800	21.45
8	IIFNLPATV	246	1.7000	20.48
9	LAPVRPLER	488	1.7000	20.48
10	VEASVTIAS	570	1.7000	20.48
11	INGVETEIS	519	1.6000	19.28
12	IVHFYNSTS	164	1.5000	18.07
13	VGIAPSITT	620	1.5000	18.07
14	LVTLGLNLF	323	1.4000	16.87
15	VEYCNQLPV	351	1.4000	16.87
16	VVSAVNRAA	634	1.3000	15.66
17	IQVLTQCRP	139	1.2000	14.46
18	LSLPRRLQI	446	1.2000	14.46
19	VKPAGPPRV	19	1.1500	13.86
20	VIDRAPLWC	66	1.1000	13.25
21	FDLLVRMGY	98	1.1000	13.25
22	IEWMSRNLA	266	1.1000	13.25
23	LNLFSRGVD	328	1.1000	13.25
24	LRAVVSAVN	631	1.1000	13.25
25	IRLRNRTWP	55	0.9000	10.84
26	FYNSTSILQ	167	0.9000	10.84
27	ILSLHPHND	280	0.9000	10.84
28	VTLGLNLFS	324	0.9000	10.84
29	WRFEYSPES	210	0.8500	10.24
30	IRVNSQSGK	425	0.8000	9.64
31	VKINGVETE	517	0.8000	9.64
32	IMKTDHGLS	439	0.7000	8.43
33	VTIASPAQP	574	0.7000	8.43
34	VTIASPAQP	593	0.7000	8.43
35	IERTFQACS	150	0.6000	7.23
36	YNSTSILQR	168	0.6000	7.23
37	YLPIDPRDV	409	0.6000	7.23
38	YEAVIRVNS	421	0.6000	7.23

39	VLTQCRPEL	141	0.5500	6.63
40	MSPARKRRM	89	0.5000	6.02
41	ITATVKING	513	0.5000	6.02
42	VYTAFSGSH	370	0.4800	5.78
43	MFDLLVRMG	97	0.4000	4.82
44	FRANRAEVQ	180	0.4000	4.82
45	LVYTAFSGS	369	0.3000	3.61
46	IQKIAEGTA	460	0.3000	3.61
47	LAAFVHALA	534	0.3000	3.61
48	IDPMSPARK	86	0.2000	2.41
49	VRMGYKEIE	102	0.2000	2.41
50	VQAIATDGA	187	0.2000	2.41
51	VEPIRLRNR	52	0.1000	1.20
52	LWQVPYLPI	404	0.1000	1.20
53	VSAVNRAAR	635	0.1000	1.20
54	ILQRRVVFR	173	-0.1000	0
55	VAVLDYYEH	548	-0.1200	0
56	VILSLHPHN	279	-0.1500	0
57	VAAAELGFA	293	-0.2000	0
58	VCLVTLGLN	321	-0.2000	0
59	YVEASVTIA	569	-0.2000	0
60	VTSKTVWGV	612	-0.2000	0

ALLELE: DRB1_1107	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 9.1

Rank	Sequence	At Position	Score	% of Highest Score
1	VRPLERIRQ	491	4.4000	48.35
2	VRMGYKEIE	102	3.5000	38.46
3	VYADSIEWM	261	3.3000	36.26
4	YGGDLVYTA	365	3.1500	34.62
5	IEFSQVIQK	454	2.9000	31.87
6	LPIDPRDVG	410	2.7000	29.67
7	VEASVTIAS	570	2.7000	29.67

8	LQRRVVFRA	174	2.6000	28.57
9	VAYIMKTDH	436	2.5800	28.35
10	IAPSITTAS	622	2.4000	26.37
11	IEVGFPSAS	109	2.3700	26.04
12	IRVNSQSGK	425	2.3700	26.04
13	WRFEYSPES	210	2.3000	25.27
14	INGVETEIS	519	2.3000	25.27
15	VKINGVETE	517	2.1000	23.08
16	VGFDVAVLD	544	2.1000	23.08
17	VILSLHPHN	279	2.0000	21.98
18	VKPAGPPRV	19	1.9000	20.88
19	FYNSTSILQ	167	1.9000	20.88
20	VQAIATDGA	187	1.9000	20.88
21	IIFNLPATV	246	1.9000	20.88
22	MKTDHGLSL	440	1.9000	20.88
23	IRLRNRTWP	55	1.8000	19.78
24	VFRANRAEV	179	1.8000	19.78
25	VTLGLNLFS	324	1.8000	19.78
26	VLTQCRPEL	141	1.7000	18.68
27	FRANRAEVQ	180	1.7000	18.68
28	VTIQVLTQC	137	1.6000	17.58
29	VWGVGIAPS	617	1.5000	16.48
30	IVHFYNSTS	164	1.4700	16.15
31	IATDGARKC	190	1.4000	15.38
32	VTTSESPDA	0	1.3000	14.29
33	LVYTAFSGS	369	1.2700	13.96
34	LVTLGLNLF	323	1.2100	13.30
35	LQIEFSQVI	452	1.2000	13.19
36	LFSRGVDPQ	330	1.1000	12.09
37	VGIAPSITT	620	1.1000	12.09
38	IEWMSRNLA	266	1.0100	11.10
39	IPDDVTIQV	133	1.0000	10.99
40	YEAVIRVNS	421	1.0000	10.99
41	YVEASVTIA	569	1.0000	10.99

42	VYTAFSGSH	370	0.9800	10.77
43	WGVGIAPSI	618	0.9000	9.89
44	LRDGNQALI	78	0.8000	8.79
45	IMKTDHGLS	439	0.8000	8.79
46	VVSAVNRAA	634	0.8000	8.79
47	VTIASPAQP	574	0.7000	7.69
48	VTIASPAQP	593	0.7000	7.69
49	LRAVVSAVN	631	0.7000	7.69
50	VIRVNSQSG	424	0.6000	6.59
51	LSLPRRLQI	446	0.6000	6.59
52	ILQRRVVFR	173	0.4000	4.40
53	FNLPATVEM	248	0.4000	4.40
54	IQKIAEGTA	460	0.4000	4.40
55	VEQAAKYPG	199	0.3500	3.85
56	FVREIIEQG	123	0.3000	3.30
57	IEQGAIPDD	128	0.3000	3.30
58	VAAAELGFA	293	0.3000	3.30
59	MKLDADAAD	389	0.3000	3.30
60	LVRMGYKEI	101	0.2000	2.20
61	IERTFQACS	150	0.2000	2.20
62	LNLFSRGVD	328	0.2000	2.20
63	MLWQVPYLP	403	0.1500	1.65
64	IVKPAGPPR	18	0.1000	1.10

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	LQRRVVFRA	174	2.9000	34.52
2	VRPLERIRQ	491	2.9000	34.52
3	WRFEYSPES	210	2.0000	23.81
4	VVSAVNRAA	634	1.9000	22.62
5	FRANRAEVQ	180	1.8000	21.43
6	YLPIDPRDV	409	1.7000	20.24

7	FGAHTIVKP	13	1.3000	15.48
8	IVHFYNSTS	164	1.3000	15.48
9	IRLRNRTWP	55	1.2000	14.29
10	YVEASVTIA	569	1.2000	14.29
11	MSPARKRRM	89	1.1000	13.10
12	VVFRANRAE	178	1.0000	11.90
13	IEWMSRNLA	266	1.0000	11.90
14	LVRMGYKEI	101	0.9000	10.71
15	VTSKTVWGV	612	0.9000	10.71
16	VFRANRAEV	179	0.8000	9.52
17	IIFNLPATV	246	0.8000	9.52
18	LVTLGLNLF	323	0.8000	9.52
19	LPVHERHPY	357	0.8000	9.52
20	YEAVIRVNS	421	0.8000	9.52
21	FYNSTSILQ	167	0.7000	8.33
22	WMSRNLANR	268	0.7000	8.33
23	FNLPATVEM	248	0.6000	7.14
24	WNPQRASSM	32	0.4000	4.76
25	FVREIIEQG	123	0.4000	4.76
26	VTIQVLTQC	137	0.4000	4.76
27	LFSRGVDPQ	330	0.4000	4.76
28	VNRYRPFAE	42	0.3000	3.57
29	MFDLLVRMG	97	0.3000	3.57
30	ILQRRVVFR	173	0.3000	3.57
31	YGGDLVYTA	365	0.3000	3.57
32	IRVNSQSGK	425	0.3000	3.57
33	LSLHPHNDR	281	0.2000	2.38
34	YIMKTDHGL	438	0.2000	2.38
35	VKINGVETE	517	0.2000	2.38
36	FDLLVRMGY	98	0.1000	1.19
37	VLTQCRPEL	141	0.1000	1.19
38	VIDRAPLWC	66	-0.1000	0
39	MGYKEIEVG	104	-0.2000	0
40	YCNQLPVHE	353	-0.2000	0

41	LQIEFSQVI	452	-0.2000	0
42	FVHALADVG	537	-0.2000	0
43	VKPAGPPRV	19	-0.3000	0
44	VRMGYKEIE	102	-0.3000	0
45	VHFYNSTSI	165	-0.3000	0
46	ILSLHPHND	280	-0.3000	0
47	YTAFSGSHQ	371	-0.3000	0
48	IEFSQVIQK	454	-0.3000	0
49	LAAFVHALA	534	-0.3000	0
50	VTIASPAQP	574	-0.3000	0
51	VTIASPAQP	593	-0.3000	0
52	ITTASLRAV	626	-0.3000	0
53	VAYIMKTDH	436	-0.3200	0
54	MLWQVPYLP	403	-0.4000	0
55	INGVETEIS	519	-0.4000	0
56	VWGVGIAPS	617	-0.4000	0
57	WCAVDLRDG	73	-0.5000	0
58	IQVLTQCRP	139	-0.5000	0
59	FQACSGAPR	154	-0.5000	0
60	LDYYEHAMS	551	-0.5000	0
61	VEASVTIAS	570	-0.5000	0
62	LNLFSRGVD	328	-0.6000	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	LQRRVVFRA	174	2.9000	32.95
2	LVTLGLNLF	323	2.7000	30.68
3	YLPIDPRDV	409	2.7000	30.68
4	MSPARKRRM	89	2.6000	29.55
5	VVFRANRAE	178	2.4000	27.27
6	WRFEYSPES	210	2.4000	27.27
7	FGAHTIVKP	13	2.3000	26.14

8	IRLRNRTWP	55	2.2000	25.00
9	WMSRNLANR	268	2.2000	25.00
10	VRPLERIRQ	491	2.2000	25.00
11	FNLPATVEM	248	2.1000	23.86
12	LPVHERHPY	357	2.1000	23.86
13	WNPQRASSM	32	1.9000	21.59
14	VTSKTVWGV	612	1.9000	21.59
15	VVSAVNRAA	634	1.9000	21.59
16	LVRMGYKEI	101	1.8000	20.45
17	FVREIIEQG	123	1.8000	20.45
18	ILQRRVVFR	173	1.8000	20.45
19	VFRANRAEV	179	1.8000	20.45
20	IIFNLPATV	246	1.8000	20.45
21	VNRYRPFAE	42	1.7000	19.32
22	MFDLLVRMG	97	1.7000	19.32
23	IVHFYNSTS	164	1.7000	19.32
24	LSLHPHNDR	281	1.7000	19.32
25	VKINGVETE	517	1.6000	18.18
26	YNSTSILQR	168	1.5000	17.05
27	FDLLVRMGY	98	1.4000	15.91
28	MGYKEIEVG	104	1.2000	13.64
29	YCNQLPVHE	353	1.2000	13.64
30	YEAVIRVNS	421	1.2000	13.64
31	FVHALADVG	537	1.2000	13.64
32	YVEASVTIA	569	1.2000	13.64
33	YIMKTDHGL	438	1.1600	13.18
34	VRMGYKEIE	102	1.1000	12.50
35	FRANRAEVQ	180	1.1000	12.50
36	VLTQCRPEL	141	1.0600	12.05
37	FQACSGAPR	154	1.0000	11.36
38	IEWMSRNLA	266	1.0000	11.36
39	WCAVDLRDG	73	0.9000	10.23
40	ILSLHPHND	280	0.8000	9.09
41	VKPAGPPRV	19	0.7000	7.95

42	VEPIRLRNR	52	0.7000	7.95
43	LQIEFSQVI	452	0.7000	7.95
44	VTIASPAQP	574	0.7000	7.95
45	VTIASPAQP	593	0.7000	7.95
46	ITTASLRAV	626	0.7000	7.95
47	YRPFAEEVE	45	0.6000	6.82
48	VHFYNSTSI	165	0.6000	6.82
49	VEQAAKYPG	199	0.6000	6.82
50	MLWQVPYLP	403	0.6000	6.82
51	LRNRTWPDR	57	0.5000	5.68
52	IQVLTQCRP	139	0.5000	5.68
53	LNLFSRGVD	328	0.5000	5.68
54	VTIQVLTQC	137	0.4000	4.55
55	IRVNSQSGK	425	0.4000	4.55
56	VEMTTPNVY	254	0.3000	3.41
57	LFGNGERTG	311	0.3000	3.41
58	VEYCNQLPV	351	0.3000	3.41
59	YGGDLVYTA	365	0.3000	3.41
60	VNSQSGKGG	427	0.3000	3.41
61	LSLPRRLQI	446	0.2000	2.27
62	LGFAAGADR	298	0.1000	1.14

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	LQRRVVFRA	174	3.9000	46.43
2	VRPLERIRQ	491	3.9000	46.43
3	VVSAVNRAA	634	2.9000	34.52
4	IVHFYNSTS	164	2.3000	27.38
5	IRLRNRTWP	55	2.2000	26.19
6	MSPARKRRM	89	2.1000	25.00
7	VVFRANRAE	178	2.0000	23.81
8	IEWMSRNLA	266	2.0000	23.81

9	LVRMGYKEI	101	1.9000	22.62
10	VTSKTVWGV	612	1.9000	22.62
11	VFRANRAEV	179	1.8000	21.43
12	IIFNLPATV	246	1.8000	21.43
13	LVTLGLNLF	323	1.8000	21.43
14	LPVHERHPY	357	1.8000	21.43
15	VTIQVLTQC	137	1.4000	16.67
16	LFSRGVDPQ	330	1.4000	16.67
17	VNRYRPFAE	42	1.3000	15.48
18	MFDLLVRMG	97	1.3000	15.48
19	ILQRRVVFR	173	1.3000	15.48
20	IRVNSQSGK	425	1.3000	15.48
21	LSLHPHNDR	281	1.2000	14.29
22	VKINGVETE	517	1.2000	14.29
23	VLTQCRPEL	141	1.1000	13.10
24	WRFEYSPES	210	1.0000	11.90
25	VIDRAPLWC	66	0.9000	10.71
26	MGYKEIEVG	104	0.8000	9.52
27	FRANRAEVQ	180	0.8000	9.52
28	LQIEFSQVI	452	0.8000	9.52
29	VKPAGPPRV	19	0.7000	8.33
30	VRMGYKEIE	102	0.7000	8.33
31	VHFYNSTSI	165	0.7000	8.33
32	ILSLHPHND	280	0.7000	8.33
33	YLPIDPRDV	409	0.7000	8.33
34	IEFSQVIQK	454	0.7000	8.33
35	LAAFVHALA	534	0.7000	8.33
36	VTIASPAQP	574	0.7000	8.33
37	VTIASPAQP	593	0.7000	8.33
38	ITTASLRAV	626	0.7000	8.33
39	VAYIMKTDH	436	0.6800	8.10
40	MLWQVPYLP	403	0.6000	7.14
41	INGVETEIS	519	0.6000	7.14
42	VWGVGIAPS	617	0.6000	7.14

43	IQVLTQCRP	139	0.5000	5.95
44	LDYYEHAMS	551	0.5000	5.95
45	VEASVTIAS	570	0.5000	5.95
46	LNLFSRGVD	328	0.4000	4.76
47	FGAHTIVKP	13	0.3000	3.57
48	VEYCNQLPV	351	0.3000	3.57
49	LSLPRRLQI	446	0.3000	3.57
50	VSPKEMWDA	474	0.3000	3.57
51	IAPSITTAS	622	0.3000	3.57
52	VEPIRLRNR	52	0.2000	2.38
53	VEQAAKYPG	199	0.2000	2.38
54	LHPHNDRGT	283	0.2000	2.38
55	LVYTAFSGS	369	0.2000	2.38
56	YVEASVTIA	569	0.2000	2.38
57	VGIAPSITT	620	0.2000	2.38
58	IERTFQACS	150	0.1000	1.19

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VRPLERIRQ	491	4.2000	48.28
2	FDLLVRMGY	98	3.4000	39.08
3	YNSTSILQR	168	3.1000	35.63
4	YLPIDPRDV	409	2.6000	29.89
5	LVTLGLNLF	323	2.3000	26.44
6	WRFEYSPES	210	2.2500	25.86
7	LAPVRPLER	488	2.2000	25.29
8	YEAVIRVNS	421	2.0000	22.99
9	LVRMGYKEI	101	1.8000	20.69
10	VFRANRAEV	179	1.8000	20.69
11	IIFNLPATV	246	1.7000	19.54
12	FNLPATVEM	248	1.4000	16.09
13	VEYCNQLPV	351	1.4000	16.09

14	YKEIEVGFP	106	1.3000	14.94
15	WMSRNLANR	268	1.3000	14.94
16	VWGVGIAPS	617	1.3000	14.94
17	IQVLTQCRP	139	1.2000	13.79
18	FYNSTSILQ	167	1.2000	13.79
19	LNLFSRGVD	328	1.2000	13.79
20	VKINGVETE	517	1.2000	13.79
21	VGIAPSITT	620	1.2000	13.79
22	VKPAGPPRV	19	1.1500	13.22
23	LSLPRRLQI	446	1.1000	12.64
24	VEASVTIAS	570	1.1000	12.64
25	MSPARKRRM	89	1.0000	11.49
26	FQACSGAPR	154	1.0000	11.49
27	LQRRVVFRA	174	1.0000	11.49
28	ILSLHPHND	280	1.0000	11.49
29	FSNIDEIRR	341	1.0000	11.49
30	IEFSQVIQK	454	1.0000	11.49
31	INGVETEIS	519	1.0000	11.49
32	IRLRNRTWP	55	0.9000	10.34
33	FVREIIEQG	123	0.9000	10.34
34	IVHFYNSTS	164	0.9000	10.34
35	ITATVKING	513	0.9000	10.34
36	LRAVVSAVN	631	0.9000	10.34
37	MFDLLVRMG	97	0.8000	9.20
38	YVEASVTIA	569	0.8000	9.20
39	FRANRAEVQ	180	0.7000	8.05
40	VTIASPAQP	574	0.7000	8.05
41	VTIASPAQP	593	0.7000	8.05
42	VEPIRLRNR	52	0.6000	6.90
43	WCAVDLRDG	73	0.6000	6.90
44	VRMGYKEIE	102	0.6000	6.90
45	VSAVNRAAR	635	0.6000	6.90
46	VLTQCRPEL	141	0.5100	5.86
47	WNPQRASSM	32	0.5000	5.75

48	ILQRRVVFR	173	0.4000	4.60
49	VEQAAKYPG	199	0.4000	4.60
50	VIRVNSQSG	424	0.4000	4.60
51	VTLGLNLFS	324	0.3000	3.45
52	VVSAVNRAA	634	0.3000	3.45
53	VAYIMKTDH	436	0.2000	2.30
54	VIDRAPLWC	66	0.1000	1.15
55	IEWMSRNLA	266	0.1000	1.15
56	LGFAAGADR	298	0.1000	1.15
57	IMKTDHGLS	439	0.1000	1.15
58	LRNRTWPDR	57	0.0500	0.57
59	YLAPVRPLE	487	-0.0500	0
60	YRPFAEEVE	45	-0.1000	0

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	LQRRVVFRA	174	3.9000	44.32
2	LVTLGLNLF	323	3.7000	42.05
3	MSPARKRRM	89	3.6000	40.91
4	VVFRANRAE	178	3.4000	38.64
5	IRLRNRTWP	55	3.2000	36.36
6	VRPLERIRQ	491	3.2000	36.36
7	LPVHERHPY	357	3.1000	35.23
8	VTSKTVWGV	612	2.9000	32.95
9	VVSAVNRAA	634	2.9000	32.95
10	LVRMGYKEI	101	2.8000	31.82
11	ILQRRVVFR	173	2.8000	31.82
12	VFRANRAEV	179	2.8000	31.82
13	IIFNLPATV	246	2.8000	31.82
14	VNRYRPFAE	42	2.7000	30.68
15	MFDLLVRMG	97	2.7000	30.68
16	IVHFYNSTS	164	2.7000	30.68

17	LSLHPHNDR	281	2.7000	30.68
18	VKINGVETE	517	2.6000	29.55
19	MGYKEIEVG	104	2.2000	25.00
20	VRMGYKEIE	102	2.1000	23.86
21	VLTQCRPEL	141	2.0600	23.41
22	IEWMSRNLA	266	2.0000	22.73
23	ILSLHPHND	280	1.8000	20.45
24	VKPAGPPRV	19	1.7000	19.32
25	VEPIRLRNR	52	1.7000	19.32
26	YLPIDPRDV	409	1.7000	19.32
27	LQIEFSQVI	452	1.7000	19.32
28	VTIASPAQP	574	1.7000	19.32
29	VTIASPAQP	593	1.7000	19.32
30	ITTASLRAV	626	1.7000	19.32
31	VHFYNSTSI	165	1.6000	18.18
32	VEQAAKYPG	199	1.6000	18.18
33	MLWQVPYLP	403	1.6000	18.18
34	LRNRTWPDR	57	1.5000	17.05
35	IQVLTQCRP	139	1.5000	17.05
36	LNLFSRGVD	328	1.5000	17.05
37	VTIQVLTQC	137	1.4000	15.91
38	WRFEYSPES	210	1.4000	15.91
39	IRVNSQSGK	425	1.4000	15.91
40	FGAHTIVKP	13	1.3000	14.77
41	VEMTTPNVY	254	1.3000	14.77
42	LFGNGERTG	311	1.3000	14.77
43	VEYCNQLPV	351	1.3000	14.77
44	VNSQSGKGG	427	1.3000	14.77
45	WMSRNLANR	268	1.2000	13.64
46	LSLPRRLQI	446	1.2000	13.64
47	FNLPATVEM	248	1.1000	12.50
48	LGFAAGADR	298	1.1000	12.50
49	INGVETEIS	519	1.0000	11.36
50	VWGVGIAPS	617	1.0000	11.36

51	WNPQRASSM	32	0.9000	10.23
52	VIDRAPLWC	66	0.9000	10.23
53	LHPHNDRGT	283	0.9000	10.23
54	LDYYEHAMS	551	0.9000	10.23
55	VEASVTIAS	570	0.9000	10.23
56	VGIAPSITT	620	0.9000	10.23
57	MPVNRYRPF	40	0.8000	9.09
58	FVREIIEQG	123	0.8000	9.09
59	VIRVNSQSG	424	0.8000	9.09
60	IEFSQVIQK	454	0.8000	9.09
61	LAPVRPLER	488	0.8000	9.09
62	LFSRGVDPQ	330	0.7000	7.95
63	IRQHVDAAD	497	0.7000	7.95
64	LAAFVHALA	534	0.7000	7.95

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	LQRRVVFRA	174	2.9000	32.95
2	LVTLGLNLF	323	2.7000	30.68
3	YLPIDPRDV	409	2.7000	30.68
4	MSPARKRRM	89	2.6000	29.55
5	VVFRANRAE	178	2.4000	27.27
6	WRFEYSPES	210	2.4000	27.27
7	FGAHTIVKP	13	2.3000	26.14
8	IRLRNRTWP	55	2.2000	25.00
9	WMSRNLANR	268	2.2000	25.00
10	VRPLERIRQ	491	2.2000	25.00
11	FNLPATVEM	248	2.1000	23.86
12	LPVHERHPY	357	2.1000	23.86
13	WNPQRASSM	32	1.9000	21.59
14	VTSKTVWGV	612	1.9000	21.59
15	VVSAVNRAA	634	1.9000	21.59

16	LVRMGYKEI	101	1.8000	20.45
17	FVREIIEQG	123	1.8000	20.45
18	ILQRRVVFR	173	1.8000	20.45
19	VFRANRAEV	179	1.8000	20.45
20	IIFNLPATV	246	1.8000	20.45
21	VNRYRPFAE	42	1.7000	19.32
22	MFDLLVRMG	97	1.7000	19.32
23	IVHFYNSTS	164	1.7000	19.32
24	LSLHPHNDR	281	1.7000	19.32
25	VKINGVETE	517	1.6000	18.18
26	YNSTSILQR	168	1.5000	17.05
27	FDLLVRMGY	98	1.4000	15.91
28	MGYKEIEVG	104	1.2000	13.64
29	YCNQLPVHE	353	1.2000	13.64
30	YEAVIRVNS	421	1.2000	13.64
31	FVHALADVG	537	1.2000	13.64
32	YVEASVTIA	569	1.2000	13.64
33	YIMKTDHGL	438	1.1600	13.18
34	VRMGYKEIE	102	1.1000	12.50
35	FRANRAEVQ	180	1.1000	12.50
36	VLTQCRPEL	141	1.0600	12.05
37	FQACSGAPR	154	1.0000	11.36
38	IEWMSRNLA	266	1.0000	11.36
39	WCAVDLRDG	73	0.9000	10.23
40	ILSLHPHND	280	0.8000	9.09
41	VKPAGPPRV	19	0.7000	7.95
42	VEPIRLRNR	52	0.7000	7.95
43	LQIEFSQVI	452	0.7000	7.95
44	VTIASPAQP	574	0.7000	7.95
45	VTIASPAQP	593	0.7000	7.95
46	ITTASLRAV	626	0.7000	7.95
47	YRPFAEEVE	45	0.6000	6.82
48	VHFYNSTSI	165	0.6000	6.82
49	VEQAAKYPG	199	0.6000	6.82

50	MLWQVPYLP	403	0.6000	6.82
51	LRNRTWPDR	57	0.5000	5.68
52	IQVLTQCRP	139	0.5000	5.68
53	LNLFSRGVD	328	0.5000	5.68
54	VTIQVLTQC	137	0.4000	4.55
55	IRVNSQSGK	425	0.4000	4.55
56	VEMTTPNVY	254	0.3000	3.41
57	LFGNGERTG	311	0.3000	3.41
58	VEYCNQLPV	351	0.3000	3.41
59	YGGDLVYTA	365	0.3000	3.41
60	VNSQSGKGG	427	0.3000	3.41
61	LSLPRRLQI	446	0.2000	2.27
62	LGFAAGADR	298	0.1000	1.14

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	VVFRANRAE	178	5.0000	55.56
2	VRPLERIRQ	491	4.7000	52.22
3	VNRYRPFAE	42	4.3000	47.78
4	VKINGVETE	517	4.2000	46.67
5	LQRRVVFRA	174	3.9000	43.33
6	VRMGYKEIE	102	3.7000	41.11
7	ILSLHPHND	280	3.4000	37.78
8	MSPARKRRM	89	3.2000	35.56
9	LNLFSRGVD	328	3.1000	34.44
10	LPVHERHPY	357	2.9000	32.22
11	VVSAVNRAA	634	2.9000	32.22
12	LVTLGLNLF	323	2.7000	30.00
13	IRLRNRTWP	55	2.6000	28.89
14	MFDLLVRMG	97	2.6000	28.89
15	IVHFYNSTS	164	2.3000	25.56
16	IRQHVDAAD	497	2.3000	25.56

17	LFSRGVDPQ	330	2.2000	24.44
18	VTSKTVWGV	612	2.2000	24.44
19	LLVRMGYKE	100	2.1000	23.33
20	LVRMGYKEI	101	2.1000	23.33
21	MGYKEIEVG	104	2.1000	23.33
22	VLTQCRPEL	141	2.1000	23.33
23	VFRANRAEV	179	2.1000	23.33
24	IIFNLPATV	246	2.1000	23.33
25	IFNLPATVE	247	2.1000	23.33
26	IEWMSRNLA	266	2.0000	22.22
27	MSRNLANRE	269	1.9000	21.11
28	VAYIMKTDH	436	1.9000	21.11
29	YCNQLPVHE	353	1.8000	20.00
30	LRAVVSAVN	631	1.8000	20.00
31	FRANRAEVQ	180	1.6000	17.78
32	VEQAAKYPG	199	1.5000	16.67
33	LEYAKQVCD	224	1.5000	16.67
34	VILSLHPHN	279	1.5000	16.67
35	VTIQVLTQC	137	1.4000	15.56
36	ILQRRVVFR	173	1.3000	14.44
37	YRPFAEEVE	45	1.2000	13.33
38	LSLHPHNDR	281	1.2000	13.33
39	LFGNGERTG	311	1.2000	13.33
40	VNSQSGKGG	427	1.2000	13.33
41	LERIRQHVD	494	1.2000	13.33
42	VEMTTPNVY	254	1.1000	12.22
43	LHPHNDRGT	283	1.1000	12.22
44	VTIASPAQP	574	1.1000	12.22
45	VTIASPAQP	593	1.1000	12.22
46	VGIAPSITT	620	1.1000	12.22
47	VKPAGPPRV	19	1.0000	11.11
48	IIEQGAIPD	127	1.0000	11.11
49	WRFEYSPES	210	1.0000	11.11
50	MLWQVPYLP	403	1.0000	11.11

51	YLPIDPRDV	409	1.0000	11.11
52	LQIEFSQVI	452	1.0000	11.11
53	ITTASLRAV	626	1.0000	11.11
54	VIDRAPLWC	66	0.9000	10.00
55	IQVLTQCRP	139	0.9000	10.00
56	VHFYNSTSI	165	0.9000	10.00
57	IRRTVEYCN	347	0.8000	8.89
58	VGFDVAVLD	544	0.8000	8.89
59	FGAHTIVKP	13	0.7000	7.78
60	FVREIIEQG	123	0.7000	7.78
61	FNLPATVEM	248	0.7000	7.78
62	VIRVNSQSG	424	0.7000	7.78
63	LAAFVHALA	534	0.7000	7.78
64	VEYCNQLPV	351	0.6000	6.67

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	VRPLERIRQ	491	4.2000	48.28
2	FDLLVRMGY	98	3.4000	39.08
3	YNSTSILQR	168	3.1000	35.63
4	YLPIDPRDV	409	2.6000	29.89
5	LVTLGLNLF	323	2.3000	26.44
6	WRFEYSPES	210	2.2500	25.86
7	LAPVRPLER	488	2.2000	25.29
8	YEAVIRVNS	421	2.0000	22.99
9	LVRMGYKEI	101	1.8000	20.69
10	VFRANRAEV	179	1.8000	20.69
11	IIFNLPATV	246	1.7000	19.54
12	FNLPATVEM	248	1.4000	16.09
13	VEYCNQLPV	351	1.4000	16.09
14	YKEIEVGFP	106	1.3000	14.94
15	WMSRNLANR	268	1.3000	14.94

16	VWGVGIAPS	617	1.3000	14.94
17	IQVLTQCRP	139	1.2000	13.79
18	FYNSTSILQ	167	1.2000	13.79
19	LNLFSRGVD	328	1.2000	13.79
20	VKINGVETE	517	1.2000	13.79
21	VGIAPSITT	620	1.2000	13.79
22	VKPAGPPRV	19	1.1500	13.22
23	LSLPRRLQI	446	1.1000	12.64
24	VEASVTIAS	570	1.1000	12.64
25	MSPARKRRM	89	1.0000	11.49
26	FQACSGAPR	154	1.0000	11.49
27	LQRRVVFRA	174	1.0000	11.49
28	ILSLHPHND	280	1.0000	11.49
29	FSNIDEIRR	341	1.0000	11.49
30	IEFSQVIQK	454	1.0000	11.49
31	INGVETEIS	519	1.0000	11.49
32	IRLRNRTWP	55	0.9000	10.34
33	FVREIIEQG	123	0.9000	10.34
34	IVHFYNSTS	164	0.9000	10.34
35	ITATVKING	513	0.9000	10.34
36	LRAVVSAVN	631	0.9000	10.34
37	MFDLLVRMG	97	0.8000	9.20
38	YVEASVTIA	569	0.8000	9.20
39	FRANRAEVQ	180	0.7000	8.05
40	VTIASPAQP	574	0.7000	8.05
41	VTIASPAQP	593	0.7000	8.05
42	VEPIRLRNR	52	0.6000	6.90
43	WCAVDLRDG	73	0.6000	6.90
44	VRMGYKEIE	102	0.6000	6.90
45	VSAVNRAAR	635	0.6000	6.90
46	VLTQCRPEL	141	0.5100	5.86
47	WNPQRASSM	32	0.5000	5.75
48	ILQRRVVFR	173	0.4000	4.60
49	VEQAAKYPG	199	0.4000	4.60

50	VIRVNSQSG	424	0.4000	4.60
51	VTLGLNLFS	324	0.3000	3.45
52	VVSAVNRAA	634	0.3000	3.45
53	VAYIMKTDH	436	0.2000	2.30
54	VIDRAPLWC	66	0.1000	1.15
55	IEWMSRNLA	266	0.1000	1.15
56	LGFAAGADR	298	0.1000	1.15
57	IMKTDHGLS	439	0.1000	1.15
58	LRNRTWPDR	57	0.0500	0.57
59	YLAPVRPLE	487	-0.0500	0
60	YRPFAEEVE	45	-0.1000	0

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	VRPLERIRQ	491	3.3000	48.53
2	YLPIDPRDV	409	1.4000	20.59
3	YEAVIRVNS	421	1.1000	16.18
4	VWGVGIAPS	617	0.9000	13.24
5	VFRANRAEV	179	0.8000	11.76
6	WRFEYSPES	210	0.7000	10.29
7	IIFNLPATV	246	0.7000	10.29
8	FDLLVRMGY	98	0.5000	7.35
9	IVHFYNSTS	164	0.5000	7.35
10	LQRRVVFRA	174	0.5000	7.35
11	LVRMGYKEI	101	0.3000	4.41
12	FYNSTSILQ	167	0.3000	4.41
13	FRANRAEVQ	180	0.3000	4.41
14	YKEIEVGFP	106	0.2000	2.94
15	IQVLTQCRP	139	0.2000	2.94
16	LVTLGLNLF	323	0.1000	1.47
17	LRAVVSAVN	631	0.1000	1.47
18	VVSAVNRAA	634	0.1000	1.47

19	YNSTSILQR	168	-0.2000	0
20	IEWMSRNLA	266	-0.2000	0
21	WMSRNLANR	268	-0.2000	0
22	IRVNSQSGK	425	-0.2000	0
23	YVEASVTIA	569	-0.3000	0
24	VTIASPAQP	574	-0.3000	0
25	VTIASPAQP	593	-0.3000	0
26	VAYIMKTDH	436	-0.3200	0
27	IERTFQACS	150	-0.4000	0
28	IMKTDHGLS	439	-0.4000	0
29	FQACSGAPR	154	-0.5000	0
30	VQAIATDGA	187	-0.5000	0
31	INGVETEIS	519	-0.5000	0
32	FNLPATVEM	248	-0.6000	0
33	VYTAFSGSH	370	-0.6200	0
34	MSPARKRRM	89	-0.7000	0
35	LVYTAFSGS	369	-0.7000	0
36	IEFSQVIQK	454	-0.7000	0
37	LAAFVHALA	534	-0.7000	0
38	IDPMSPARK	86	-0.8000	0
39	MFDLLVRMG	97	-0.8000	0
40	ILSLHPHND	280	-0.8000	0
41	IQKIAEGTA	460	-0.8000	0
42	YGGDLVYTA	365	-0.9000	0
43	VEASVTIAS	570	-0.9000	0
44	VSAVNRAAR	635	-0.9000	0
45	VKPAGPPRV	19	-1.0000	0
46	WNPQRASSM	32	-1.0000	0
47	WCAVDLRDG	73	-1.0000	0
48	FSQVIQKIA	456	-1.0000	0
49	VEPIRLRNR	52	-1.1000	0
50	YTAFSGSHQ	371	-1.1000	0
51	VIRVNSQSG	424	-1.1000	0
52	LAPVRPLER	488	-1.1000	0

53	FVHALADVG	537	-1.1000	0
54	VGIAPSITT	620	-1.1000	0
55	IRLRNRTWP	55	-1.2000	0
56	VAAAELGFA	293	-1.3000	0
57	VCLVTLGLN	321	-1.3000	0
58	VKINGVETE	517	-1.3000	0
59	LGFAAGADR	298	-1.4000	0
60	LFSRGVDPQ	330	-1.4000	0
61	VEYCNQLPV	351	-1.4000	0
62	YEHAMSAGD	554	-1.5000	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	VRPLERIRQ	491	5.9000	71.08
2	LQRRVVFRA	174	2.0000	24.10
3	LVRMGYKEI	101	1.9000	22.89
4	IEFSQVIQK	454	1.9000	22.89
5	VWGVGIAPS	617	1.9000	22.89
6	VFRANRAEV	179	1.8000	21.69
7	VAYIMKTDH	436	1.7800	21.45
8	IIFNLPATV	246	1.7000	20.48
9	LAPVRPLER	488	1.7000	20.48
10	VEASVTIAS	570	1.7000	20.48
11	INGVETEIS	519	1.6000	19.28
12	IVHFYNSTS	164	1.5000	18.07
13	VGIAPSITT	620	1.5000	18.07
14	LVTLGLNLF	323	1.4000	16.87
15	VEYCNQLPV	351	1.4000	16.87
16	VVSAVNRAA	634	1.3000	15.66
17	IQVLTQCRP	139	1.2000	14.46
18	LSLPRRLQI	446	1.2000	14.46
19	VKPAGPPRV	19	1.1500	13.86

20	VIDRAPLWC	66	1.1000	13.25
21	FDLLVRMGY	98	1.1000	13.25
22	IEWMSRNLA	266	1.1000	13.25
23	LNLFSRGVD	328	1.1000	13.25
24	LRAVVSAVN	631	1.1000	13.25
25	IRLRNRTWP	55	0.9000	10.84
26	FYNSTSILQ	167	0.9000	10.84
27	ILSLHPHND	280	0.9000	10.84
28	VTLGLNLFS	324	0.9000	10.84
29	WRFEYSPES	210	0.8500	10.24
30	IRVNSQSGK	425	0.8000	9.64
31	VKINGVETE	517	0.8000	9.64
32	IMKTDHGLS	439	0.7000	8.43
33	VTIASPAQP	574	0.7000	8.43
34	VTIASPAQP	593	0.7000	8.43
35	IERTFQACS	150	0.6000	7.23
36	YNSTSILQR	168	0.6000	7.23
37	YLPIDPRDV	409	0.6000	7.23
38	YEAVIRVNS	421	0.6000	7.23
39	VLTQCRPEL	141	0.5500	6.63
40	MSPARKRRM	89	0.5000	6.02
41	ITATVKING	513	0.5000	6.02
42	VYTAFSGSH	370	0.4800	5.78
43	MFDLLVRMG	97	0.4000	4.82
44	FRANRAEVQ	180	0.4000	4.82
45	LVYTAFSGS	369	0.3000	3.61
46	IQKIAEGTA	460	0.3000	3.61
47	LAAFVHALA	534	0.3000	3.61
48	IDPMSPARK	86	0.2000	2.41
49	VRMGYKEIE	102	0.2000	2.41
50	VQAIATDGA	187	0.2000	2.41
51	VEPIRLRNR	52	0.1000	1.20
52	LWQVPYLPI	404	0.1000	1.20
53	VSAVNRAAR	635	0.1000	1.20

54	ILQRRVVFR	173	-0.1000	0
55	VAVLDYYEH	548	-0.1200	0
56	VILSLHPHN	279	-0.1500	0
57	VAAAELGFA	293	-0.2000	0
58	VCLVTLGLN	321	-0.2000	0
59	YVEASVTIA	569	-0.2000	0
60	VTSKTVWGV	612	-0.2000	0

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	VRPLERIRQ	491	5.7000	64.04
2	FDLLVRMGY	98	3.2000	35.96
3	LNLFSRGVD	328	2.8000	31.46
4	VKINGVETE	517	2.8000	31.46
5	FYNSTSILQ	167	2.7000	30.34
6	ILSLHPHND	280	2.6000	29.21
7	VRMGYKEIE	102	2.2000	24.72
8	FRANRAEVQ	180	2.2000	24.72
9	LRAVVSAVN	631	2.1000	23.60
10	VAYIMKTDH	436	2.0000	22.47
11	YLPIDPRDV	409	1.9000	21.35
12	WRFEYSPES	210	1.8500	20.79
13	YNSTSILQR	168	1.6000	17.98
14	YEAVIRVNS	421	1.6000	17.98
15	YLAPVRPLE	487	1.5500	17.42
16	YRPFAEEVE	45	1.5000	16.85
17	VVFRANRAE	178	1.5000	16.85
18	IFNLPATVE	247	1.4000	15.73
19	VGIAPSITT	620	1.4000	15.73
20	LVTLGLNLF	323	1.3000	14.61
21	YCNQLPVHE	353	1.3000	14.61
22	VNRYRPFAE	42	1.2000	13.48

23	LERIRQHVD	494	1.2000	13.48
24	YEHAMSAGD	554	1.2000	13.48
25	WQVPYLPID	405	1.1500	12.92
26	LVRMGYKEI	101	1.1000	12.36
27	VFRANRAEV	179	1.1000	12.36
28	LQRRVVFRA	174	1.0000	11.24
29	IIFNLPATV	246	1.0000	11.24
30	FNLPATVEM	248	1.0000	11.24
31	VWGVGIAPS	617	0.9000	10.11
32	VILSLHPHN	279	0.8500	9.55
33	FVREIIEQG	123	0.8000	8.99
34	VCLVTLGLN	321	0.8000	8.99
35	ITATVKING	513	0.8000	8.99
36	YVEASVTIA	569	0.8000	8.99
37	MFDLLVRMG	97	0.7000	7.87
38	YKEIEVGFP	106	0.7000	7.87
39	VEYCNQLPV	351	0.7000	7.87
40	VYTAFSGSH	370	0.7000	7.87
41	LAPVRPLER	488	0.7000	7.87
42	VEASVTIAS	570	0.7000	7.87
43	MSPARKRRM	89	0.6000	6.74
44	FDFVREIIE	121	0.6000	6.74
45	IQVLTQCRP	139	0.6000	6.74
46	INGVETEIS	519	0.6000	6.74
47	VLTQCRPEL	141	0.5500	6.18
48	WCAVDLRDG	73	0.5000	5.62
49	IVHFYNSTS	164	0.5000	5.62
50	VKPAGPPRV	19	0.4500	5.06
51	LSLPRRLQI	446	0.4000	4.49
52	IRLRNRTWP	55	0.3000	3.37
53	IIEQGAIPD	127	0.3000	3.37
54	VEQAAKYPG	199	0.3000	3.37
55	VIRVNSQSG	424	0.3000	3.37
56	VVSAVNRAA	634	0.3000	3.37

57	IEFSQVIQK	454	0.2000	2.25
58	WNPQRASSM	32	0.1000	1.12
59	VIDRAPLWC	66	0.1000	1.12
60	IEWMSRNLA	266	0.1000	1.12
61	IRRTVEYCN	347	0.1000	1.12
62	VAVLDYYEH	548	0.1000	1.12
63	VTIASPAQP	574	0.1000	1.12
64	VTIASPAQP	593	0.1000	1.12

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	LQRRVVFRA	174	3.9000	46.43
2	VRPLERIRQ	491	3.9000	46.43
3	VVSAVNRAA	634	2.9000	34.52
4	IVHFYNSTS	164	2.3000	27.38
5	IRLRNRTWP	55	2.2000	26.19
6	MSPARKRRM	89	2.1000	25.00
7	VVFRANRAE	178	2.0000	23.81
8	IEWMSRNLA	266	2.0000	23.81
9	LVRMGYKEI	101	1.9000	22.62
10	VTSKTVWGV	612	1.9000	22.62
11	VFRANRAEV	179	1.8000	21.43
12	IIFNLPATV	246	1.8000	21.43
13	LVTLGLNLF	323	1.8000	21.43
14	LPVHERHPY	357	1.8000	21.43
15	VTIQVLTQC	137	1.4000	16.67
16	LFSRGVDPQ	330	1.4000	16.67
17	VNRYRPFAE	42	1.3000	15.48
18	MFDLLVRMG	97	1.3000	15.48
19	ILQRRVVFR	173	1.3000	15.48
20	IRVNSQSGK	425	1.3000	15.48
21	LSLHPHNDR	281	1.2000	14.29

22	VKINGVETE	517	1.2000	14.29
23	VLTQCRPEL	141	1.1000	13.10
24	WRFEYSPES	210	1.0000	11.90
25	VIDRAPLWC	66	0.9000	10.71
26	MGYKEIEVG	104	0.8000	9.52
27	FRANRAEVQ	180	0.8000	9.52
28	LQIEFSQVI	452	0.8000	9.52
29	VKPAGPPRV	19	0.7000	8.33
30	VRMGYKEIE	102	0.7000	8.33
31	VHFYNSTSI	165	0.7000	8.33
32	ILSLHPHND	280	0.7000	8.33
33	YLPIDPRDV	409	0.7000	8.33
34	IEFSQVIQK	454	0.7000	8.33
35	LAAFVHALA	534	0.7000	8.33
36	VTIASPAQP	574	0.7000	8.33
37	VTIASPAQP	593	0.7000	8.33
38	ITTASLRAV	626	0.7000	8.33
39	VAYIMKTDH	436	0.6800	8.10
40	MLWQVPYLP	403	0.6000	7.14
41	INGVETEIS	519	0.6000	7.14
42	VWGVGIAPS	617	0.6000	7.14
43	IQVLTQCRP	139	0.5000	5.95
44	LDYYEHAMS	551	0.5000	5.95
45	VEASVTIAS	570	0.5000	5.95
46	LNLFSRGVD	328	0.4000	4.76
47	FGAHTIVKP	13	0.3000	3.57
48	VEYCNQLPV	351	0.3000	3.57
49	LSLPRRLQI	446	0.3000	3.57
50	VSPKEMWDA	474	0.3000	3.57
51	IAPSITTAS	622	0.3000	3.57
52	VEPIRLRNR	52	0.2000	2.38
53	VEQAAKYPG	199	0.2000	2.38
54	LHPHNDRGT	283	0.2000	2.38
55	LVYTAFSGS	369	0.2000	2.38

56	YVEASVTIA	569	0.2000	2.38
57	VGIAPSITT	620	0.2000	2.38
58	IERTFQACS	150	0.1000	1.19

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LQRRVVFRA	174	2.9000	34.52
2	VRPLERIRQ	491	2.9000	34.52
3	WRFEYSPES	210	2.0000	23.81
4	VVSAVNRAA	634	1.9000	22.62
5	FRANRAEVQ	180	1.8000	21.43
6	YLPIDPRDV	409	1.7000	20.24
7	FGAHTIVKP	13	1.3000	15.48
8	IVHFYNSTS	164	1.3000	15.48
9	IRLRNRTWP	55	1.2000	14.29
10	YVEASVTIA	569	1.2000	14.29
11	MSPARKRRM	89	1.1000	13.10
12	VVFRANRAE	178	1.0000	11.90
13	IEWMSRNLA	266	1.0000	11.90
14	LVRMGYKEI	101	0.9000	10.71
15	VTSKTVWGV	612	0.9000	10.71
16	VFRANRAEV	179	0.8000	9.52
17	IIFNLPATV	246	0.8000	9.52
18	LVTLGLNLF	323	0.8000	9.52
19	LPVHERHPY	357	0.8000	9.52
20	YEAVIRVNS	421	0.8000	9.52
21	FYNSTSILQ	167	0.7000	8.33
22	WMSRNLANR	268	0.7000	8.33
23	FNLPATVEM	248	0.6000	7.14
24	WNPQRASSM	32	0.4000	4.76
25	FVREIIEQG	123	0.4000	4.76
26	VTIQVLTQC	137	0.4000	4.76

27	LFSRGVDPQ	330	0.4000	4.76
28	VNRYRPFAE	42	0.3000	3.57
29	MFDLLVRMG	97	0.3000	3.57
30	ILQRRVVFR	173	0.3000	3.57
31	YGGDLVYTA	365	0.3000	3.57
32	IRVNSQSGK	425	0.3000	3.57
33	LSLHPHNDR	281	0.2000	2.38
34	YIMKTDHGL	438	0.2000	2.38
35	VKINGVETE	517	0.2000	2.38
36	FDLLVRMGY	98	0.1000	1.19
37	VLTQCRPEL	141	0.1000	1.19
38	VIDRAPLWC	66	-0.1000	0
39	MGYKEIEVG	104	-0.2000	0
40	YCNQLPVHE	353	-0.2000	0
41	LQIEFSQVI	452	-0.2000	0
42	FVHALADVG	537	-0.2000	0
43	VKPAGPPRV	19	-0.3000	0
44	VRMGYKEIE	102	-0.3000	0
45	VHFYNSTSI	165	-0.3000	0
46	ILSLHPHND	280	-0.3000	0
47	YTAFSGSHQ	371	-0.3000	0
48	IEFSQVIQK	454	-0.3000	0
49	LAAFVHALA	534	-0.3000	0
50	VTIASPAQP	574	-0.3000	0
51	VTIASPAQP	593	-0.3000	0
52	ITTASLRAV	626	-0.3000	0
53	VAYIMKTDH	436	-0.3200	0
54	MLWQVPYLP	403	-0.4000	0
55	INGVETEIS	519	-0.4000	0
56	VWGVGIAPS	617	-0.4000	0
57	WCAVDLRDG	73	-0.5000	0
58	IQVLTQCRP	139	-0.5000	0
59	FQACSGAPR	154	-0.5000	0
60	LDYYEHAMS	551	-0.5000	0

61	VEASVTIAS	570	-0.5000	0
62	LNLFSRGVD	328	-0.6000	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	LQRRVVFRA	174	3.9000	44.32
2	LVTLGLNLF	323	3.7000	42.05
3	MSPARKRRM	89	3.6000	40.91
4	VVFRANRAE	178	3.4000	38.64
5	IRLRNRTWP	55	3.2000	36.36
6	VRPLERIRQ	491	3.2000	36.36
7	LPVHERHPY	357	3.1000	35.23
8	VTSKTVWGV	612	2.9000	32.95
9	VVSAVNRAA	634	2.9000	32.95
10	LVRMGYKEI	101	2.8000	31.82
11	ILQRRVVFR	173	2.8000	31.82
12	VFRANRAEV	179	2.8000	31.82
13	IIFNLPATV	246	2.8000	31.82
14	VNRYRPFAE	42	2.7000	30.68
15	MFDLLVRMG	97	2.7000	30.68
16	IVHFYNSTS	164	2.7000	30.68
17	LSLHPHNDR	281	2.7000	30.68
18	VKINGVETE	517	2.6000	29.55
19	MGYKEIEVG	104	2.2000	25.00
20	VRMGYKEIE	102	2.1000	23.86
21	VLTQCRPEL	141	2.0600	23.41
22	IEWMSRNLA	266	2.0000	22.73
23	ILSLHPHND	280	1.8000	20.45
24	VKPAGPPRV	19	1.7000	19.32
25	VEPIRLRNR	52	1.7000	19.32
26	YLPIDPRDV	409	1.7000	19.32
27	LQIEFSQVI	452	1.7000	19.32

28	VTIASPAQP	574	1.7000	19.32
29	VTIASPAQP	593	1.7000	19.32
30	ITTASLRAV	626	1.7000	19.32
31	VHFYNSTSI	165	1.6000	18.18
32	VEQAAKYPG	199	1.6000	18.18
33	MLWQVPYLP	403	1.6000	18.18
34	LRNRTWPDR	57	1.5000	17.05
35	IQVLTQCRP	139	1.5000	17.05
36	LNLFSRGVD	328	1.5000	17.05
37	VTIQVLTQC	137	1.4000	15.91
38	WRFEYSPES	210	1.4000	15.91
39	IRVNSQSGK	425	1.4000	15.91
40	FGAHTIVKP	13	1.3000	14.77
41	VEMTTPNVY	254	1.3000	14.77
42	LFGNGERTG	311	1.3000	14.77
43	VEYCNQLPV	351	1.3000	14.77
44	VNSQSGKGG	427	1.3000	14.77
45	WMSRNLANR	268	1.2000	13.64
46	LSLPRRLQI	446	1.2000	13.64
47	FNLPATVEM	248	1.1000	12.50
48	LGFAAGADR	298	1.1000	12.50
49	INGVETEIS	519	1.0000	11.36
50	VWGVGIAPS	617	1.0000	11.36
51	WNPQRASSM	32	0.9000	10.23
52	VIDRAPLWC	66	0.9000	10.23
53	LHPHNDRGT	283	0.9000	10.23
54	LDYYEHAMS	551	0.9000	10.23
55	VEASVTIAS	570	0.9000	10.23
56	VGIAPSITT	620	0.9000	10.23
57	MPVNRYRPF	40	0.8000	9.09
58	FVREIIEQG	123	0.8000	9.09
59	VIRVNSQSG	424	0.8000	9.09
60	IEFSQVIQK	454	0.8000	9.09
61	LAPVRPLER	488	0.8000	9.09

62	LFSRGVDPQ	330	0.7000	7.95
63	IRQHVDAAD	497	0.7000	7.95
64	LAAFVHALA	534	0.7000	7.95

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	LQRRVVFRA	174	3.9000	44.32
2	LVTLGLNLF	323	3.7000	42.05
3	MSPARKRRM	89	3.6000	40.91
4	VVFRANRAE	178	3.4000	38.64
5	IRLRNRTWP	55	3.2000	36.36
6	VRPLERIRQ	491	3.2000	36.36
7	LPVHERHPY	357	3.1000	35.23
8	VTSKTVWGV	612	2.9000	32.95
9	VVSAVNRAA	634	2.9000	32.95
10	LVRMGYKEI	101	2.8000	31.82
11	ILQRRVVFR	173	2.8000	31.82
12	VFRANRAEV	179	2.8000	31.82
13	IIFNLPATV	246	2.8000	31.82
14	VNRYRPFAE	42	2.7000	30.68
15	MFDLLVRMG	97	2.7000	30.68
16	IVHFYNSTS	164	2.7000	30.68
17	LSLHPHNDR	281	2.7000	30.68
18	VKINGVETE	517	2.6000	29.55
19	MGYKEIEVG	104	2.2000	25.00
20	VRMGYKEIE	102	2.1000	23.86
21	VLTQCRPEL	141	2.0600	23.41
22	IEWMSRNLA	266	2.0000	22.73
23	ILSLHPHND	280	1.8000	20.45
24	VKPAGPPRV	19	1.7000	19.32
25	VEPIRLRNR	52	1.7000	19.32
26	YLPIDPRDV	409	1.7000	19.32

27	LQIEFSQVI	452	1.7000	19.32
28	VTIASPAQP	574	1.7000	19.32
29	VTIASPAQP	593	1.7000	19.32
30	ITTASLRAV	626	1.7000	19.32
31	VHFYNSTSI	165	1.6000	18.18
32	VEQAAKYPG	199	1.6000	18.18
33	MLWQVPYLP	403	1.6000	18.18
34	LRNRTWPDR	57	1.5000	17.05
35	IQVLTQCRP	139	1.5000	17.05
36	LNLFSRGVD	328	1.5000	17.05
37	VTIQVLTQC	137	1.4000	15.91
38	WRFEYSPES	210	1.4000	15.91
39	IRVNSQSGK	425	1.4000	15.91
40	FGAHTIVKP	13	1.3000	14.77
41	VEMTTPNVY	254	1.3000	14.77
42	LFGNGERTG	311	1.3000	14.77
43	VEYCNQLPV	351	1.3000	14.77
44	VNSQSGKGG	427	1.3000	14.77
45	WMSRNLANR	268	1.2000	13.64
46	LSLPRRLQI	446	1.2000	13.64
47	FNLPATVEM	248	1.1000	12.50
48	LGFAAGADR	298	1.1000	12.50
49	INGVETEIS	519	1.0000	11.36
50	VWGVGIAPS	617	1.0000	11.36
51	WNPQRASSM	32	0.9000	10.23
52	VIDRAPLWC	66	0.9000	10.23
53	LHPHNDRGT	283	0.9000	10.23
54	LDYYEHAMS	551	0.9000	10.23
55	VEASVTIAS	570	0.9000	10.23
56	VGIAPSITT	620	0.9000	10.23
57	MPVNRYRPF	40	0.8000	9.09
58	FVREIIEQG	123	0.8000	9.09
59	VIRVNSQSG	424	0.8000	9.09
60	IEFSQVIQK	454	0.8000	9.09

61	LAPVRPLER	488	0.8000	9.09
62	LFSRGVDPQ	330	0.7000	7.95
63	IRQHVDAAD	497	0.7000	7.95
64	LAAFVHALA	534	0.7000	7.95

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	VHFYNSTSI	165	5.6000	57.14
2	IVHFYNSTS	164	5.4000	55.10
3	LVRMGYKEI	101	4.6000	46.94
4	LSLPRRLQI	446	4.0000	40.82
5	VRPLERIRQ	491	3.9000	39.80
6	VGIAPSITT	620	3.9000	39.80
7	MKTDHGLSL	440	3.6000	36.73
8	IRLRNRTWP	55	3.5000	35.71
9	VNRYRPFAE	42	3.3000	33.67
10	VTLGLNLFS	324	3.3000	33.67
11	LNLFSRGVD	328	3.3000	33.67
12	LQRRVVFRA	174	3.2000	32.65
13	LVTLGLNLF	323	3.1000	31.63
14	LWQVPYLPI	404	3.1000	31.63
15	LQIEFSQVI	452	3.1000	31.63
16	VFRANRAEV	179	2.8000	28.57
17	IEWMSRNLA	266	2.8000	28.57
18	VVSAVNRAA	634	2.5000	25.51
19	VEYCNQLPV	351	2.3000	23.47
20	LVYTAFSGS	369	2.3000	23.47
21	LANRESVIL	273	2.1000	21.43
22	VLTQCRPEL	141	2.0000	20.41
23	WRFEYSPES	210	2.0000	20.41
24	LAAFVHALA	534	1.9000	19.39
25	VLDYYEHAM	550	1.8800	19.18

26	VKPAGPPRV	19	1.8000	18.37
27	LRNRTWPDR	57	1.8000	18.37
28	IIFNLPATV	246	1.8000	18.37
29	LPVHERHPY	357	1.8000	18.37
30	LRAVVSAVN	631	1.8000	18.37
31	VIDRAPLWC	66	1.7000	17.35
32	IVKPAGPPR	18	1.6000	16.33
33	VIRVNSQSG	424	1.5000	15.31
34	YIMKTDHGL	438	1.5000	15.31
35	VVFRANRAE	178	1.4000	14.29
36	LAPVRPLER	488	1.2000	12.24
37	LDYYEHAMS	551	1.2000	12.24
38	VDLRDGNQA	76	1.1000	11.22
39	VGFPSASQT	111	1.1000	11.22
40	VTIQVLTQC	137	1.1000	11.22
41	LHPHNDRGT	283	1.1000	11.22
42	IRRTVEYCN	347	1.1000	11.22
43	VQAIATDGA	187	1.0600	10.82
44	FDLLVRMGY	98	1.0000	10.20
45	LLVRMGYKE	100	1.0000	10.20
46	LSLHPHNDR	281	1.0000	10.20
47	IRQHVDAAD	497	1.0000	10.20
48	VAVLDYYEH	548	1.0000	10.20
49	WGVGIAPSI	618	1.0000	10.20
50	VEASVTIAS	570	0.9600	9.80
51	FNLPATVEM	248	0.8400	8.57
52	LRDGNQALI	78	0.8000	8.16
53	VEMTTPNVY	254	0.8000	8.16
54	LGFAAGADR	298	0.8000	8.16
55	IQKIAEGTA	460	0.8000	8.16
56	ISGSGNGPL	526	0.8000	8.16
57	VHALADVGF	538	0.8000	8.16
58	VRMGYKEIE	102	0.7000	7.14
59	LPRRLQIEF	448	0.7000	7.14

60	YNSTSILQR	168	0.6500	6.63
61	VTTSESPDA	0	0.6000	6.12
62	FYNSTSILQ	167	0.6000	6.12
63	YTAFSGSHQ	371	0.6000	6.12
64	VGRTYEAVI	417	0.6000	6.12

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	VHFYNSTSI	165	4.6000	46.94
2	IVHFYNSTS	164	4.4000	44.90
3	LVRMGYKEI	101	3.6000	36.73
4	WRFEYSPES	210	3.0000	30.61
5	LSLPRRLQI	446	3.0000	30.61
6	VRPLERIRQ	491	2.9000	29.59
7	VGIAPSITT	620	2.9000	29.59
8	MKTDHGLSL	440	2.6000	26.53
9	IRLRNRTWP	55	2.5000	25.51
10	YIMKTDHGL	438	2.5000	25.51
11	VNRYRPFAE	42	2.3000	23.47
12	VTLGLNLFS	324	2.3000	23.47
13	LNLFSRGVD	328	2.3000	23.47
14	LQRRVVFRA	174	2.2000	22.45
15	LVTLGLNLF	323	2.1000	21.43
16	LWQVPYLPI	404	2.1000	21.43
17	LQIEFSQVI	452	2.1000	21.43
18	FDLLVRMGY	98	2.0000	20.41
19	WGVGIAPSI	618	2.0000	20.41
20	FNLPATVEM	248	1.8400	18.78
21	VFRANRAEV	179	1.8000	18.37
22	IEWMSRNLA	266	1.8000	18.37
23	YNSTSILQR	168	1.6500	16.84
24	FYNSTSILQ	167	1.6000	16.33

25	YTAFSGSHQ	371	1.6000	16.33
26	YLPIDPRDV	409	1.5000	15.31
27	VVSAVNRAA	634	1.5000	15.31
28	YRPFAEEVE	45	1.3000	13.27
29	VEYCNQLPV	351	1.3000	13.27
30	LVYTAFSGS	369	1.3000	13.27
31	YEAVIRVNS	421	1.3000	13.27
32	LANRESVIL	273	1.1000	11.22
33	VLTQCRPEL	141	1.0000	10.20
34	FGNGERTGN	312	1.0000	10.20
35	FSRGVDPQI	331	1.0000	10.20
36	LAAFVHALA	534	0.9000	9.18
37	VLDYYEHAM	550	0.8800	8.98
38	FGAHTIVKP	13	0.8500	8.67
39	VKPAGPPRV	19	0.8000	8.16
40	LRNRTWPDR	57	0.8000	8.16
41	IIFNLPATV	246	0.8000	8.16
42	LPVHERHPY	357	0.8000	8.16
43	FVHALADVG	537	0.8000	8.16
44	YVEASVTIA	569	0.8000	8.16
45	LRAVVSAVN	631	0.8000	8.16
46	FVREIIEQG	123	0.7500	7.65
47	VIDRAPLWC	66	0.7000	7.14
48	FQACSGAPR	154	0.7000	7.14
49	WMSRNLANR	268	0.7000	7.14
50	YGGDLVYTA	365	0.7000	7.14
51	WNPQRASSM	32	0.6800	6.94
52	IVKPAGPPR	18	0.6000	6.12
53	VIRVNSQSG	424	0.5000	5.10
54	VVFRANRAE	178	0.4000	4.08
55	YYEHAMSAG	553	0.4000	4.08
56	FSNIDEIRR	341	0.3000	3.06
57	LAPVRPLER	488	0.2000	2.04
58	LDYYEHAMS	551	0.2000	2.04

59	VDLRDGNQA	76	0.1000	1.02
60	VGFPSASQT	111	0.1000	1.02
61	VTIQVLTQC	137	0.1000	1.02
62	LHPHNDRGT	283	0.1000	1.02
63	IRRTVEYCN	347	0.1000	1.02
64	YLAPVRPLE	487	0.1000	1.02

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	VHFYNSTSI	165	5.6000	57.14
2	IVHFYNSTS	164	5.4000	55.10
3	LVRMGYKEI	101	4.6000	46.94
4	LSLPRRLQI	446	4.0000	40.82
5	VRPLERIRQ	491	3.9000	39.80
6	VGIAPSITT	620	3.9000	39.80
7	MKTDHGLSL	440	3.6000	36.73
8	IRLRNRTWP	55	3.5000	35.71
9	VNRYRPFAE	42	3.3000	33.67
10	VTLGLNLFS	324	3.3000	33.67
11	LNLFSRGVD	328	3.3000	33.67
12	LQRRVVFRA	174	3.2000	32.65
13	LVTLGLNLF	323	3.1000	31.63
14	LWQVPYLPI	404	3.1000	31.63
15	LQIEFSQVI	452	3.1000	31.63
16	VFRANRAEV	179	2.8000	28.57
17	IEWMSRNLA	266	2.8000	28.57
18	VVSAVNRAA	634	2.5000	25.51
19	VEYCNQLPV	351	2.3000	23.47
20	LVYTAFSGS	369	2.3000	23.47
21	LANRESVIL	273	2.1000	21.43
22	VLTQCRPEL	141	2.0000	20.41
23	WRFEYSPES	210	2.0000	20.41

24	LAAFVHALA	534	1.9000	19.39
25	VLDYYEHAM	550	1.8800	19.18
26	VKPAGPPRV	19	1.8000	18.37
27	LRNRTWPDR	57	1.8000	18.37
28	IIFNLPATV	246	1.8000	18.37
29	LPVHERHPY	357	1.8000	18.37
30	LRAVVSAVN	631	1.8000	18.37
31	VIDRAPLWC	66	1.7000	17.35
32	IVKPAGPPR	18	1.6000	16.33
33	VIRVNSQSG	424	1.5000	15.31
34	YIMKTDHGL	438	1.5000	15.31
35	VVFRANRAE	178	1.4000	14.29
36	LAPVRPLER	488	1.2000	12.24
37	LDYYEHAMS	551	1.2000	12.24
38	VDLRDGNQA	76	1.1000	11.22
39	VGFPSASQT	111	1.1000	11.22
40	VTIQVLTQC	137	1.1000	11.22
41	LHPHNDRGT	283	1.1000	11.22
42	IRRTVEYCN	347	1.1000	11.22
43	VQAIATDGA	187	1.0600	10.82
44	FDLLVRMGY	98	1.0000	10.20
45	LLVRMGYKE	100	1.0000	10.20
46	LSLHPHNDR	281	1.0000	10.20
47	IRQHVDAAD	497	1.0000	10.20
48	VAVLDYYEH	548	1.0000	10.20
49	WGVGIAPSI	618	1.0000	10.20
50	VEASVTIAS	570	0.9600	9.80
51	FNLPATVEM	248	0.8400	8.57
52	LRDGNQALI	78	0.8000	8.16
53	VEMTTPNVY	254	0.8000	8.16
54	LGFAAGADR	298	0.8000	8.16
55	IQKIAEGTA	460	0.8000	8.16
56	ISGSGNGPL	526	0.8000	8.16
57	VHALADVGF	538	0.8000	8.16

58	VRMGYKEIE	102	0.7000	7.14
59	LPRRLQIEF	448	0.7000	7.14
60	YNSTSILQR	168	0.6500	6.63
61	VTTSESPDA	0	0.6000	6.12
62	FYNSTSILQ	167	0.6000	6.12
63	YTAFSGSHQ	371	0.6000	6.12
64	VGRTYEAVI	417	0.6000	6.12

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	LVRMGYKEI	101	4.6000	46.94
2	YLPIDPRDV	409	3.9000	39.80
3	LAPVRPLER	488	3.7000	37.76
4	VEPIRLRNR	52	3.5000	35.71
5	FQACSGAPR	154	3.4000	34.69
6	FSNIDEIRR	341	3.2000	32.65
7	YNSTSILQR	168	3.0000	30.61
8	VEMTTPNVY	254	2.8000	28.57
9	VRPLERIRQ	491	2.7000	27.55
10	IDPMSPARK	86	2.6000	26.53
11	LGFAAGADR	298	2.5000	25.51
12	VIRVNSQSG	424	2.5000	25.51
13	LVTLGLNLF	323	2.4000	24.49
14	FYNSTSILQ	167	2.3000	23.47
15	IEFSQVIQK	454	2.0000	20.41
16	WCAVDLRDG	73	1.8000	18.37
17	LQIEFSQVI	452	1.8000	18.37
18	LRAVVSAVN	631	1.8000	18.37
19	VGIAPSITT	620	1.5000	15.31
20	IRRTVEYCN	347	1.4000	14.29
21	WRFEYSPES	210	1.3000	13.27
22	YIMKTDHGL	438	1.3000	13.27

23	VAVLDYYEH	548	1.3000	13.27
24	VVSAVNRAA	634	1.3000	13.27
25	IVKPAGPPR	18	1.2000	12.24
26	FVHALADVG	537	1.2000	12.24
27	WMSRNLANR	268	1.1000	11.22
28	IRVNSQSGK	425	1.1000	11.22
29	VNRYRPFAE	42	1.0000	10.20
30	VHFYNSTSI	165	1.0000	10.20
31	LVYTAFSGS	369	1.0000	10.20
32	VYTAFSGSH	370	1.0000	10.20
33	VSAVNRAAR	635	1.0000	10.20
34	VAYIMKTDH	436	0.9000	9.18
35	LWQVPYLPI	404	0.8000	8.16
36	WNPQRASSM	32	0.7000	7.14
37	FDLLVRMGY	98	0.7000	7.14
38	ILSLHPHND	280	0.7000	7.14
39	VCLVTLGLN	321	0.7000	7.14
40	IFNLPATVE	247	0.6000	6.12
41	IMKTDHGLS	439	0.5000	5.10
42	FRANRAEVQ	180	0.3000	3.06
43	YEAVIRVNS	421	0.3000	3.06
44	VNSQSGKGG	427	0.3000	3.06
45	FSQVIQKIA	456	0.3000	3.06
46	LRNRTWPDR	57	0.2000	2.04
47	IAPTPERPI	238	0.1000	1.02
48	LSLHPHNDR	281	0.1000	1.02
49	IQKIAEGTA	460	0.1000	1.02
50	INGVETEIS	519	0.1000	1.02
51	IVHFYNSTS	164	-0.1000	0
52	MLWQVPYLP	403	-0.1000	0
53	YVEASVTIA	569	-0.1000	0
54	VTIASPAQP	574	-0.1000	0
55	VTIASPAQP	593	-0.1000	0
56	VKPAGPPRV	19	-0.2000	0

57	FPSASQTDF	113	-0.2000	0
58	MKTDHGLSL	440	-0.2000	0
59	YKEIEVGFP	106	-0.3000	0
60	FNLPATVEM	248	-0.3000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVRMGYKEI	101	4.6000	46.94
2	YLPIDPRDV	409	3.9000	39.80
3	LAPVRPLER	488	3.7000	37.76
4	VEPIRLRNR	52	3.5000	35.71
5	FQACSGAPR	154	3.4000	34.69
6	FSNIDEIRR	341	3.2000	32.65
7	YNSTSILQR	168	3.0000	30.61
8	VEMTTPNVY	254	2.8000	28.57
9	VRPLERIRQ	491	2.7000	27.55
10	IDPMSPARK	86	2.6000	26.53
11	LGFAAGADR	298	2.5000	25.51
12	VIRVNSQSG	424	2.5000	25.51
13	LVTLGLNLF	323	2.4000	24.49
14	FYNSTSILQ	167	2.3000	23.47
15	IEFSQVIQK	454	2.0000	20.41
16	WCAVDLRDG	73	1.8000	18.37
17	LQIEFSQVI	452	1.8000	18.37
18	LRAVVSAVN	631	1.8000	18.37
19	VGIAPSITT	620	1.5000	15.31
20	IRRTVEYCN	347	1.4000	14.29
21	WRFEYSPES	210	1.3000	13.27
22	YIMKTDHGL	438	1.3000	13.27
23	VAVLDYYEH	548	1.3000	13.27
24	VVSAVNRAA	634	1.3000	13.27
25	IVKPAGPPR	18	1.2000	12.24

26	FVHALADVG	537	1.2000	12.24
27	WMSRNLANR	268	1.1000	11.22
28	IRVNSQSGK	425	1.1000	11.22
29	VNRYRPFAE	42	1.0000	10.20
30	VHFYNSTSI	165	1.0000	10.20
31	LVYTAFSGS	369	1.0000	10.20
32	VYTAFSGSH	370	1.0000	10.20
33	VSAVNRAAR	635	1.0000	10.20
34	VAYIMKTDH	436	0.9000	9.18
35	LWQVPYLPI	404	0.8000	8.16
36	WNPQRASSM	32	0.7000	7.14
37	FDLLVRMGY	98	0.7000	7.14
38	ILSLHPHND	280	0.7000	7.14
39	VCLVTLGLN	321	0.7000	7.14
40	IFNLPATVE	247	0.6000	6.12
41	IMKTDHGLS	439	0.5000	5.10
42	FRANRAEVQ	180	0.3000	3.06
43	YEAVIRVNS	421	0.3000	3.06
44	VNSQSGKGG	427	0.3000	3.06
45	FSQVIQKIA	456	0.3000	3.06
46	LRNRTWPDR	57	0.2000	2.04
47	IAPTPERPI	238	0.1000	1.02
48	LSLHPHNDR	281	0.1000	1.02
49	IQKIAEGTA	460	0.1000	1.02
50	INGVETEIS	519	0.1000	1.02
51	IVHFYNSTS	164	-0.1000	0
52	MLWQVPYLP	403	-0.1000	0
53	YVEASVTIA	569	-0.1000	0
54	VTIASPAQP	574	-0.1000	0
55	VTIASPAQP	593	-0.1000	0
56	VKPAGPPRV	19	-0.2000	0
57	FPSASQTDF	113	-0.2000	0
58	MKTDHGLSL	440	-0.2000	0
59	YKEIEVGFP	106	-0.3000	0

60	FNLPATVEM	248	-0.3000	0