MHC Class-II Binding Peptide Prediction Results

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INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Sun Feb 14 16:17:06 2010
Length of input sequence	575 amino acids
Number of nanomers from input sequence	567
Number of nanomers with obligatory P1 anchor residue	173
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	57

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	YVKLVSSAA	560	2.2000	36.67
2	VLRALANPI	383	1.5000	25.00
3	FENAIAVVM	276	1.3800	23.00
4	VTIIDAFEA	177	1.3000	21.67
5	LVSSAAVGA	563	1.3000	21.67
6	VVMAFGGST	282	0.9000	15.00
7	ITILHGSLA	397	0.9000	15.00
8	VKLVSSAAV	561	0.7500	12.50

9	VFSAGGYPL	78	0.7000	11.67
10	FLYAGSILP	156	0.7000	11.67
11	VLHLLAIAH	293	0.6000	10.00
12	MREMLAITG	462	0.6000	10.00
13	WNEITPCNL	57	0.4000	6.67
14	IHPSGGITI	391	0.4000	6.67
15	IRYEGPKGG	451	0.4000	6.67
16	LRNGDRIRL	514	0.3000	5.00
17	ITVGDAVVI	443	0.2000	3.33
18	LLHGDCLTV	354	0.1000	1.67
19	LRALANPIH	384	-0.0300	0
20	VVKTAGFDS	410	-0.2000	0
21	VVELLRRGI	257	-0.2100	0
22	VFLYAGSIL	155	-0.3000	0
23	VGHIAPEAV	498	-0.3000	0
24	YPLEFGTIS	84	-0.4100	0
25	MLMAAARLD	143	-0.4100	0
26	LLLTDGRFS	482	-0.5100	0
27	FGGSTNAVL	286	-0.6000	0
28	LAITGAIKG	466	-0.7000	0
29	LEKAAARGM	27	-0.7300	0
30	LMAAARLDL	144	-0.9000	0
31	ILPGRAKLS	162	-0.9000	0
32	VDHIGGVPV	336	-0.9000	0
33	FEAVGACSR	183	-0.9500	0
34	IRLDVAGRV	520	-1.0000	0
35	FSLVSREVI	106	-1.0500	0
36	IAVVMAFGG	280	-1.0500	0
37	FGTISVSDG	88	-1.1000	0
38	LGMSLPGSA	229	-1.1000	0
39	IAHEANVAL	299	-1.1000	0
40	IGSGVPHLA	315	-1.1000	0
41	ISVSDGISM	91	-1.1200	0
42	VKPFGRHVM	325	-1.1400	0

43	FARRSGQAV	249	-1.2000	0
44	FGRHVMSDV	328	-1.2000	0
45	MKALLDAGL	346	-1.2000	0
46	VLLAGCDKS	131	-1.3000	0
47	VVMKALLDA	344	-1.3000	0
48	VIRYEGPKG	450	-1.3300	0
49	MLRAVGMDD	35	-1.4100	0
50	MAFGGSTNA	284	-1.4100	0
51	LHGSLAPEG	400	-1.4300	0
52	MLAITGAIK	465	-1.5000	0
53	MYTANTMAS	216	-1.5100	0
54	IDAFEAVGA	180	-1.5200	0
55	VMAFGGSTN	283	-1.5200	0
56	LAIAHEANV	297	-1.6000	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	VLRALANPI	383	2.5000	41.67
2	VTIIDAFEA	177	2.3000	38.33
3	LVSSAAVGA	563	2.3000	38.33
4	VVMAFGGST	282	1.9000	31.67
5	ITILHGSLA	397	1.9000	31.67
6	VKLVSSAAV	561	1.7500	29.17
7	VFSAGGYPL	78	1.7000	28.33
8	VLHLLAIAH	293	1.6000	26.67
9	MREMLAITG	462	1.6000	26.67
10	IHPSGGITI	391	1.4000	23.33
11	IRYEGPKGG	451	1.4000	23.33
12	FENAIAVVM	276	1.3800	23.00
13	LRNGDRIRL	514	1.3000	21.67
14	ITVGDAVVI	443	1.2000	20.00
15	YVKLVSSAA	560	1.2000	20.00

16	LLHGDCLTV	354	1.1000	18.33
17	LRALANPIH	384	0.9700	16.17
18	VVKTAGFDS	410	0.8000	13.33
19	VVELLRRGI	257	0.7900	13.17
20	VFLYAGSIL	155	0.7000	11.67
21	FLYAGSILP	156	0.7000	11.67
22	VGHIAPEAV	498	0.7000	11.67
23	MLMAAARLD	143	0.5900	9.83
24	LLLTDGRFS	482	0.4900	8.17
25	LAITGAIKG	466	0.3000	5.00
26	LEKAAARGM	27	0.2700	4.50
27	LMAAARLDL	144	0.1000	1.67
28	ILPGRAKLS	162	0.1000	1.67
29	VDHIGGVPV	336	0.1000	1.67
30	IAVVMAFGG	280	-0.0500	0
31	LGMSLPGSA	229	-0.1000	0
32	IAHEANVAL	299	-0.1000	0
33	IGSGVPHLA	315	-0.1000	0
34	ISVSDGISM	91	-0.1200	0
35	VKPFGRHVM	325	-0.1400	0
36	MKALLDAGL	346	-0.2000	0
37	VLLAGCDKS	131	-0.3000	0
38	VVMKALLDA	344	-0.3000	0
39	VIRYEGPKG	450	-0.3300	0
40	MLRAVGMDD	35	-0.4100	0
41	MAFGGSTNA	284	-0.4100	0
42	LHGSLAPEG	400	-0.4300	0
43	MLAITGAIK	465	-0.5000	0
44	MYTANTMAS	216	-0.5100	0
45	IDAFEAVGA	180	-0.5200	0
46	VMAFGGSTN	283	-0.5200	0
47	WNEITPCNL	57	-0.6000	0
48	FGGSTNAVL	286	-0.6000	0
49	LAIAHEANV	297	-0.6000	0

50	VVMQAERLD	120	-0.6100	0
51	LAAITPPDP	371	-0.7300	0
52	LSLQDFSRI	307	-0.8000	0
53	LRRGITARD	261	-0.9000	0
54	LPGSAAPPA	233	-0.9300	0
55	FEAVGACSR	183	-0.9500	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	IRLDVAGRV	520	5.9000	62.11
2	LLTDGRFSG	483	5.2000	54.74
3	VIADSVEVV	113	4.7000	49.47
4	LRNGDRIRL	514	4.5600	48.00
5	MYTANTMAS	216	3.9000	41.05
6	LRRGITARD	261	3.6000	37.89
7	LEFGTISVS	86	3.2700	34.42
8	MHFSLVSRE	104	3.2700	34.42
9	LSLDRLANA	65	3.2000	33.68
10	LGMSLPGSA	229	3.2000	33.68
11	LVSSAAVGA	563	3.2000	33.68
12	VLADPAEFA	531	3.1000	32.63
13	VVMKALLDA	344	2.9000	30.53
14	LHGDCLTVT	355	2.9000	30.53
15	LHGSLAPEG	400	2.8000	29.47
16	VMQAERLDG	121	2.7000	28.42
17	LYAGSILPG	157	2.7000	28.42
18	VGACSRGLM	186	2.7000	28.42
19	LGKDVLLLT	477	2.7000	28.42
20	VLLAGCDKS	131	2.5000	26.32
21	VTIIDAFEA	177	2.5000	26.32
22	VVMAFGGST	282	2.4000	25.26
23	LVSREVIAD	108	2.3000	24.21

24	VKLVSSAAV	561	2.3000	24.21
25	LMAAARLDL	144	2.2600	23.79
26	VLRALANPI	383	2.2100	23.26
27	VGMDDEDFA	39	2.2000	23.16
28	LHLLAIAHE	294	2.2000	23.16
29	LLHGDCLTV	354	2.2000	23.16
30	IHPSGGITI	391	2.1000	22.11
31	ILPGRAKLS	162	2.0000	21.05
32	VVKTAGFDS	410	2.0000	21.05
33	IRYEGPKGG	451	2.0000	21.05
34	ITGAIKGAG	468	2.0000	21.05
35	LANAVKEGV	70	1.9000	20.00
36	VALSLQDFS	305	1.9000	20.00
37	IGGVPVVMK	339	1.9000	20.00
38	LLRRGITAR	260	1.8000	18.95
39	LRALANPIH	384	1.8000	18.95
40	ITVGDAVVI	443	1.8000	18.95
41	MREMLAITG	462	1.8000	18.95
42	VGHIAPEAV	498	1.8000	18.95
43	ISVSDGISM	91	1.7000	17.89
44	LDLAAVFLY	150	1.7000	17.89
45	VELLRRGIT	258	1.7000	17.89
46	VKPFGRHVM	325	1.7000	17.89
47	FGTISVSDG	88	1.6700	17.58
48	MSRADVDAI	194	1.6000	16.84
49	VVELLRRGI	257	1.6000	16.84
50	ILHGSLAPE	399	1.6000	16.84
51	MLRAVGMDD	35	1.5000	15.79
52	VSSAAVGAV	564	1.5000	15.79
53	IAVVMAFGG	280	1.4000	14.74
54	LQDFSRIGS	309	1.4000	14.74
55	LAAITPPDP	371	1.4000	14.74
56	LCVGHIAPE	496	1.4000	14.74
57	YAGSILPGR	158	1.3000	13.68

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IRLDVAGRV	520	3.9000	42.86
2	LLTDGRFSG	483	2.8000	30.77
3	VIADSVEVV	113	2.7000	29.67
4	LRNGDRIRL	514	2.6000	28.57
5	MYTANTMAS	216	2.5000	27.47
6	LSLDRLANA	65	2.2000	24.18
7	LGMSLPGSA	229	2.2000	24.18
8	LVSSAAVGA	563	2.2000	24.18
9	VLADPAEFA	531	2.1000	23.08
10	YVKLVSSAA	560	2.0700	22.75
11	VVMKALLDA	344	1.9000	20.88
12	LEFGTISVS	86	1.8700	20.55
13	VTIIDAFEA	177	1.5000	16.48
14	LRRGITARD	261	1.5000	16.48
15	LRALANPIH	384	1.3800	15.16
16	FSGGTTGLC	489	1.3000	14.29
17	FGTISVSDG	88	1.2700	13.96
18	VGMDDEDFA	39	1.2000	13.19
19	FSLVSREVI	106	1.2000	13.19
20	LHGDCLTVT	355	1.2000	13.19
21	VLLAGCDKS	131	1.1000	12.09
22	LGKDVLLLT	477	1.0000	10.99
23	MHFSLVSRE	104	0.8700	9.56
24	FLYAGSILP	156	0.8000	8.79
25	YAGSILPGR	158	0.8000	8.79
26	IGGVPVVMK	339	0.8000	8.79
27	VVMAFGGST	282	0.7000	7.69
28	VLHLLAIAH	293	0.6800	7.47
29	ILPGRAKLS	162	0.6000	6.59
30	VVKTAGFDS	410	0.6000	6.59

31	VALSLQDFS	305	0.5000	5.49
32	FENAIAVVM	276	0.4000	4.40
33	LHGSLAPEG	400	0.4000	4.40
34	VLRALANPI	383	0.3100	3.41
35	VMQAERLDG	121	0.3000	3.30
36	LMAAARLDL	144	0.3000	3.30
37	LYAGSILPG	157	0.3000	3.30
38	VKLVSSAAV	561	0.3000	3.30
39	LVSREVIAD	108	0.2000	2.20
40	VGACSRGLM	186	0.2000	2.20
41	LLHGDCLTV	354	0.2000	2.20
42	IHPSGGITI	391	0.2000	2.20
43	LPGSAAPPA	233	0.1000	1.10
44	MAFGGSTNA	284	0.1000	1.10
45	LANAVKEGV	70	-0.1000	0
46	IGSGVPHLA	315	-0.1000	0
47	ITVGDAVVI	443	-0.1000	0
48	LSKYVKLVS	557	-0.1000	0
49	ITILHGSLA	397	-0.1300	0
50	FAKPQIGVA	46	-0.2000	0
51	VSREVIADS	109	-0.2000	0
52	FGGSTNAVL	286	-0.2000	0
53	LHLLAIAHE	294	-0.2000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VIADSVEVV	113	4.1000	46.59
2	IRLDVAGRV	520	3.5000	39.77
3	VLADPAEFA	531	3.5000	39.77
4	VVMKALLDA	344	3.4000	38.64
5	LRNGDRIRL	514	3.2800	37.27
6	LSLDRLANA	65	3.2000	36.36

7	MYTANTMAS	216	3.2000	36.36
8	LVSSAAVGA	563	3.0800	35.00
9	LEFGTISVS	86	2.6000	29.55
10	VGMDDEDFA	39	2.5000	28.41
11	LRRGITARD	261	2.5000	28.41
12	LGKDVLLLT	477	2.5000	28.41
13	VLLAGCDKS	131	2.4000	27.27
14	LLTDGRFSG	483	2.3000	26.14
15	ILPGRAKLS	162	2.2000	25.00
16	LHGDCLTVT	355	2.2000	25.00
17	VLRALANPI	383	2.0000	22.73
18	VMQAERLDG	121	1.8000	20.45
19	LMAAARLDL	144	1.8000	20.45
20	LYAGSILPG	157	1.8000	20.45
21	LGMSLPGSA	229	1.8000	20.45
22	VALSLQDFS	305	1.8000	20.45
23	IGSGVPHLA	315	1.7000	19.32
24	LLHGDCLTV	354	1.7000	19.32
25	IGGVPVVMK	339	1.6800	19.09
26	MHFSLVSRE	104	1.6000	18.18
27	LSKYVKLVS	557	1.4000	15.91
28	VLHLLAIAH	293	1.3600	15.45
29	LANAVKEGV	70	1.3000	14.77
30	VKLVSSAAV	561	1.3000	14.77
31	IRYEGPKGG	451	1.2000	13.64
32	VGHIAPEAV	498	1.2000	13.64
33	MAFGGSTNA	284	1.1000	12.50
34	VTIIDAFEA	177	1.0000	11.36
35	MSRADVDAI	194	1.0000	11.36
36	VKPFGRHVM	325	1.0000	11.36
37	LRALANPIH	384	0.9800	11.14
38	LVSREVIAD	108	0.8800	10.00
39	IHPSGGITI	391	0.8800	10.00
40	VSREVIADS	109	0.8000	9.09

41	MQAERLDGS	122	0.8000	9.09
42	LHLLAIAHE	294	0.8000	9.09
43	YVKLVSSAA	560	0.8000	9.09
44	ITVGDAVVI	443	0.7800	8.86
45	LQDFSRIGS	309	0.6800	7.73
46	FSLVSREVI	106	0.6000	6.82
47	ITILHGSLA	397	0.6000	6.82
48	MLAITGAIK	465	0.5000	5.68
49	VVELLRRGI	257	0.4000	4.55
50	VLSKYVKLV	556	0.4000	4.55
51	LLRRGITAR	260	0.3000	3.41
52	VVMAFGGST	282	0.3000	3.41
53	VPVVMKALL	342	0.3000	3.41
54	VDAIERAIC	199	0.2000	2.27
55	LLAIAHEAN	296	0.2000	2.27
56	VMSDVDHIG	332	0.2000	2.27
57	ILHGSLAPE	399	0.2000	2.27

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	VIADSVEVV	113	4.1000	46.59
2	IRLDVAGRV	520	3.5000	39.77
3	VLADPAEFA	531	3.5000	39.77
4	VVMKALLDA	344	3.4000	38.64
5	LRNGDRIRL	514	3.2800	37.27
6	LSLDRLANA	65	3.2000	36.36
7	MYTANTMAS	216	3.2000	36.36
8	LVSSAAVGA	563	3.0800	35.00
9	LEFGTISVS	86	2.6000	29.55
10	VGMDDEDFA	39	2.5000	28.41
11	LRRGITARD	261	2.5000	28.41
12	LGKDVLLLT	477	2.5000	28.41

13	VLLAGCDKS	131	2.4000	27.27
14	LLTDGRFSG	483	2.3000	26.14
15	ILPGRAKLS	162	2.2000	25.00
16	LHGDCLTVT	355	2.2000	25.00
17	VLRALANPI	383	2.0000	22.73
18	VMQAERLDG	121	1.8000	20.45
19	LMAAARLDL	144	1.8000	20.45
20	LYAGSILPG	157	1.8000	20.45
21	LGMSLPGSA	229	1.8000	20.45
22	VALSLQDFS	305	1.8000	20.45
23	IGSGVPHLA	315	1.7000	19.32
24	LLHGDCLTV	354	1.7000	19.32
25	IGGVPVVMK	339	1.6800	19.09
26	MHFSLVSRE	104	1.6000	18.18
27	LSKYVKLVS	557	1.4000	15.91
28	VLHLLAIAH	293	1.3600	15.45
29	LANAVKEGV	70	1.3000	14.77
30	VKLVSSAAV	561	1.3000	14.77
31	IRYEGPKGG	451	1.2000	13.64
32	VGHIAPEAV	498	1.2000	13.64
33	MAFGGSTNA	284	1.1000	12.50
34	VTIIDAFEA	177	1.0000	11.36
35	MSRADVDAI	194	1.0000	11.36
36	VKPFGRHVM	325	1.0000	11.36
37	LRALANPIH	384	0.9800	11.14
38	LVSREVIAD	108	0.8800	10.00
39	IHPSGGITI	391	0.8800	10.00
40	VSREVIADS	109	0.8000	9.09
41	MQAERLDGS	122	0.8000	9.09
42	LHLLAIAHE	294	0.8000	9.09
43	YVKLVSSAA	560	0.8000	9.09
44	ITVGDAVVI	443	0.7800	8.86
45	LQDFSRIGS	309	0.6800	7.73
46	FSLVSREVI	106	0.6000	6.82

47	ITILHGSLA	397	0.6000	6.82
48	MLAITGAIK	465	0.5000	5.68
49	VVELLRRGI	257	0.4000	4.55
50	VLSKYVKLV	556	0.4000	4.55
51	LLRRGITAR	260	0.3000	3.41
52	VVMAFGGST	282	0.3000	3.41
53	VPVVMKALL	342	0.3000	3.41
54	VDAIERAIC	199	0.2000	2.27
55	LLAIAHEAN	296	0.2000	2.27
56	VMSDVDHIG	332	0.2000	2.27
57	ILHGSLAPE	399	0.2000	2.27

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	VIADSVEVV	113	4.1000	46.59
2	IRLDVAGRV	520	3.5000	39.77
3	VLADPAEFA	531	3.5000	39.77
4	VVMKALLDA	344	3.4000	38.64
5	LRNGDRIRL	514	3.2800	37.27
6	LSLDRLANA	65	3.2000	36.36
7	MYTANTMAS	216	3.2000	36.36
8	LVSSAAVGA	563	3.0800	35.00
9	LEFGTISVS	86	2.6000	29.55
10	VGMDDEDFA	39	2.5000	28.41
11	LRRGITARD	261	2.5000	28.41
12	LGKDVLLLT	477	2.5000	28.41
13	VLLAGCDKS	131	2.4000	27.27
14	LLTDGRFSG	483	2.3000	26.14
15	ILPGRAKLS	162	2.2000	25.00
16	LHGDCLTVT	355	2.2000	25.00
17	VLRALANPI	383	2.0000	22.73
18	VMQAERLDG	121	1.8000	20.45

19	LMAAARLDL	144	1.8000	20.45
20	LYAGSILPG	157	1.8000	20.45
21	LGMSLPGSA	229	1.8000	20.45
22	VALSLQDFS	305	1.8000	20.45
23	IGSGVPHLA	315	1.7000	19.32
24	LLHGDCLTV	354	1.7000	19.32
25	IGGVPVVMK	339	1.6800	19.09
26	MHFSLVSRE	104	1.6000	18.18
27	LSKYVKLVS	557	1.4000	15.91
28	VLHLLAIAH	293	1.3600	15.45
29	LANAVKEGV	70	1.3000	14.77
30	VKLVSSAAV	561	1.3000	14.77
31	IRYEGPKGG	451	1.2000	13.64
32	VGHIAPEAV	498	1.2000	13.64
33	MAFGGSTNA	284	1.1000	12.50
34	VTIIDAFEA	177	1.0000	11.36
35	MSRADVDAI	194	1.0000	11.36
36	VKPFGRHVM	325	1.0000	11.36
37	LRALANPIH	384	0.9800	11.14
38	LVSREVIAD	108	0.8800	10.00
39	IHPSGGITI	391	0.8800	10.00
40	VSREVIADS	109	0.8000	9.09
41	MQAERLDGS	122	0.8000	9.09
42	LHLLAIAHE	294	0.8000	9.09
43	YVKLVSSAA	560	0.8000	9.09
44	ITVGDAVVI	443	0.7800	8.86
45	LQDFSRIGS	309	0.6800	7.73
46	FSLVSREVI	106	0.6000	6.82
47	ITILHGSLA	397	0.6000	6.82
48	MLAITGAIK	465	0.5000	5.68
49	VVELLRRGI	257	0.4000	4.55
50	VLSKYVKLV	556	0.4000	4.55
51	LLRRGITAR	260	0.3000	3.41
52	VVMAFGGST	282	0.3000	3.41

53	VPVVMKALL	342	0.3000	3.41
54	VDAIERAIC	199	0.2000	2.27
55	LLAIAHEAN	296	0.2000	2.27
56	VMSDVDHIG	332	0.2000	2.27
57	ILHGSLAPE	399	0.2000	2.27

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	IRLDVAGRV	520	4.9000	51.58
2	LLTDGRFSG	483	4.2000	44.21
3	VIADSVEVV	113	3.7000	38.95
4	LRNGDRIRL	514	3.5600	37.47
5	MYTANTMAS	216	2.9000	30.53
6	FGTISVSDG	88	2.6700	28.11
7	LRRGITARD	261	2.6000	27.37
8	YAGSILPGR	158	2.3000	24.21
9	LEFGTISVS	86	2.2700	23.89
10	MHFSLVSRE	104	2.2700	23.89
11	LSLDRLANA	65	2.2000	23.16
12	LGMSLPGSA	229	2.2000	23.16
13	LVSSAAVGA	563	2.2000	23.16
14	FSLVSREVI	106	2.1000	22.11
15	VLADPAEFA	531	2.1000	22.11
16	YVKLVSSAA	560	2.0700	21.79
17	FENAIAVVM	276	1.9000	20.00
18	VVMKALLDA	344	1.9000	20.00
19	LHGDCLTVT	355	1.9000	20.00
20	FLYAGSILP	156	1.8000	18.95
21	LHGSLAPEG	400	1.8000	18.95
22	VMQAERLDG	121	1.7000	17.89
23	LYAGSILPG	157	1.7000	17.89
24	VGACSRGLM	186	1.7000	17.89

25	LGKDVLLLT	477	1.7000	17.89
26	VLLAGCDKS	131	1.5000	15.79
27	VTIIDAFEA	177	1.5000	15.79
28	VVMAFGGST	282	1.4000	14.74
29	LVSREVIAD	108	1.3000	13.68
30	FSGGTTGLC	489	1.3000	13.68
31	VKLVSSAAV	561	1.3000	13.68
32	LMAAARLDL	144	1.2600	13.26
33	VLRALANPI	383	1.2100	12.74
34	VGMDDEDFA	39	1.2000	12.63
35	LHLLAIAHE	294	1.2000	12.63
36	LLHGDCLTV	354	1.2000	12.63
37	IHPSGGITI	391	1.1000	11.58
38	YTTGVLSKY	552	1.0700	11.26
39	ILPGRAKLS	162	1.0000	10.53
40	VVKTAGFDS	410	1.0000	10.53
41	IRYEGPKGG	451	1.0000	10.53
42	ITGAIKGAG	468	1.0000	10.53
43	LANAVKEGV	70	0.9000	9.47
44	VALSLQDFS	305	0.9000	9.47
45	IGGVPVVMK	339	0.9000	9.47
46	LLRRGITAR	260	0.8000	8.42
47	LRALANPIH	384	0.8000	8.42
48	ITVGDAVVI	443	0.8000	8.42
49	MREMLAITG	462	0.8000	8.42
50	VGHIAPEAV	498	0.8000	8.42
51	FGGSTNAVL	286	0.7600	8.00
52	ISVSDGISM	91	0.7000	7.37
53	LDLAAVFLY	150	0.7000	7.37
54	VELLRRGIT	258	0.7000	7.37
55	VKPFGRHVM	325	0.7000	7.37
56	FGRHVMSDV	328	0.6700	7.05
57	FEAVGACSR	183	0.6000	6.32

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	VIADSVEVV	113	4.1000	46.59
2	IRLDVAGRV	520	3.5000	39.77
3	VLADPAEFA	531	3.5000	39.77
4	VVMKALLDA	344	3.4000	38.64
5	LRNGDRIRL	514	3.2800	37.27
6	LSLDRLANA	65	3.2000	36.36
7	MYTANTMAS	216	3.2000	36.36
8	LVSSAAVGA	563	3.0800	35.00
9	LEFGTISVS	86	2.6000	29.55
10	VGMDDEDFA	39	2.5000	28.41
11	LRRGITARD	261	2.5000	28.41
12	LGKDVLLLT	477	2.5000	28.41
13	VLLAGCDKS	131	2.4000	27.27
14	LLTDGRFSG	483	2.3000	26.14
15	ILPGRAKLS	162	2.2000	25.00
16	LHGDCLTVT	355	2.2000	25.00
17	VLRALANPI	383	2.0000	22.73
18	VMQAERLDG	121	1.8000	20.45
19	LMAAARLDL	144	1.8000	20.45
20	LYAGSILPG	157	1.8000	20.45
21	LGMSLPGSA	229	1.8000	20.45
22	VALSLQDFS	305	1.8000	20.45
23	IGSGVPHLA	315	1.7000	19.32
24	LLHGDCLTV	354	1.7000	19.32
25	IGGVPVVMK	339	1.6800	19.09
26	MHFSLVSRE	104	1.6000	18.18
27	LSKYVKLVS	557	1.4000	15.91
28	VLHLLAIAH	293	1.3600	15.45
29	LANAVKEGV	70	1.3000	14.77
30	VKLVSSAAV	561	1.3000	14.77

31	IRYEGPKGG	451	1.2000	13.64
32	VGHIAPEAV	498	1.2000	13.64
33	MAFGGSTNA	284	1.1000	12.50
34	VTIIDAFEA	177	1.0000	11.36
35	MSRADVDAI	194	1.0000	11.36
36	VKPFGRHVM	325	1.0000	11.36
37	LRALANPIH	384	0.9800	11.14
38	LVSREVIAD	108	0.8800	10.00
39	IHPSGGITI	391	0.8800	10.00
40	VSREVIADS	109	0.8000	9.09
41	MQAERLDGS	122	0.8000	9.09
42	LHLLAIAHE	294	0.8000	9.09
43	YVKLVSSAA	560	0.8000	9.09
44	ITVGDAVVI	443	0.7800	8.86
45	LQDFSRIGS	309	0.6800	7.73
46	FSLVSREVI	106	0.6000	6.82
47	ITILHGSLA	397	0.6000	6.82
48	MLAITGAIK	465	0.5000	5.68
49	VVELLRRGI	257	0.4000	4.55
50	VLSKYVKLV	556	0.4000	4.55
51	LLRRGITAR	260	0.3000	3.41
52	VVMAFGGST	282	0.3000	3.41
53	VPVVMKALL	342	0.3000	3.41
54	VDAIERAIC	199	0.2000	2.27
55	LLAIAHEAN	296	0.2000	2.27
56	VMSDVDHIG	332	0.2000	2.27
57	ILHGSLAPE	399	0.2000	2.27

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	YVKLVSSAA	560	3.7000	43.02
2	MYTANTMAS	216	3.3000	38.37

3	LRALANPIH	384	2.6800	31.16
4	IRYEGPKGG	451	2.2000	25.58
5	LVSSAAVGA	563	2.1800	25.35
6	VIADSVEVV	113	1.9000	22.09
7	FGGSTNAVL	286	1.8000	20.93
8	IRLDVAGRV	520	1.6000	18.60
9	VLADPAEFA	531	1.6000	18.60
10	FLYAGSILP	156	1.5800	18.37
11	VSREVIADS	109	1.5000	17.44
12	VLLAGCDKS	131	1.4000	16.28
13	VLHLLAIAH	293	1.1600	13.49
14	YPLEFGTIS	84	1.1000	12.79
15	IAHEANVAL	299	1.0800	12.56
16	FGTISVSDG	88	1.0000	11.63
17	MQAERLDGS	122	1.0000	11.63
18	VLRALANPI	383	1.0000	11.63
19	MGHEGMHFS	99	0.8000	9.30
20	LAPEGAVVK	404	0.5800	6.74
21	LRRGITARD	261	0.5000	5.81
22	VKLVSSAAV	561	0.5000	5.81
23	MHFSLVSRE	104	0.4000	4.65
24	LGMSLPGSA	229	0.4000	4.65
25	VVMKALLDA	344	0.4000	4.65
26	IAPEAVDGG	501	0.4000	4.65
27	VASSWNEIT	53	0.3000	3.49
28	VTIIDAFEA	177	0.3000	3.49
29	FGRHVMSDV	328	0.3000	3.49
30	FENAIAVVM	276	0.2800	3.26
31	LAITGAIKG	466	0.2800	3.26
32	LDRLANAVK	67	0.2000	2.33
33	MREMLAITG	462	-0.0200	0
34	YTANTMASA	217	-0.2000	0
35	LHLLAIAHE	294	-0.2000	0
36	IALLRNGDR	511	-0.2000	0

37	MSRADVDAI	194	-0.3000	0
38	VALSLQDFS	305	-0.3000	0
39	LLLTDGRFS	482	-0.3000	0
40	VGMDDEDFA	39	-0.4000	0
41	LTKEAFENA	271	-0.4000	0
42	FSRIGSGVP	312	-0.4000	0
43	VMSDVDHIG	332	-0.4000	0
44	ITILHGSLA	397	-0.4000	0
45	IGGVPVVMK	339	-0.5200	0
46	WNEITPCNL	57	-0.6000	0
47	LGKDVLLLT	477	-0.7000	0
48	IHPSGGITI	391	-0.8200	0
49	ILPGRAKLS	162	-0.9000	0
50	MAFGGSTNA	284	-0.9000	0
51	LHGSLAPEG	400	-0.9000	0
52	LHGDCLTVT	355	-1.0000	0
53	MLAITGAIK	465	-1.0000	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	MYTANTMAS	216	4.3000	44.79
2	VVMKALLDA	344	3.5000	36.46
3	LVSREVIAD	108	3.0000	31.25
4	MLMAAARLD	143	2.4000	25.00
5	LRRGITARD	261	2.4000	25.00
6	LLLTDGRFS	482	2.4000	25.00
7	VTIIDAFEA	177	2.0800	21.67
8	VLRALANPI	383	2.0000	20.83
9	LRALANPIH	384	1.9800	20.62
10	IGVASSWNE	51	1.7000	17.71
11	LLRRGITAR	260	1.7000	17.71
12	VKLVSSAAV	561	1.7000	17.71

13	ITARDILTK	265	1.6000	16.67
14	VLSKYVKLV	556	1.5000	15.62
15	LVSSAAVGA	563	1.5000	15.62
16	LEKAAARGM	27	1.4000	14.58
17	LMSRADVDA	193	1.4000	14.58
18	ILPGRAKLS	162	1.3000	13.54
19	VVKTAGFDS	410	1.3000	13.54
20	MAFGGSTNA	284	1.2000	12.50
21	VLHLLAIAH	293	1.1800	12.29
22	MREMLAITG	462	1.1000	11.46
23	YVKLVSSAA	560	1.1000	11.46
24	FLYAGSILP	156	1.0000	10.42
25	LLRNGDRIR	513	0.9000	9.38
26	IGGVPVVMK	339	0.8000	8.33
27	LLHGDCLTV	354	0.8000	8.33
28	VVMQAERLD	120	0.7000	7.29
29	VLLAGCDKS	131	0.6000	6.25
30	IGSGVPHLA	315	0.5000	5.21
31	LAITGAIKG	466	0.5000	5.21
32	LEFGTISVS	86	0.4000	4.17
33	ILTKEAFEN	270	0.2000	2.08
34	LDLAAVFLY	150	0.1000	1.04
35	LYAGSILPG	157	0.1000	1.04
36	LDRLANAVK	67	-0.2000	0
37	VVIRYEGPK	449	-0.2000	0
38	ITVGDAVVI	443	-0.3000	0
39	IRYEGPKGG	451	-0.3000	0
40	FARRSGQAV	249	-0.4000	0
41	VFEGTARVF	420	-0.4000	0
42	VGDAVVIRY	445	-0.4000	0
43	VSDGISMGH	93	-0.4200	0
44	VADIKPRSR	13	-0.5200	0
45	VFSAGGYPL	78	-0.6000	0
46	MHFSLVSRE	104	-0.6000	0

47	FENAIAVVM	276	-0.6000	0
48	LHLLAIAHE	294	-0.6000	0
49	VKPFGRHVM	325	-0.6000	0
50	MLRAVGMDD	35	-0.7000	0
51	VVELLRRGI	257	-0.7000	0
52	IAVVMAFGG	280	-0.7000	0
53	MLAITGAIK	465	-0.7200	0
54	LPGMLMAAA	140	-0.8000	0
55	IDAFEAVGA	180	-0.8000	0
56	FGRHVMSDV	328	-0.8000	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	MYTANTMAS	216	4.2000	47.73
2	YVKLVSSAA	560	3.6000	40.91
3	LRALANPIH	384	3.5800	40.68
4	VKLVSSAAV	561	2.9000	32.95
5	VTIIDAFEA	177	2.5500	28.98
6	VLHLLAIAH	293	2.3600	26.82
7	VLRALANPI	383	2.1000	23.86
8	MREMLAITG	462	1.8800	21.36
9	IGGVPVVMK	339	1.7000	19.32
10	VLLAGCDKS	131	1.5000	17.05
11	ITILHGSLA	397	1.5000	17.05
12	LVSSAAVGA	563	1.5000	17.05
13	LDRLANAVK	67	1.4000	15.91
14	VVMKALLDA	344	1.2000	13.64
15	IALLRNGDR	511	1.1000	12.50
16	FGTISVSDG	88	1.0000	11.36
17	LHLLAIAHE	294	1.0000	11.36
18	LRRGITARD	261	0.7000	7.95
19	MHFSLVSRE	104	0.6000	6.82

20	FLYAGSILP	156	0.5800	6.59
21	LPGMLMAAA	140	0.4000	4.55
22	VGHIAPEAV	498	0.4000	4.55
23	VVKTAGFDS	410	0.3500	3.98
24	MLAITGAIK	465	0.3000	3.41
25	IRLDVAGRV	520	0.2000	2.27
26	IAVVMAFGG	280	-0.0500	0
27	VSREVIADS	109	-0.1000	0
28	MLMAAARLD	143	-0.2000	0
29	MSRADVDAI	194	-0.2000	0
30	MAFGGSTNA	284	-0.2000	0
31	LSLQDFSRI	307	-0.2000	0
32	VMAFGGSTN	283	-0.3000	0
33	VLLLTDGRF	481	-0.3000	0
34	LAITGAIKG	466	-0.3200	0
35	IGVASSWNE	51	-0.4000	0
36	LEFGTISVS	86	-0.4000	0
37	IDAFEAVGA	180	-0.4000	0
38	VVMAFGGST	282	-0.4000	0
39	IRYEGPKGG	451	-0.4000	0
40	LDLAAVFLY	150	-0.4500	0
41	VIADSVEVV	113	-0.5000	0
42	VFLYAGSIL	155	-0.6000	0
43	LLLTDGRFS	482	-0.6000	0
44	FGGSTNAVL	286	-0.7000	0
45	IAHEANVAL	299	-0.7000	0
46	LQDFSRIGS	309	-0.7200	0
47	MLRAVGMDD	35	-0.8000	0
48	VKPFGRHVM	325	-0.8000	0
49	VLADPAEFA	531	-0.8000	0
50	LVSREVIAD	108	-0.8200	0
51	VGDAVVIRY	445	-0.8200	0
52	MSLPGSAAP	231	-0.9000	0
53	FENAIAVVM	276	-0.9000	0

54	FSRIGSGVP	312	-1.0000	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	YVKLVSSAA	560	4.6000	48.94
2	LRALANPIH	384	3.8000	40.43
3	FGTISVSDG	88	3.3000	35.11
4	MYTANTMAS	216	3.2000	34.04
5	LHLLAIAHE	294	3.0000	31.91
6	MHFSLVSRE	104	2.6000	27.66
7	VLHLLAIAH	293	2.5800	27.45
8	LRRGITARD	261	2.4000	25.53
9	VKLVSSAAV	561	2.2000	23.40
10	MREMLAITG	462	2.1800	23.19
11	FLYAGSILP	156	1.9800	21.06
12	IGVASSWNE	51	1.6000	17.02
13	VTIIDAFEA	177	1.5500	16.49
14	MLMAAARLD	143	1.5000	15.96
15	FGGSTNAVL	286	1.3000	13.83
16	VLRALANPI	383	1.3000	13.83
17	FENAIAVVM	276	1.2000	12.77
18	MLRAVGMDD	35	0.9000	9.57
19	LVSREVIAD	108	0.8800	9.36
20	LRAVGMDDE	36	0.7000	7.45
21	WNEITPCNL	57	0.7000	7.45
22	VMAFGGSTN	283	0.7000	7.45
23	VLLAGCDKS	131	0.5000	5.32
24	ITILHGSLA	397	0.5000	5.32
25	LVSSAAVGA	563	0.5000	5.32
26	FSRIGSGVP	312	0.4000	4.26
27	IAVVMAFGG	280	0.2500	2.66
28	VVMQAERLD	120	0.2000	2.13

29	VVMKALLDA	344	0.2000	2.13
30	IERAICPGE	202	0.1000	1.06
31	IALLRNGDR	511	0.1000	1.06
32	LAITGAIKG	466	-0.0200	0
33	IRYEGPKGG	451	-0.1000	0
34	ITPCNLSLD	60	-0.3000	0
35	LDRLANAVK	67	-0.3000	0
36	VGHIAPEAV	498	-0.3000	0
37	LDLAAVFLY	150	-0.3500	0
38	FEAVGACSR	183	-0.4000	0
39	LLAIAHEAN	296	-0.4000	0
40	VLLLTDGRF	481	-0.4000	0
41	VVMAFGGST	282	-0.5000	0
42	IRLDVAGRV	520	-0.5000	0
43	LPGMLMAAA	140	-0.6000	0
44	VFLYAGSIL	155	-0.6000	0
45	VVKTAGFDS	410	-0.6500	0
46	IAHEANVAL	299	-0.7000	0
47	VKPFGRHVM	325	-0.7000	0
48	VGDAVVIRY	445	-0.7200	0
49	FGRHVMSDV	328	-0.8000	0
50	ILTKEAFEN	270	-0.9500	0
51	YPLEFGTIS	84	-1.0000	0
52	MSRADVDAI	194	-1.0000	0
53	LGMSLPGSA	229	-1.0000	0
54	LSLQDFSRI	307	-1.0000	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	YVKLVSSAA	560	4.6000	52.27
2	MYTANTMAS	216	3.2000	36.36
3	LRALANPIH	384	2.5800	29.32

4	FGTISVSDG	88	2.0000	22.73
5	VKLVSSAAV	561	1.9000	21.59
6	FLYAGSILP	156	1.5800	17.95
7	VTIIDAFEA	177	1.5500	17.61
8	VLHLLAIAH	293	1.3600	15.45
9	VLRALANPI	383	1.1000	12.50
10	MREMLAITG	462	0.8800	10.00
11	IGGVPVVMK	339	0.7000	7.95
12	VLLAGCDKS	131	0.5000	5.68
13	ITILHGSLA	397	0.5000	5.68
14	LVSSAAVGA	563	0.5000	5.68
15	LDRLANAVK	67	0.4000	4.55
16	FGGSTNAVL	286	0.3000	3.41
17	VVMKALLDA	344	0.2000	2.27
18	FENAIAVVM	276	0.1000	1.14
19	IALLRNGDR	511	0.1000	1.14
20	WNEITPCNL	57	-0.3000	0
21	LRRGITARD	261	-0.3000	0
22	MHFSLVSRE	104	-0.4000	0
23	FEAVGACSR	183	-0.4000	0
24	LPGMLMAAA	140	-0.6000	0
25	VGHIAPEAV	498	-0.6000	0
26	VVKTAGFDS	410	-0.6500	0
27	MLAITGAIK	465	-0.7000	0
28	IRLDVAGRV	520	-0.8000	0
29	YPLEFGTIS	84	-1.0000	0
30	LGMSLPGSA	229	-1.0000	0
31	MKALLDAGL	346	-1.0000	0
32	IAVVMAFGG	280	-1.0500	0
33	VSREVIADS	109	-1.1000	0
34	FGRHVMSDV	328	-1.1000	0
35	MLMAAARLD	143	-1.2000	0
36	MSRADVDAI	194	-1.2000	0
37	MAFGGSTNA	284	-1.2000	0

38	LSLQDFSRI	307	-1.2000	0
39	VMAFGGSTN	283	-1.3000	0
40	VLLLTDGRF	481	-1.3000	0
41	LAITGAIKG	466	-1.3200	0
42	IGVASSWNE	51	-1.4000	0
43	LEFGTISVS	86	-1.4000	0
44	IDAFEAVGA	180	-1.4000	0
45	VVMAFGGST	282	-1.4000	0
46	IRYEGPKGG	451	-1.4000	0
47	LDLAAVFLY	150	-1.4500	0
48	VIADSVEVV	113	-1.5000	0
49	VFLYAGSIL	155	-1.6000	0
50	LLLTDGRFS	482	-1.6000	0
51	IAHEANVAL	299	-1.7000	0
52	LQDFSRIGS	309	-1.7200	0
53	MLRAVGMDD	35	-1.8000	0
54	YTANTMASA	217	-1.8000	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	LRALANPIH	384	4.8000	51.06
2	MYTANTMAS	216	4.2000	44.68
3	LHLLAIAHE	294	4.0000	42.55
4	MHFSLVSRE	104	3.6000	38.30
5	YVKLVSSAA	560	3.6000	38.30
6	VLHLLAIAH	293	3.5800	38.09
7	LRRGITARD	261	3.4000	36.17
8	VKLVSSAAV	561	3.2000	34.04
9	MREMLAITG	462	3.1800	33.83
10	IGVASSWNE	51	2.6000	27.66
11	VTIIDAFEA	177	2.5500	27.13
12	MLMAAARLD	143	2.5000	26.60

13	FGTISVSDG	88	2.3000	24.47
14	VLRALANPI	383	2.3000	24.47
15	MLRAVGMDD	35	1.9000	20.21
16	LVSREVIAD	108	1.8800	20.00
17	LRAVGMDDE	36	1.7000	18.09
18	VMAFGGSTN	283	1.7000	18.09
19	VLLAGCDKS	131	1.5000	15.96
20	ITILHGSLA	397	1.5000	15.96
21	LVSSAAVGA	563	1.5000	15.96
22	IAVVMAFGG	280	1.2500	13.30
23	VVMQAERLD	120	1.2000	12.77
24	VVMKALLDA	344	1.2000	12.77
25	IERAICPGE	202	1.1000	11.70
26	IALLRNGDR	511	1.1000	11.70
27	IGGVPVVMK	339	1.0000	10.64
28	MKALLDAGL	346	1.0000	10.64
29	FLYAGSILP	156	0.9800	10.43
30	LAITGAIKG	466	0.9800	10.43
31	IRYEGPKGG	451	0.9000	9.57
32	ITPCNLSLD	60	0.7000	7.45
33	LDRLANAVK	67	0.7000	7.45
34	VGHIAPEAV	498	0.7000	7.45
35	LDLAAVFLY	150	0.6500	6.91
36	LLAIAHEAN	296	0.6000	6.38
37	VLLLTDGRF	481	0.6000	6.38
38	VVMAFGGST	282	0.5000	5.32
39	IRLDVAGRV	520	0.5000	5.32
40	LPGMLMAAA	140	0.4000	4.26
41	VFLYAGSIL	155	0.4000	4.26
42	VVKTAGFDS	410	0.3500	3.72
43	FGGSTNAVL	286	0.3000	3.19
44	IAHEANVAL	299	0.3000	3.19
45	VKPFGRHVM	325	0.3000	3.19
46	VGDAVVIRY	445	0.2800	2.98

47	FENAIAVVM	276	0.2000	2.13
48	ILTKEAFEN	270	0.0500	0.53
49	LEKAAARGM	27	-0.1000	0
50	VSREVIADS	109	-0.1000	0
51	VASSWNEIT	53	-0.2000	0
52	VIADSVEVV	113	-0.2000	0

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	MYTANTMAS	216	3.7000	41.11
2	YVKLVSSAA	560	3.7000	41.11
3	IRYEGPKGG	451	3.6000	40.00
4	VIADSVEVV	113	2.9000	32.22
5	FGGSTNAVL	286	2.7600	30.67
6	IRLDVAGRV	520	2.6000	28.89
7	FLYAGSILP	156	2.5800	28.67
8	FGTISVSDG	88	2.4000	26.67
9	LVSSAAVGA	563	2.1800	24.22
10	LRALANPIH	384	2.1000	23.33
11	IAHEANVAL	299	2.0400	22.67
12	VSREVIADS	109	1.9000	21.11
13	VLRALANPI	383	1.9000	21.11
14	MHFSLVSRE	104	1.8000	20.00
15	VLLAGCDKS	131	1.8000	20.00
16	IAPEAVDGG	501	1.8000	20.00
17	FENAIAVVM	276	1.7800	19.78
18	LAITGAIKG	466	1.6800	18.67
19	LRRGITARD	261	1.6000	17.78
20	VLADPAEFA	531	1.6000	17.78
21	YPLEFGTIS	84	1.5000	16.67
22	VKLVSSAAV	561	1.5000	16.67
23	MQAERLDGS	122	1.4000	15.56

24	MREMLAITG	462	1.3800	15.33
25	FGRHVMSDV	328	1.3000	14.44
26	IALLRNGDR	511	1.3000	14.44
27	MGHEGMHFS	99	1.2000	13.33
28	LHLLAIAHE	294	1.2000	13.33
29	VASSWNEIT	53	1.0000	11.11
30	VMSDVDHIG	332	1.0000	11.11
31	VGHIAPEAV	498	1.0000	11.11
32	LAPEGAVVK	404	0.6800	7.56
33	MSRADVDAI	194	0.6000	6.67
34	FSRIGSGVP	312	0.6000	6.67
35	VLHLLAIAH	293	0.5800	6.44
36	LHGSLAPEG	400	0.5000	5.56
37	LGMSLPGSA	229	0.4000	4.44
38	VVMKALLDA	344	0.4000	4.44
39	VVKTAGFDS	410	0.4000	4.44
40	WNEITPCNL	57	0.3600	4.00
41	LDRLANAVK	67	0.3000	3.33
42	VTIIDAFEA	177	0.3000	3.33
43	VLLLTDGRF	481	0.3000	3.33
44	VALSLQDFS	305	0.1000	1.11
45	LLLTDGRFS	482	0.1000	1.11
46	IHPSGGITI	391	0.0800	0.89
47	YTANTMASA	217	-0.2000	0
48	LSLQDFSRI	307	-0.2000	0
49	FDGERAALD	428	-0.2000	0
50	LLRNGDRIR	513	-0.2000	0
51	LVSREVIAD	108	-0.2200	0
52	MKALLDAGL	346	-0.2400	0
53	YAGSILPGR	158	-0.3000	0
54	FEAVGACSR	183	-0.3000	0

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

	1.68	8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	MYTANTMAS	216	4.2000	47.73
2	YVKLVSSAA	560	3.6000	40.91
3	LRALANPIH	384	3.5800	40.68
4	VKLVSSAAV	561	2.9000	32.95
5	VTIIDAFEA	177	2.5500	28.98
6	VLHLLAIAH	293	2.3600	26.82
7	VLRALANPI	383	2.1000	23.86
8	MREMLAITG	462	1.8800	21.36
9	IGGVPVVMK	339	1.7000	19.32
10	VLLAGCDKS	131	1.5000	17.05
11	ITILHGSLA	397	1.5000	17.05
12	LVSSAAVGA	563	1.5000	17.05
13	LDRLANAVK	67	1.4000	15.91
14	VVMKALLDA	344	1.2000	13.64
15	IALLRNGDR	511	1.1000	12.50
16	FGTISVSDG	88	1.0000	11.36
17	LHLLAIAHE	294	1.0000	11.36
18	LRRGITARD	261	0.7000	7.95
19	MHFSLVSRE	104	0.6000	6.82
20	FLYAGSILP	156	0.5800	6.59
21	LPGMLMAAA	140	0.4000	4.55
22	VGHIAPEAV	498	0.4000	4.55
23	VVKTAGFDS	410	0.3500	3.98
24	MLAITGAIK	465	0.3000	3.41
25	IRLDVAGRV	520	0.2000	2.27
26	IAVVMAFGG	280	-0.0500	0
27	VSREVIADS	109	-0.1000	0
28	MLMAAARLD	143	-0.2000	0
29	MSRADVDAI	194	-0.2000	0
30	MAFGGSTNA	284	-0.2000	0
31	LSLQDFSRI	307	-0.2000	0
32	VMAFGGSTN	283	-0.3000	0

33	VLLLTDGRF	481	-0.3000	0
34	LAITGAIKG	466	-0.3200	0
35	IGVASSWNE	51	-0.4000	0
36	LEFGTISVS	86	-0.4000	0
37	IDAFEAVGA	180	-0.4000	0
38	VVMAFGGST	282	-0.4000	0
39	IRYEGPKGG	451	-0.4000	0
40	LDLAAVFLY	150	-0.4500	0
41	VIADSVEVV	113	-0.5000	0
42	VFLYAGSIL	155	-0.6000	0
43	LLLTDGRFS	482	-0.6000	0
44	FGGSTNAVL	286	-0.7000	0
45	IAHEANVAL	299	-0.7000	0
46	LQDFSRIGS	309	-0.7200	0
47	MLRAVGMDD	35	-0.8000	0
48	VKPFGRHVM	325	-0.8000	0
49	VLADPAEFA	531	-0.8000	0
50	LVSREVIAD	108	-0.8200	0
51	VGDAVVIRY	445	-0.8200	0
52	MSLPGSAAP	231	-0.9000	0
53	FENAIAVVM	276	-0.9000	0
54	FSRIGSGVP	312	-1.0000	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	YVKLVSSAA	560	3.7000	43.02
2	MYTANTMAS	216	3.3000	38.37
3	LRALANPIH	384	2.6800	31.16
4	IRYEGPKGG	451	2.2000	25.58
5	LVSSAAVGA	563	2.1800	25.35
6	VIADSVEVV	113	1.9000	22.09
7	FGGSTNAVL	286	1.8000	20.93

8	IRLDVAGRV	520	1.6000	18.60
9	VLADPAEFA	531	1.6000	18.60
10	FLYAGSILP	156	1.5800	18.37
11	VSREVIADS	109	1.5000	17.44
12	VLLAGCDKS	131	1.4000	16.28
13	VLHLLAIAH	293	1.1600	13.49
14	YPLEFGTIS	84	1.1000	12.79
15	IAHEANVAL	299	1.0800	12.56
16	FGTISVSDG	88	1.0000	11.63
17	MQAERLDGS	122	1.0000	11.63
18	VLRALANPI	383	1.0000	11.63
19	MGHEGMHFS	99	0.8000	9.30
20	LAPEGAVVK	404	0.5800	6.74
21	LRRGITARD	261	0.5000	5.81
22	VKLVSSAAV	561	0.5000	5.81
23	MHFSLVSRE	104	0.4000	4.65
24	LGMSLPGSA	229	0.4000	4.65
25	VVMKALLDA	344	0.4000	4.65
26	IAPEAVDGG	501	0.4000	4.65
27	VASSWNEIT	53	0.3000	3.49
28	VTIIDAFEA	177	0.3000	3.49
29	FGRHVMSDV	328	0.3000	3.49
30	FENAIAVVM	276	0.2800	3.26
31	LAITGAIKG	466	0.2800	3.26
32	LDRLANAVK	67	0.2000	2.33
33	MREMLAITG	462	-0.0200	0
34	YTANTMASA	217	-0.2000	0
35	LHLLAIAHE	294	-0.2000	0
36	IALLRNGDR	511	-0.2000	0
37	MSRADVDAI	194	-0.3000	0
38	VALSLQDFS	305	-0.3000	0
39	LLLTDGRFS	482	-0.3000	0
40	VGMDDEDFA	39	-0.4000	0
41	LTKEAFENA	271	-0.4000	0

42	FSRIGSGVP	312	-0.4000	0
43	VMSDVDHIG	332	-0.4000	0
44	ITILHGSLA	397	-0.4000	0
45	IGGVPVVMK	339	-0.5200	0
46	WNEITPCNL	57	-0.6000	0
47	LGKDVLLLT	477	-0.7000	0
48	IHPSGGITI	391	-0.8200	0
49	ILPGRAKLS	162	-0.9000	0
50	MAFGGSTNA	284	-0.9000	0
51	LHGSLAPEG	400	-0.9000	0
52	LHGDCLTVT	355	-1.0000	0
53	MLAITGAIK	465	-1.0000	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	IHPSGGITI	391	6.8000	58.62
2	VLRALANPI	383	5.5000	47.41
3	LRNGDRIRL	514	5.3000	45.69
4	FGGSTNAVL	286	5.0000	43.10
5	FSLVSREVI	106	4.8000	41.38
6	LMAAARLDL	144	4.6000	39.66
7	VKLVSSAAV	561	4.6000	39.66
8	VFSAGGYPL	78	4.5000	38.79
9	ISVSDGISM	91	4.5000	38.79
10	LVSSAAVGA	563	4.4000	37.93
11	FLYAGSILP	156	4.2000	36.21
12	FENAIAVVM	276	4.2000	36.21
13	VTIIDAFEA	177	3.7000	31.90
14	VVKTAGFDS	410	3.7000	31.90
15	LAITGAIKG	466	3.7000	31.90
16	WNEITPCNL	57	3.6000	31.03
17	ITVGDAVVI	443	3.4000	29.31

18	LLHGDCLTV	354	3.3000	28.45
19	VGHIAPEAV	498	3.2000	27.59
20	VFLYAGSIL	155	3.1000	26.72
21	FGRHVMSDV	328	2.9000	25.00
22	IRLDVAGRV	520	2.6000	22.41
23	VVMKALLDA	344	2.5000	21.55
24	VKPFGRHVM	325	2.4000	20.69
25	MHFSLVSRE	104	2.3000	19.83
26	VVMAFGGST	282	2.3000	19.83
27	YVKLVSSAA	560	2.3000	19.83
28	IAHEANVAL	299	2.2000	18.97
29	VPVVMKALL	342	2.2000	18.97
30	LLLTDGRFS	482	2.2000	18.97
31	FARRSGQAV	249	2.1000	18.10
32	VVELLRRGI	257	2.1000	18.10
33	LDLAAVFLY	150	2.0000	17.24
34	VDHIGGVPV	336	2.0000	17.24
35	LGMSLPGSA	229	1.9000	16.38
36	IAVVMAFGG	280	1.9000	16.38
37	LEKAAARGM	27	1.8000	15.52
38	VGDAVVIRY	445	1.8000	15.52
39	IGVASSWNE	51	1.7000	14.66
40	MSRADVDAI	194	1.6000	13.79
41	VLHLLAIAH	293	1.6000	13.79
42	FGTISVSDG	88	1.5000	12.93
43	LVSREVIAD	108	1.5000	12.93
44	VIADSVEVV	113	1.5000	12.93
45	FSRIGSGVP	312	1.5000	12.93
46	VLSKYVKLV	556	1.5000	12.93
47	VASSWNEIT	53	1.4000	12.07
48	MREMLAITG	462	1.4000	12.07
49	MYTANTMAS	216	1.3200	11.38
50	LANAVKEGV	70	1.3000	11.21
51	LSLQDFSRI	307	1.2000	10.34

52	IGGVPVVMK	339	1.2000	10.34
53	LTVTGHTMA	360	1.0000	8.62
54	FEGTARVFD	421	1.0000	8.62
55	VSSAAVGAV	564	1.0000	8.62
56	MLMAAARLD	143	0.9000	7.76
57	MLRAVGMDD	35	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	IHPSGGITI	391	6.8000	58.62
2	VLRALANPI	383	5.5000	47.41
3	LRNGDRIRL	514	5.3000	45.69
4	FGGSTNAVL	286	5.0000	43.10
5	FSLVSREVI	106	4.8000	41.38
6	LMAAARLDL	144	4.6000	39.66
7	VKLVSSAAV	561	4.6000	39.66
8	VFSAGGYPL	78	4.5000	38.79
9	ISVSDGISM	91	4.5000	38.79
10	LVSSAAVGA	563	4.4000	37.93
11	FLYAGSILP	156	4.2000	36.21
12	FENAIAVVM	276	4.2000	36.21
13	VTIIDAFEA	177	3.7000	31.90
14	VVKTAGFDS	410	3.7000	31.90
15	LAITGAIKG	466	3.7000	31.90
16	WNEITPCNL	57	3.6000	31.03
17	ITVGDAVVI	443	3.4000	29.31
18	LLHGDCLTV	354	3.3000	28.45
19	VGHIAPEAV	498	3.2000	27.59
20	VFLYAGSIL	155	3.1000	26.72
21	FGRHVMSDV	328	2.9000	25.00
22	IRLDVAGRV	520	2.6000	22.41
23	VVMKALLDA	344	2.5000	21.55

24	VKPFGRHVM	325	2.4000	20.69
25	MHFSLVSRE	104	2.3000	19.83
26	VVMAFGGST	282	2.3000	19.83
27	YVKLVSSAA	560	2.3000	19.83
28	IAHEANVAL	299	2.2000	18.97
29	VPVVMKALL	342	2.2000	18.97
30	LLLTDGRFS	482	2.2000	18.97
31	FARRSGQAV	249	2.1000	18.10
32	VVELLRRGI	257	2.1000	18.10
33	LDLAAVFLY	150	2.0000	17.24
34	VDHIGGVPV	336	2.0000	17.24
35	LGMSLPGSA	229	1.9000	16.38
36	IAVVMAFGG	280	1.9000	16.38
37	LEKAAARGM	27	1.8000	15.52
38	VGDAVVIRY	445	1.8000	15.52
39	IGVASSWNE	51	1.7000	14.66
40	MSRADVDAI	194	1.6000	13.79
41	VLHLLAIAH	293	1.6000	13.79
42	FGTISVSDG	88	1.5000	12.93
43	LVSREVIAD	108	1.5000	12.93
44	VIADSVEVV	113	1.5000	12.93
45	FSRIGSGVP	312	1.5000	12.93
46	VLSKYVKLV	556	1.5000	12.93
47	VASSWNEIT	53	1.4000	12.07
48	MREMLAITG	462	1.4000	12.07
49	MYTANTMAS	216	1.3200	11.38
50	LANAVKEGV	70	1.3000	11.21
51	LSLQDFSRI	307	1.2000	10.34
52	IGGVPVVMK	339	1.2000	10.34
53	LTVTGHTMA	360	1.0000	8.62
54	FEGTARVFD	421	1.0000	8.62
55	VSSAAVGAV	564	1.0000	8.62
56	MLMAAARLD	143	0.9000	7.76
57	MLRAVGMDD	35	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	LVSREVIAD	108	5.0000	58.14
2	VVMKALLDA	344	4.7000	54.65
3	LHLLAIAHE	294	3.5000	40.70
4	LPGRAKLSD	163	3.0000	34.88
5	LRRGITARD	261	2.7000	31.40
6	LSKYVKLVS	557	2.6000	30.23
7	VLSKYVKLV	556	2.5000	29.07
8	ILTKEAFEN	270	2.0000	23.26
9	VVIRYEGPK	449	2.0000	23.26
10	MLMAAARLD	143	1.8000	20.93
11	VKPFGRHVM	325	1.7000	19.77
12	VLHLLAIAH	293	1.4000	16.28
13	LRALANPIH	384	1.4000	16.28
14	VIRYEGPKG	450	1.4000	16.28
15	YVKLVSSAA	560	1.4000	16.28
16	VMQAERLDG	121	1.1000	12.79
17	MYTANTMAS	216	1.1000	12.79
18	IKPRSRDVT	16	1.0000	11.63
19	FGTISVSDG	88	1.0000	11.63
20	VFLYAGSIL	155	1.0000	11.63
21	VELLRRGIT	258	1.0000	11.63
22	VVMAFGGST	282	1.0000	11.63
23	IRYEGPKGG	451	1.0000	11.63
24	IKGAGLGKD	472	1.0000	11.63
25	VVELLRRGI	257	0.9000	10.47
26	MREMLAITG	462	0.9000	10.47
27	LRNGDRIRL	514	0.9000	10.47
28	VKLVSSAAV	561	0.9000	10.47
29	MHFSLVSRE	104	0.8000	9.30
30	LMAAARLDL	144	0.8000	9.30

31	MLRAVGMDD	35	0.7000	8.14
32	VGACSRGLM	186	0.7000	8.14
33	FARRSGQAV	249	0.7000	8.14
34	ITARDILTK	265	0.7000	8.14
35	ILHGSLAPE	399	0.7000	8.14
36	VPVVMKALL	342	0.6000	6.98
37	VVMQAERLD	120	0.5000	5.81
38	LCVGHIAPE	496	0.5000	5.81
39	FASRQQDFS	538	0.5000	5.81
40	WNEITPCNL	57	0.4000	4.65
41	LLRRGITAR	260	0.3000	3.49
42	LQDFSRIGS	309	0.3000	3.49
43	ITGAIKGAG	468	0.3000	3.49
44	IRLDVAGRV	520	0.3000	3.49
45	FENAIAVVM	276	0.2000	2.33
46	FEGTARVFD	421	0.2000	2.33
47	VTIIDAFEA	177	-0.1000	0
48	IERAICPGE	202	-0.1000	0
49	LGMSLPGSA	229	-0.1000	0
50	VSREVIADS	109	-0.2000	0
51	LYAGSILPG	157	-0.4000	0
52	LRAVGMDDE	36	-0.5000	0
53	FSLVSREVI	106	-0.5000	0
54	FEAVGACSR	183	-0.6000	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	VVMKALLDA	344	4.7000	58.75
2	VVIRYEGPK	449	2.7000	33.75
3	LSKYVKLVS	557	2.6000	32.50
4	LVSREVIAD	108	2.3000	28.75
5	VLSKYVKLV	556	2.2000	27.50

6	ITARDILTK	265	1.4000	17.50
7	YVKLVSSAA	560	1.4000	17.50
8	MYTANTMAS	216	1.1000	13.75
9	VVELLRRGI	257	0.7000	8.75
10	VKPFGRHVM	325	0.6000	7.50
11	VKLVSSAAV	561	0.6000	7.50
12	LHLLAIAHE	294	0.5000	6.25
13	FASRQQDFS	538	0.5000	6.25
14	FARRSGQAV	249	0.4000	5.00
15	LPGRAKLSD	163	0.3000	3.75
16	LLRRGITAR	260	0.3000	3.75
17	LQDFSRIGS	309	0.3000	3.75
18	VLHLLAIAH	293	0.1800	2.25
19	LRALANPIH	384	0.1800	2.25
20	IKPRSRDVT	16	0.1000	1.25
21	VELLRRGIT	258	0.1000	1.25
22	VVMAFGGST	282	0.1000	1.25
23	VIRYEGPKG	450	0.1000	1.25
24	VTIIDAFEA	177	-0.1000	0
25	LGMSLPGSA	229	-0.1000	0
26	LRNGDRIRL	514	-0.1000	0
27	VSREVIADS	109	-0.2000	0
28	VMQAERLDG	121	-0.2000	0
29	LMAAARLDL	144	-0.2000	0
30	IGGVPVVMK	339	-0.2000	0
31	FGTISVSDG	88	-0.3000	0
32	IRYEGPKGG	451	-0.3000	0
33	FLYAGSILP	156	-0.4000	0
34	VGACSRGLM	186	-0.4000	0
35	VPVVMKALL	342	-0.4000	0
36	MREMLAITG	462	-0.4000	0
37	WNEITPCNL	57	-0.6000	0
38	FEAVGACSR	183	-0.6000	0
39	LLLTDGRFS	482	-0.6000	0

40	FSLVSREVI	106	-0.7000	0
41	VLLAGCDKS	131	-0.7000	0
42	MLAITGAIK	465	-0.7000	0
43	FAKPQIGVA	46	-0.8000	0
44	LPGMLMAAA	140	-0.8000	0
45	ILPGRAKLS	162	-0.8000	0
46	ITILHGSLA	397	-0.8000	0
47	VVKTAGFDS	410	-0.8000	0
48	FSGGTTGLC	489	-0.8000	0
49	LVSSAAVGA	563	-0.8000	0
50	MLMAAARLD	143	-0.9000	0
51	LMSRADVDA	193	-0.9000	0
52	YTANTMASA	217	-0.9000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VVMKALLDA	344	5.7000	71.25
2	VVIRYEGPK	449	3.7000	46.25
3	LSKYVKLVS	557	3.6000	45.00
4	LVSREVIAD	108	3.3000	41.25
5	VLSKYVKLV	556	3.2000	40.00
6	ITARDILTK	265	2.4000	30.00
7	MYTANTMAS	216	2.1000	26.25
8	VVELLRRGI	257	1.7000	21.25
9	VKPFGRHVM	325	1.6000	20.00
10	VKLVSSAAV	561	1.6000	20.00
11	LHLLAIAHE	294	1.5000	18.75
12	LPGRAKLSD	163	1.3000	16.25
13	LLRRGITAR	260	1.3000	16.25
14	LQDFSRIGS	309	1.3000	16.25
15	VLHLLAIAH	293	1.1800	14.75
16	LRALANPIH	384	1.1800	14.75

17	IKPRSRDVT	16	1.1000	13.75
18	VELLRRGIT	258	1.1000	13.75
19	VVMAFGGST	282	1.1000	13.75
20	VIRYEGPKG	450	1.1000	13.75
21	VFLYAGSIL	155	1.0000	12.50
22	LRRGITARD	261	1.0000	12.50
23	ILTKEAFEN	270	1.0000	12.50
24	IRLDVAGRV	520	1.0000	12.50
25	VTIIDAFEA	177	0.9000	11.25
26	LGMSLPGSA	229	0.9000	11.25
27	LRNGDRIRL	514	0.9000	11.25
28	VSREVIADS	109	0.8000	10.00
29	VMQAERLDG	121	0.8000	10.00
30	LMAAARLDL	144	0.8000	10.00
31	IGGVPVVMK	339	0.8000	10.00
32	IRYEGPKGG	451	0.7000	8.75
33	VGACSRGLM	186	0.6000	7.50
34	VPVVMKALL	342	0.6000	7.50
35	MREMLAITG	462	0.6000	7.50
36	LLLTDGRFS	482	0.4000	5.00
37	YVKLVSSAA	560	0.4000	5.00
38	VLLAGCDKS	131	0.3000	3.75
39	MLAITGAIK	465	0.3000	3.75
40	LPGMLMAAA	140	0.2000	2.50
41	ILPGRAKLS	162	0.2000	2.50
42	ITILHGSLA	397	0.2000	2.50
43	VVKTAGFDS	410	0.2000	2.50
44	LVSSAAVGA	563	0.2000	2.50
45	MLMAAARLD	143	0.1000	1.25
46	LMSRADVDA	193	0.1000	1.25
47	VLRALANPI	383	0.1000	1.25
48	LSLDRLANA	65	-0.1000	0
49	VSSAAVGAV	564	-0.1000	0
50	VEVVMQAER	118	-0.4000	0

51	IALLRNGDR	511	-0.4000	0
52	FASRQQDFS	538	-0.5000	0
53	FARRSGQAV	249	-0.6000	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	LVSREVIAD	108	6.0000	69.77
2	VVMKALLDA	344	5.7000	66.28
3	LHLLAIAHE	294	4.5000	52.33
4	LPGRAKLSD	163	4.0000	46.51
5	LRRGITARD	261	3.7000	43.02
6	LSKYVKLVS	557	3.6000	41.86
7	VLSKYVKLV	556	3.5000	40.70
8	ILTKEAFEN	270	3.0000	34.88
9	VVIRYEGPK	449	3.0000	34.88
10	MLMAAARLD	143	2.8000	32.56
11	VKPFGRHVM	325	2.7000	31.40
12	VLHLLAIAH	293	2.4000	27.91
13	LRALANPIH	384	2.4000	27.91
14	VIRYEGPKG	450	2.4000	27.91
15	VMQAERLDG	121	2.1000	24.42
16	MYTANTMAS	216	2.1000	24.42
17	IKPRSRDVT	16	2.0000	23.26
18	VFLYAGSIL	155	2.0000	23.26
19	VELLRRGIT	258	2.0000	23.26
20	VVMAFGGST	282	2.0000	23.26
21	IRYEGPKGG	451	2.0000	23.26
22	IKGAGLGKD	472	2.0000	23.26
23	VVELLRRGI	257	1.9000	22.09
24	MREMLAITG	462	1.9000	22.09
25	LRNGDRIRL	514	1.9000	22.09
26	VKLVSSAAV	561	1.9000	22.09

27	MHFSLVSRE	104	1.8000	20.93
28	LMAAARLDL	144	1.8000	20.93
29	MLRAVGMDD	35	1.7000	19.77
30	VGACSRGLM	186	1.7000	19.77
31	ITARDILTK	265	1.7000	19.77
32	ILHGSLAPE	399	1.7000	19.77
33	VPVVMKALL	342	1.6000	18.60
34	VVMQAERLD	120	1.5000	17.44
35	LCVGHIAPE	496	1.5000	17.44
36	LLRRGITAR	260	1.3000	15.12
37	LQDFSRIGS	309	1.3000	15.12
38	ITGAIKGAG	468	1.3000	15.12
39	IRLDVAGRV	520	1.3000	15.12
40	IGVASSWNE	51	1.0000	11.63
41	VTIIDAFEA	177	0.9000	10.47
42	IERAICPGE	202	0.9000	10.47
43	LGMSLPGSA	229	0.9000	10.47
44	VSREVIADS	109	0.8000	9.30
45	LYAGSILPG	157	0.6000	6.98
46	LRAVGMDDE	36	0.5000	5.81
47	LLLTDGRFS	482	0.4000	4.65
48	LLTDGRFSG	483	0.4000	4.65
49	YVKLVSSAA	560	0.4000	4.65
50	VLLAGCDKS	131	0.3000	3.49
51	VLRALANPI	383	0.3000	3.49
52	VAGRVLDVL	524	0.3000	3.49
53	LEKAAARGM	27	0.2000	2.33
54	ITPCNLSLD	60	0.2000	2.33
55	LPGMLMAAA	140	0.2000	2.33
56	ILPGRAKLS	162	0.2000	2.33
57	IAVVMAFGG	280	0.2000	2.33

ALLELE: DRB1_0813	Threshold for 3 % with score:	Highest Score achievable by any peptide:

	1.9	8.7

Rank	Sequence	At Position	Score	% of Highest Score
1	VVMKALLDA	344	5.3000	60.92
2	LSKYVKLVS	557	3.2000	36.78
3	YVKLVSSAA	560	3.2000	36.78
4	LVSREVIAD	108	3.1800	36.55
5	LLRRGITAR	260	3.1000	35.63
6	MYTANTMAS	216	2.1000	24.14
7	ITARDILTK	265	2.0000	22.99
8	VVIRYEGPK	449	2.0000	22.99
9	VFLYAGSIL	155	1.8000	20.69
10	FASRQQDFS	538	1.7000	19.54
11	VLSKYVKLV	556	1.7000	19.54
12	FGTISVSDG	88	1.5000	17.24
13	FARRSGQAV	249	1.4000	16.09
14	IKPRSRDVT	16	1.3000	14.94
15	LQDFSRIGS	309	1.1800	13.56
16	VKPFGRHVM	325	1.1000	12.64
17	VLRALANPI	383	1.1000	12.64
18	VLHLLAIAH	293	1.0600	12.18
19	FSLVSREVI	106	1.0000	11.49
20	ITILHGSLA	397	1.0000	11.49
21	LPGRAKLSD	163	0.9000	10.34
22	ILTKEAFEN	270	0.8500	9.77
23	LEFGTISVS	86	0.8000	9.20
24	IGGVPVVMK	339	0.8000	9.20
25	LRNGDRIRL	514	0.7800	8.97
26	VTIIDAFEA	177	0.7500	8.62
27	VKLVSSAAV	561	0.6000	6.90
28	VLLAGCDKS	131	0.5000	5.75
29	LHLLAIAHE	294	0.5000	5.75
30	FLYAGSILP	156	0.4800	5.52
31	MREMLAITG	462	0.4800	5.52
32	VMQAERLDG	121	0.4000	4.60

33	LMAAARLDL	144	0.4000	4.60
34	VVELLRRGI	257	0.4000	4.60
35	LRALANPIH	384	0.3800	4.37
36	VIRYEGPKG	450	0.3000	3.45
37	LVSSAAVGA	563	0.2000	2.30
38	LMSRADVDA	193	0.1000	1.15
39	FENAIAVVM	276	0.1000	1.15
40	VVKTAGFDS	410	0.0500	0.57
41	YPLEFGTIS	84	-0.1000	0
42	VSREVIADS	109	-0.2000	0
43	LAGCDKSLP	133	-0.3000	0
44	MHFSLVSRE	104	-0.4000	0
45	VPVVMKALL	342	-0.4000	0
46	VAGRVLDVL	524	-0.5000	0
47	WNEITPCNL	57	-0.6000	0
48	LANAVKEGV	70	-0.6000	0
49	FEAVGACSR	183	-0.6000	0
50	VELLRRGIT	258	-0.6000	0
51	VVMAFGGST	282	-0.6000	0
52	MLAITGAIK	465	-0.7000	0
53	IRLDVAGRV	520	-0.7000	0
54	LPGMLMAAA	140	-0.8000	0
55	LGMSLPGSA	229	-0.8000	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	LVSREVIAD	108	6.6000	65.35
2	VVMKALLDA	344	6.5000	64.36
3	LPGRAKLSD	163	4.8000	47.52
4	LSKYVKLVS	557	4.4000	43.56
5	LHLLAIAHE	294	3.5000	34.65
6	VLSKYVKLV	556	3.1000	30.69

7	VLHLLAIAH	293	3.0000	29.70
8	VMQAERLDG	121	2.9000	28.71
9	MYTANTMAS	216	2.7000	26.73
10	LRRGITARD	261	2.7000	26.73
11	LMAAARLDL	144	2.6000	25.74
12	LRALANPIH	384	2.5500	25.25
13	VIRYEGPKG	450	2.5500	25.25
14	ITARDILTK	265	2.5000	24.75
15	ILTKEAFEN	270	2.5000	24.75
16	MREMLAITG	462	2.5000	24.75
17	LRNGDRIRL	514	2.5000	24.75
18	VKPFGRHVM	325	2.4000	23.76
19	MLRAVGMDD	35	2.3000	22.77
20	VVIRYEGPK	449	2.1000	20.79
21	MLMAAARLD	143	2.0000	19.80
22	LQDFSRIGS	309	1.9000	18.81
23	FLYAGSILP	156	1.6000	15.84
24	IRYEGPKGG	451	1.6000	15.84
25	LYAGSILPG	157	1.4000	13.86
26	LLRRGITAR	260	1.4000	13.86
27	YVKLVSSAA	560	1.4000	13.86
28	VVELLRRGI	257	1.1000	10.89
29	VELLRRGIT	258	1.1000	10.89
30	VVMAFGGST	282	1.1000	10.89
31	IKGAGLGKD	472	1.1000	10.89
32	IERAICPGE	202	1.0500	10.40
33	FGTISVSDG	88	1.0000	9.90
34	VFLYAGSIL	155	1.0000	9.90
35	VKLVSSAAV	561	0.9000	8.91
36	IGVASSWNE	51	0.8000	7.92
37	MHFSLVSRE	104	0.8000	7.92
38	VGACSRGLM	186	0.8000	7.92
39	FARRSGQAV	249	0.8000	7.92
40	IKPRSRDVT	16	0.7000	6.93

41	VVMQAERLD	120	0.7000	6.93
42	FENAIAVVM	276	0.7000	6.93
43	LLDAGLLHG	349	0.7000	6.93
44	ILHGSLAPE	399	0.7000	6.93
45	FEGTARVFD	421	0.7000	6.93
46	FSLVSREVI	106	0.6000	5.94
47	VPVVMKALL	342	0.6000	5.94
48	LAITGAIKG	466	0.6000	5.94
49	LCVGHIAPE	496	0.5000	4.95
50	WNEITPCNL	57	0.4000	3.96
51	VTIIDAFEA	177	0.4000	3.96
52	ITGAIKGAG	468	0.4000	3.96
53	IRLDVAGRV	520	0.4000	3.96
54	LLHGDCLTV	354	0.3000	2.97
55	VGDAVVIRY	445	0.3000	2.97
56	FASRQQDFS	538	0.2000	1.98

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	VVMKALLDA	344	3.7000	44.58
2	MYTANTMAS	216	2.7000	32.53
3	VLHLLAIAH	293	2.1800	26.27
4	LQDFSRIGS	309	1.8000	21.69
5	YVKLVSSAA	560	1.8000	21.69
6	LRALANPIH	384	1.7300	20.84
7	VMQAERLDG	121	1.6000	19.28
8	LMAAARLDL	144	1.6000	19.28
9	LSKYVKLVS	557	1.5000	18.07
10	VVELLRRGI	257	1.3000	15.66
11	FLYAGSILP	156	1.2000	14.46
12	VKPFGRHVM	325	1.2000	14.46
13	VTIIDAFEA	177	1.0000	12.05

14	LVSREVIAD	108	0.9000	10.84
15	LHLLAIAHE	294	0.9000	10.84
16	MREMLAITG	462	0.8000	9.64
17	LRNGDRIRL	514	0.8000	9.64
18	VKLVSSAAV	561	0.7000	8.43
19	VELLRRGIT	258	0.6000	7.23
20	FSLVSREVI	106	0.5000	6.02
21	IGGVPVVMK	339	0.4000	4.82
22	FGTISVSDG	88	0.3000	3.61
23	LGMSLPGSA	229	0.3000	3.61
24	ITARDILTK	265	0.2000	2.41
25	VVMAFGGST	282	0.2000	2.41
26	VVKTAGFDS	410	0.1000	1.20
27	MLAITGAIK	465	-0.1000	0
28	VVIRYEGPK	449	-0.2000	0
29	VGACSRGLM	186	-0.3000	0
30	VPVVMKALL	342	-0.3000	0
31	LAITGAIKG	466	-0.3000	0
32	MLRAVGMDD	35	-0.4000	0
33	VDAIERAIC	199	-0.4000	0
34	FENAIAVVM	276	-0.4000	0
35	ITILHGSLA	397	-0.4000	0
36	IRYEGPKGG	451	-0.4000	0
37	FEAVGACSR	183	-0.5000	0
38	FSRIGSGVP	312	-0.5000	0
39	LYAGSILPG	157	-0.6000	0
40	LLDAGLLHG	349	-0.6000	0
41	VLRALANPI	383	-0.6000	0
42	IRLDVAGRV	520	-0.6000	0
43	MLMAAARLD	143	-0.7000	0
44	LRRGITARD	261	-0.7000	0
45	LLHGDCLTV	354	-0.7000	0
46	IHPSGGITI	391	-0.8000	0
47	VGDAVVIRY	445	-0.8000	0

48	VSREVIADS	109	-0.9000	0
49	ILPGRAKLS	162	-0.9000	0
50	LPGRAKLSD	163	-0.9000	0
51	YTANTMASA	217	-0.9000	0
52	ITGAIKGAG	468	-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	VVMKALLDA	344	4.9000	58.33
2	VVELLRRGI	257	3.2000	38.10
3	VKPFGRHVM	325	3.1000	36.90
4	VLSKYVKLV	556	2.5000	29.76
5	LSKYVKLVS	557	2.5000	29.76
6	MYTANTMAS	216	2.4000	28.57
7	VVMQAERLD	120	2.2000	26.19
8	LLLTDGRFS	482	2.1000	25.00
9	MLMAAARLD	143	1.9000	22.62
10	LQDFSRIGS	309	1.9000	22.62
11	VVKTAGFDS	410	1.6000	19.05
12	LVSSAAVGA	563	1.6000	19.05
13	LRALANPIH	384	1.5800	18.81
14	LVSREVIAD	108	1.5000	17.86
15	VMQAERLDG	121	1.5000	17.86
16	LMAAARLDL	144	1.5000	17.86
17	VTIIDAFEA	177	1.5000	17.86
18	VLRALANPI	383	1.5000	17.86
19	IRYEGPKGG	451	1.4000	16.67
20	VLLAGCDKS	131	1.2000	14.29
21	LHLLAIAHE	294	1.2000	14.29
22	VLHLLAIAH	293	1.1800	14.05
23	ITARDILTK	265	1.0000	11.90
24	ILTKEAFEN	270	1.0000	11.90

25	LEKAAARGM	27	0.9000	10.71
26	VSREVIADS	109	0.7000	8.33
27	LLRRGITAR	260	0.7000	8.33
28	LRNGDRIRL	514	0.7000	8.33
29	IGGVPVVMK	339	0.6000	7.14
30	VVIRYEGPK	449	0.6000	7.14
31	LDLAAVFLY	150	0.5000	5.95
32	ILPGRAKLS	162	0.5000	5.95
33	LRRGITARD	261	0.5000	5.95
34	YVKLVSSAA	560	0.5000	5.95
35	VKLVSSAAV	561	0.4000	4.76
36	LGMSLPGSA	229	0.3000	3.57
37	ITILHGSLA	397	0.3000	3.57
38	MREMLAITG	462	0.3000	3.57
39	LLTDGRFSG	483	0.2000	2.38
40	LANAVKEGV	70	0.1000	1.19
41	VVMAFGGST	282	0.1000	1.19
42	IKPRSRDVT	16	-0.1000	0
43	LEFGTISVS	86	-0.1000	0
44	LPGRAKLSD	163	-0.1000	0
45	MSRADVDAI	194	-0.2000	0
46	VELLRRGIT	258	-0.2000	0
47	MGHEGMHFS	99	-0.3000	0
48	IGVASSWNE	51	-0.4000	0
49	MHFSLVSRE	104	-0.4000	0
50	LPGMLMAAA	140	-0.4000	0
51	VFLYAGSIL	155	-0.4000	0
52	VGACSRGLM	186	-0.4000	0
53	LLRNGDRIR	513	-0.4000	0
54	IRLDVAGRV	520	-0.4000	0

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	VVMKALLDA	344	4.7000	56.63
2	MYTANTMAS	216	3.7000	44.58
3	VLHLLAIAH	293	3.1800	38.31
4	LQDFSRIGS	309	2.8000	33.73
5	LRALANPIH	384	2.7300	32.89
6	VMQAERLDG	121	2.6000	31.33
7	LMAAARLDL	144	2.6000	31.33
8	LSKYVKLVS	557	2.5000	30.12
9	VVELLRRGI	257	2.3000	27.71
10	VKPFGRHVM	325	2.2000	26.51
11	VTIIDAFEA	177	2.0000	24.10
12	LVSREVIAD	108	1.9000	22.89
13	LHLLAIAHE	294	1.9000	22.89
14	MREMLAITG	462	1.8000	21.69
15	LRNGDRIRL	514	1.8000	21.69
16	VKLVSSAAV	561	1.7000	20.48
17	VELLRRGIT	258	1.6000	19.28
18	IGGVPVVMK	339	1.4000	16.87
19	LGMSLPGSA	229	1.3000	15.66
20	ITARDILTK	265	1.2000	14.46
21	VVMAFGGST	282	1.2000	14.46
22	VVKTAGFDS	410	1.1000	13.25
23	LLLTDGRFS	482	1.0000	12.05
24	VLSKYVKLV	556	1.0000	12.05
25	LVSSAAVGA	563	1.0000	12.05
26	MLAITGAIK	465	0.9000	10.84
27	VVIRYEGPK	449	0.8000	9.64
28	YVKLVSSAA	560	0.8000	9.64
29	VGACSRGLM	186	0.7000	8.43
30	VPVVMKALL	342	0.7000	8.43
31	LAITGAIKG	466	0.7000	8.43
32	MLRAVGMDD	35	0.6000	7.23
33	VDAIERAIC	199	0.6000	7.23

34	ITILHGSLA	397	0.6000	7.23
35	IRYEGPKGG	451	0.6000	7.23
36	LYAGSILPG	157	0.4000	4.82
37	LLDAGLLHG	349	0.4000	4.82
38	VLRALANPI	383	0.4000	4.82
39	IRLDVAGRV	520	0.4000	4.82
40	MLMAAARLD	143	0.3000	3.61
41	LRRGITARD	261	0.3000	3.61
42	LLHGDCLTV	354	0.3000	3.61
43	FLYAGSILP	156	0.2000	2.41
44	IHPSGGITI	391	0.2000	2.41
45	VGDAVVIRY	445	0.2000	2.41
46	VSREVIADS	109	0.1000	1.20
47	ILPGRAKLS	162	0.1000	1.20
48	LPGRAKLSD	163	0.1000	1.20
49	ITGAIKGAG	468	0.1000	1.20
50	VGHIAPEAV	498	0.1000	1.20
51	IALLRNGDR	511	0.1000	1.20
52	LAAITPPDP	371	0.0500	0.60
53	LANAVKEGV	70	-0.2000	0
54	LPGMLMAAA	140	-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	VVMKALLDA	344	4.7000	56.63
2	MYTANTMAS	216	3.7000	44.58
3	VLHLLAIAH	293	3.1800	38.31
4	LQDFSRIGS	309	2.8000	33.73
5	LRALANPIH	384	2.7300	32.89
6	VMQAERLDG	121	2.6000	31.33
7	LMAAARLDL	144	2.6000	31.33
8	LSKYVKLVS	557	2.5000	30.12

9	VVELLRRGI	257	2.3000	27.71
10	VKPFGRHVM	325	2.2000	26.51
11	VTIIDAFEA	177	2.0000	24.10
12	LVSREVIAD	108	1.9000	22.89
13	LHLLAIAHE	294	1.9000	22.89
14	MREMLAITG	462	1.8000	21.69
15	LRNGDRIRL	514	1.8000	21.69
16	VKLVSSAAV	561	1.7000	20.48
17	VELLRRGIT	258	1.6000	19.28
18	IGGVPVVMK	339	1.4000	16.87
19	LGMSLPGSA	229	1.3000	15.66
20	ITARDILTK	265	1.2000	14.46
21	VVMAFGGST	282	1.2000	14.46
22	VVKTAGFDS	410	1.1000	13.25
23	LLLTDGRFS	482	1.0000	12.05
24	VLSKYVKLV	556	1.0000	12.05
25	LVSSAAVGA	563	1.0000	12.05
26	MLAITGAIK	465	0.9000	10.84
27	VVIRYEGPK	449	0.8000	9.64
28	YVKLVSSAA	560	0.8000	9.64
29	VGACSRGLM	186	0.7000	8.43
30	VPVVMKALL	342	0.7000	8.43
31	LAITGAIKG	466	0.7000	8.43
32	MLRAVGMDD	35	0.6000	7.23
33	VDAIERAIC	199	0.6000	7.23
34	ITILHGSLA	397	0.6000	7.23
35	IRYEGPKGG	451	0.6000	7.23
36	LYAGSILPG	157	0.4000	4.82
37	LLDAGLLHG	349	0.4000	4.82
38	VLRALANPI	383	0.4000	4.82
39	IRLDVAGRV	520	0.4000	4.82
40	MLMAAARLD	143	0.3000	3.61
41	LRRGITARD	261	0.3000	3.61
42	LLHGDCLTV	354	0.3000	3.61

43	FLYAGSILP	156	0.2000	2.41
44	IHPSGGITI	391	0.2000	2.41
45	VGDAVVIRY	445	0.2000	2.41
46	VSREVIADS	109	0.1000	1.20
47	ILPGRAKLS	162	0.1000	1.20
48	LPGRAKLSD	163	0.1000	1.20
49	ITGAIKGAG	468	0.1000	1.20
50	VGHIAPEAV	498	0.1000	1.20
51	IALLRNGDR	511	0.1000	1.20
52	LAAITPPDP	371	0.0500	0.60
53	LANAVKEGV	70	-0.2000	0
54	LPGMLMAAA	140	-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	IRLDVAGRV	520	4.9000	53.85
2	LLTDGRFSG	483	3.8000	41.76
3	VIADSVEVV	113	3.7000	40.66
4	LRNGDRIRL	514	3.6000	39.56
5	MYTANTMAS	216	3.5000	38.46
6	LSLDRLANA	65	3.2000	35.16
7	LGMSLPGSA	229	3.2000	35.16
8	LVSSAAVGA	563	3.2000	35.16
9	VLADPAEFA	531	3.1000	34.07
10	VVMKALLDA	344	2.9000	31.87
11	LEFGTISVS	86	2.8700	31.54
12	VTIIDAFEA	177	2.5000	27.47
13	LRRGITARD	261	2.5000	27.47
14	LRALANPIH	384	2.3800	26.15
15	VGMDDEDFA	39	2.2000	24.18
16	LHGDCLTVT	355	2.2000	24.18
17	VLLAGCDKS	131	2.1000	23.08

18	LGKDVLLLT	477	2.0000	21.98
19	MHFSLVSRE	104	1.8700	20.55
20	IGGVPVVMK	339	1.8000	19.78
21	VVMAFGGST	282	1.7000	18.68
22	VLHLLAIAH	293	1.6800	18.46
23	ILPGRAKLS	162	1.6000	17.58
24	VVKTAGFDS	410	1.6000	17.58
25	VALSLQDFS	305	1.5000	16.48
26	LHGSLAPEG	400	1.4000	15.38
27	VLRALANPI	383	1.3100	14.40
28	VMQAERLDG	121	1.3000	14.29
29	LMAAARLDL	144	1.3000	14.29
30	LYAGSILPG	157	1.3000	14.29
31	VKLVSSAAV	561	1.3000	14.29
32	LVSREVIAD	108	1.2000	13.19
33	VGACSRGLM	186	1.2000	13.19
34	LLHGDCLTV	354	1.2000	13.19
35	IHPSGGITI	391	1.2000	13.19
36	LPGSAAPPA	233	1.1000	12.09
37	MAFGGSTNA	284	1.1000	12.09
38	YVKLVSSAA	560	1.0700	11.76
39	VELLRRGIT	258	1.0000	10.99
40	LQDFSRIGS	309	1.0000	10.99
41	VVIRYEGPK	449	1.0000	10.99
42	LANAVKEGV	70	0.9000	9.89
43	IGSGVPHLA	315	0.9000	9.89
44	ITVGDAVVI	443	0.9000	9.89
45	LSKYVKLVS	557	0.9000	9.89
46	ITILHGSLA	397	0.8700	9.56
47	VSREVIADS	109	0.8000	8.79
48	LHLLAIAHE	294	0.8000	8.79
49	VGHIAPEAV	498	0.8000	8.79
50	MSRADVDAI	194	0.7000	7.69
51	VVELLRRGI	257	0.7000	7.69

52	IRYEGPKGG	451	0.6000	6.59
53	ITGAIKGAG	468	0.6000	6.59
54	MQAERLDGS	122	0.5000	5.49
55	MLAITGAIK	465	0.5000	5.49
56	VSSAAVGAV	564	0.5000	5.49
57	MLRAVGMDD	35	0.4000	4.40

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	VVMKALLDA	344	3.9000	46.43
2	VVELLRRGI	257	2.2000	26.19
3	VKPFGRHVM	325	2.1000	25.00
4	VLSKYVKLV	556	1.5000	17.86
5	LSKYVKLVS	557	1.5000	17.86
6	YVKLVSSAA	560	1.5000	17.86
7	MYTANTMAS	216	1.4000	16.67
8	VVMQAERLD	120	1.2000	14.29
9	LLLTDGRFS	482	1.1000	13.10
10	MLMAAARLD	143	0.9000	10.71
11	LQDFSRIGS	309	0.9000	10.71
12	VVKTAGFDS	410	0.6000	7.14
13	LVSSAAVGA	563	0.6000	7.14
14	LRALANPIH	384	0.5800	6.90
15	LVSREVIAD	108	0.5000	5.95
16	VMQAERLDG	121	0.5000	5.95
17	LMAAARLDL	144	0.5000	5.95
18	VTIIDAFEA	177	0.5000	5.95
19	VLRALANPI	383	0.5000	5.95
20	IRYEGPKGG	451	0.4000	4.76
21	VLLAGCDKS	131	0.2000	2.38
22	LHLLAIAHE	294	0.2000	2.38
23	FGRHVMSDV	328	0.2000	2.38

24	VLHLLAIAH	293	0.1800	2.14
25	FENAIAVVM	276	0.1000	1.19
26	LEKAAARGM	27	-0.1000	0
27	FLYAGSILP	156	-0.1000	0
28	VSREVIADS	109	-0.3000	0
29	LLRRGITAR	260	-0.3000	0
30	LRNGDRIRL	514	-0.3000	0
31	IGGVPVVMK	339	-0.4000	0
32	VVIRYEGPK	449	-0.4000	0
33	FSLVSREVI	106	-0.5000	0
34	LDLAAVFLY	150	-0.5000	0
35	ILPGRAKLS	162	-0.5000	0
36	LRRGITARD	261	-0.5000	0
37	VKLVSSAAV	561	-0.6000	0
38	LGMSLPGSA	229	-0.7000	0
39	ITILHGSLA	397	-0.7000	0
40	MREMLAITG	462	-0.7000	0
41	FASRQQDFS	538	-0.7000	0
42	FGTISVSDG	88	-0.8000	0
43	YTANTMASA	217	-0.8000	0
44	LLTDGRFSG	483	-0.8000	0
45	LANAVKEGV	70	-0.9000	0
46	FARRSGQAV	249	-0.9000	0
47	VVMAFGGST	282	-0.9000	0
48	IGSGVPHLA	315	-1.0000	0
49	VIRYEGPKG	450	-1.0000	0
50	FSPPPPRYT	545	-1.0000	0
51	IKPRSRDVT	16	-1.1000	0
52	LEFGTISVS	86	-1.1000	0
53	LPGRAKLSD	163	-1.1000	0
54	MSRADVDAI	194	-1.2000	0

ALLELE: DRB1_1120	Threshold for 3 % with score:	Highest Score achievable by any peptide: 8.8

	2.1	

Rank	Sequence	At Position	Score	% of Highest Score
1	VVMKALLDA	344	3.9000	44.32
2	VKPFGRHVM	325	3.6000	40.91
3	VVELLRRGI	257	3.1000	35.23
4	VLSKYVKLV	556	2.5000	28.41
5	VVMQAERLD	120	2.3000	26.14
6	MLMAAARLD	143	2.0000	22.73
7	VMQAERLDG	121	1.9000	21.59
8	LSKYVKLVS	557	1.9000	21.59
9	MYTANTMAS	216	1.8000	20.45
10	IRYEGPKGG	451	1.8000	20.45
11	LVSREVIAD	108	1.6000	18.18
12	FENAIAVVM	276	1.6000	18.18
13	LHLLAIAHE	294	1.6000	18.18
14	LLLTDGRFS	482	1.5000	17.05
15	YVKLVSSAA	560	1.5000	17.05
16	LMAAARLDL	144	1.4600	16.59
17	LEKAAARGM	27	1.4000	15.91
18	VLRALANPI	383	1.4000	15.91
19	LQDFSRIGS	309	1.3000	14.77
20	LLRRGITAR	260	1.2000	13.64
21	FGRHVMSDV	328	1.2000	13.64
22	VVKTAGFDS	410	1.0000	11.36
23	FLYAGSILP	156	0.9000	10.23
24	LDLAAVFLY	150	0.8000	9.09
25	ILTKEAFEN	270	0.8000	9.09
26	MREMLAITG	462	0.7000	7.95
27	LRNGDRIRL	514	0.6600	7.50
28	FGTISVSDG	88	0.6000	6.82
29	VLLAGCDKS	131	0.6000	6.82
30	LRRGITARD	261	0.6000	6.82
31	LLTDGRFSG	483	0.6000	6.82
32	LVSSAAVGA	563	0.6000	6.82

33	VTIIDAFEA	177	0.5000	5.68
34	FSLVSREVI	106	0.4000	4.55
35	VIRYEGPKG	450	0.4000	4.55
36	VKLVSSAAV	561	0.4000	4.55
37	LANAVKEGV	70	0.1000	1.14
38	VSREVIADS	109	0.1000	1.14
39	VGACSRGLM	186	0.1000	1.14
40	FARRSGQAV	249	0.1000	1.14
41	ITARDILTK	265	0.1000	1.14
42	LLRNGDRIR	513	0.1000	1.14
43	LYAGSILPG	157	-0.1000	0
44	ILPGRAKLS	162	-0.1000	0
45	YAGSILPGR	158	-0.2000	0
46	VVMAFGGST	282	-0.2000	0
47	FEAVGACSR	183	-0.3000	0
48	MSRADVDAI	194	-0.3000	0
49	IGGVPVVMK	339	-0.3000	0
50	LLDAGLLHG	349	-0.3000	0
51	VVIRYEGPK	449	-0.3000	0
52	FASRQQDFS	538	-0.3000	0

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	VVMKALLDA	344	4.9000	58.33
2	VVELLRRGI	257	3.2000	38.10
3	VKPFGRHVM	325	3.1000	36.90
4	VLSKYVKLV	556	2.5000	29.76
5	LSKYVKLVS	557	2.5000	29.76
6	MYTANTMAS	216	2.4000	28.57
7	VVMQAERLD	120	2.2000	26.19
8	LLLTDGRFS	482	2.1000	25.00
9	MLMAAARLD	143	1.9000	22.62

10	LQDFSRIGS	309	1.9000	22.62
11	VVKTAGFDS	410	1.6000	19.05
12	LVSSAAVGA	563	1.6000	19.05
13	LRALANPIH	384	1.5800	18.81
14	LVSREVIAD	108	1.5000	17.86
15	VMQAERLDG	121	1.5000	17.86
16	LMAAARLDL	144	1.5000	17.86
17	VTIIDAFEA	177	1.5000	17.86
18	VLRALANPI	383	1.5000	17.86
19	IRYEGPKGG	451	1.4000	16.67
20	VLLAGCDKS	131	1.2000	14.29
21	LHLLAIAHE	294	1.2000	14.29
22	VLHLLAIAH	293	1.1800	14.05
23	ITARDILTK	265	1.0000	11.90
24	ILTKEAFEN	270	1.0000	11.90
25	LEKAAARGM	27	0.9000	10.71
26	VSREVIADS	109	0.7000	8.33
27	LLRRGITAR	260	0.7000	8.33
28	LRNGDRIRL	514	0.7000	8.33
29	IGGVPVVMK	339	0.6000	7.14
30	VVIRYEGPK	449	0.6000	7.14
31	LDLAAVFLY	150	0.5000	5.95
32	ILPGRAKLS	162	0.5000	5.95
33	LRRGITARD	261	0.5000	5.95
34	YVKLVSSAA	560	0.5000	5.95
35	VKLVSSAAV	561	0.4000	4.76
36	LGMSLPGSA	229	0.3000	3.57
37	ITILHGSLA	397	0.3000	3.57
38	MREMLAITG	462	0.3000	3.57
39	LLTDGRFSG	483	0.2000	2.38
40	LANAVKEGV	70	0.1000	1.19
41	VVMAFGGST	282	0.1000	1.19
42	IKPRSRDVT	16	-0.1000	0
43	LEFGTISVS	86	-0.1000	0

44	LPGRAKLSD	163	-0.1000	0
45	MSRADVDAI	194	-0.2000	0
46	VELLRRGIT	258	-0.2000	0
47	MGHEGMHFS	99	-0.3000	0
48	IGVASSWNE	51	-0.4000	0
49	MHFSLVSRE	104	-0.4000	0
50	LPGMLMAAA	140	-0.4000	0
51	VFLYAGSIL	155	-0.4000	0
52	VGACSRGLM	186	-0.4000	0
53	LLRNGDRIR	513	-0.4000	0
54	IRLDVAGRV	520	-0.4000	0

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	VVMKALLDA	344	3.7000	42.53
2	MYTANTMAS	216	3.1000	35.63
3	VMQAERLDG	121	3.0000	34.48
4	VKPFGRHVM	325	2.7000	31.03
5	LMAAARLDL	144	2.5600	29.43
6	LHLLAIAHE	294	2.3000	26.44
7	FLYAGSILP	156	2.2000	25.29
8	VVELLRRGI	257	2.2000	25.29
9	LQDFSRIGS	309	2.2000	25.29
10	MREMLAITG	462	2.2000	25.29
11	LVSREVIAD	108	2.0000	22.99
12	LSKYVKLVS	557	1.9000	21.84
13	YVKLVSSAA	560	1.8000	20.69
14	LRNGDRIRL	514	1.7600	20.23
15	FGTISVSDG	88	1.7000	19.54
16	VKLVSSAAV	561	1.7000	19.54
17	VLHLLAIAH	293	1.6000	18.39
18	FSLVSREVI	106	1.4000	16.09

19	VELLRRGIT	258	1.3000	14.94
20	VGACSRGLM	186	1.2000	13.79
21	LRALANPIH	384	1.1500	13.22
22	FENAIAVVM	276	1.1000	12.64
23	LAITGAIKG	466	1.1000	12.64
24	VTIIDAFEA	177	1.0000	11.49
25	FEAVGACSR	183	1.0000	11.49
26	IRYEGPKGG	451	1.0000	11.49
27	VLSKYVKLV	556	1.0000	11.49
28	WNEITPCNL	57	0.9600	11.03
29	VVMAFGGST	282	0.9000	10.34
30	LYAGSILPG	157	0.8000	9.20
31	LLDAGLLHG	349	0.8000	9.20
32	MLRAVGMDD	35	0.7000	8.05
33	VPVVMKALL	342	0.6600	7.59
34	IALLRNGDR	511	0.6000	6.90
35	FSRIGSGVP	312	0.5000	5.75
36	IGGVPVVMK	339	0.5000	5.75
37	VVKTAGFDS	410	0.5000	5.75
38	VGDAVVIRY	445	0.5000	5.75
39	ITGAIKGAG	468	0.5000	5.75
40	MLMAAARLD	143	0.4000	4.60
41	LRRGITARD	261	0.4000	4.60
42	LLLTDGRFS	482	0.4000	4.60
43	IRLDVAGRV	520	0.4000	4.60
44	LGMSLPGSA	229	0.3000	3.45
45	ITARDILTK	265	0.3000	3.45
46	LLHGDCLTV	354	0.3000	3.45
47	VLRALANPI	383	0.3000	3.45
48	VEVVMQAER	118	0.2000	2.30
49	LPGRAKLSD	163	0.2000	2.30
50	VLLLTDGRF	481	0.2000	2.30
51	YAGSILPGR	158	0.1500	1.72
52	IHPSGGITI	391	0.1000	1.15

53	VGHIAPEAV	498	0.1000	1.15
54	LAAITPPDP	371	0.0500	0.57

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	VVMKALLDA	344	4.9000	55.68
2	VKPFGRHVM	325	4.6000	52.27
3	VVELLRRGI	257	4.1000	46.59
4	VLSKYVKLV	556	3.5000	39.77
5	VVMQAERLD	120	3.3000	37.50
6	MLMAAARLD	143	3.0000	34.09
7	VMQAERLDG	121	2.9000	32.95
8	LSKYVKLVS	557	2.9000	32.95
9	MYTANTMAS	216	2.8000	31.82
10	IRYEGPKGG	451	2.8000	31.82
11	LVSREVIAD	108	2.6000	29.55
12	LHLLAIAHE	294	2.6000	29.55
13	LLLTDGRFS	482	2.5000	28.41
14	LMAAARLDL	144	2.4600	27.95
15	LEKAAARGM	27	2.4000	27.27
16	VLRALANPI	383	2.4000	27.27
17	LQDFSRIGS	309	2.3000	26.14
18	LLRRGITAR	260	2.2000	25.00
19	VVKTAGFDS	410	2.0000	22.73
20	LDLAAVFLY	150	1.8000	20.45
21	ILTKEAFEN	270	1.8000	20.45
22	MREMLAITG	462	1.7000	19.32
23	LRNGDRIRL	514	1.6600	18.86
24	VLLAGCDKS	131	1.6000	18.18
25	LRRGITARD	261	1.6000	18.18
26	LLTDGRFSG	483	1.6000	18.18
27	LVSSAAVGA	563	1.6000	18.18

28	VTIIDAFEA	177	1.5000	17.05
29	VIRYEGPKG	450	1.4000	15.91
30	VKLVSSAAV	561	1.4000	15.91
31	LANAVKEGV	70	1.1000	12.50
32	VSREVIADS	109	1.1000	12.50
33	VGACSRGLM	186	1.1000	12.50
34	ITARDILTK	265	1.1000	12.50
35	LLRNGDRIR	513	1.1000	12.50
36	IGVASSWNE	51	1.0000	11.36
37	MHFSLVSRE	104	1.0000	11.36
38	LPGRAKLSD	163	1.0000	11.36
39	LRALANPIH	384	1.0000	11.36
40	LYAGSILPG	157	0.9000	10.23
41	ILPGRAKLS	162	0.9000	10.23
42	VVMAFGGST	282	0.8000	9.09
43	MSRADVDAI	194	0.7000	7.95
44	IGGVPVVMK	339	0.7000	7.95
45	LLDAGLLHG	349	0.7000	7.95
46	VVIRYEGPK	449	0.7000	7.95
47	IKPRSRDVT	16	0.6000	6.82
48	FENAIAVVM	276	0.6000	6.82
49	IAVVMAFGG	280	0.6000	6.82
50	VLHLLAIAH	293	0.6000	6.82
51	IRLDVAGRV	520	0.6000	6.82
52	VFLYAGSIL	155	0.5600	6.36
53	VELLRRGIT	258	0.5000	5.68
54	YVKLVSSAA	560	0.5000	5.68
55	MLRAVGMDD	35	0.4000	4.55
56	LAIAHEANV	297	0.4000	4.55
57	LLHGDCLTV	354	0.4000	4.55

ALLELE: DRB1_1302	Threshold for 3 % with score: 2.1	Highest Score achievable by any peptide: 8.8

Rank	Sequence	At Position	Score	% of Highest Score
1	VVMKALLDA	344	3.9000	44.32
2	VKPFGRHVM	325	3.6000	40.91
3	VVELLRRGI	257	3.1000	35.23
4	VLSKYVKLV	556	2.5000	28.41
5	VVMQAERLD	120	2.3000	26.14
6	MLMAAARLD	143	2.0000	22.73
7	VMQAERLDG	121	1.9000	21.59
8	LSKYVKLVS	557	1.9000	21.59
9	MYTANTMAS	216	1.8000	20.45
10	IRYEGPKGG	451	1.8000	20.45
11	LVSREVIAD	108	1.6000	18.18
12	FENAIAVVM	276	1.6000	18.18
13	LHLLAIAHE	294	1.6000	18.18
14	LLLTDGRFS	482	1.5000	17.05
15	YVKLVSSAA	560	1.5000	17.05
16	LMAAARLDL	144	1.4600	16.59
17	LEKAAARGM	27	1.4000	15.91
18	VLRALANPI	383	1.4000	15.91
19	LQDFSRIGS	309	1.3000	14.77
20	LLRRGITAR	260	1.2000	13.64
21	FGRHVMSDV	328	1.2000	13.64
22	VVKTAGFDS	410	1.0000	11.36
23	FLYAGSILP	156	0.9000	10.23
24	LDLAAVFLY	150	0.8000	9.09
25	ILTKEAFEN	270	0.8000	9.09
26	MREMLAITG	462	0.7000	7.95
27	LRNGDRIRL	514	0.6600	7.50
28	FGTISVSDG	88	0.6000	6.82
29	VLLAGCDKS	131	0.6000	6.82
30	LRRGITARD	261	0.6000	6.82
31	LLTDGRFSG	483	0.6000	6.82
32	LVSSAAVGA	563	0.6000	6.82
33	VTIIDAFEA	177	0.5000	5.68

34	FSLVSREVI	106	0.4000	4.55
35	VIRYEGPKG	450	0.4000	4.55
36	VKLVSSAAV	561	0.4000	4.55
37	LANAVKEGV	70	0.1000	1.14
38	VSREVIADS	109	0.1000	1.14
39	VGACSRGLM	186	0.1000	1.14
40	FARRSGQAV	249	0.1000	1.14
41	ITARDILTK	265	0.1000	1.14
42	LLRNGDRIR	513	0.1000	1.14
43	LYAGSILPG	157	-0.1000	0
44	ILPGRAKLS	162	-0.1000	0
45	YAGSILPGR	158	-0.2000	0
46	VVMAFGGST	282	-0.2000	0
47	FEAVGACSR	183	-0.3000	0
48	MSRADVDAI	194	-0.3000	0
49	IGGVPVVMK	339	-0.3000	0
50	LLDAGLLHG	349	-0.3000	0
51	VVIRYEGPK	449	-0.3000	0
52	FASRQQDFS	538	-0.3000	0

ALLELE: DRB1_1304	Threshold for 3 % with score: 2.6	Highest Score achievable by any peptide: 9

Rank	Sequence	At Position	Score	% of Highest Score
1	VVMQAERLD	120	4.9000	54.44
2	VVMKALLDA	344	4.9000	54.44
3	MLMAAARLD	143	4.6000	51.11
4	LVSREVIAD	108	4.2000	46.67
5	LHLLAIAHE	294	4.2000	46.67
6	VKPFGRHVM	325	4.2000	46.67
7	VVELLRRGI	257	3.4000	37.78
8	LRRGITARD	261	3.2000	35.56
9	ILTKEAFEN	270	3.0000	33.33
10	VMQAERLDG	121	2.8000	31.11

11	LRALANPIH	384	2.8000	31.11
12	VLSKYVKLV	556	2.8000	31.11
13	IRYEGPKGG	451	2.7000	30.00
14	IGVASSWNE	51	2.6000	28.89
15	MHFSLVSRE	104	2.6000	28.89
16	LPGRAKLSD	163	2.6000	28.89
17	LMAAARLDL	144	2.5000	27.78
18	LSKYVKLVS	557	2.5000	27.78
19	MYTANTMAS	216	2.4000	26.67
20	VLHLLAIAH	293	2.4000	26.67
21	LLLTDGRFS	482	2.1000	23.33
22	LEKAAARGM	27	2.0000	22.22
23	MLRAVGMDD	35	2.0000	22.22
24	LQDFSRIGS	309	1.9000	21.11
25	VLRALANPI	383	1.7000	18.89
26	LRNGDRIRL	514	1.7000	18.89
27	LDLAAVFLY	150	1.6000	17.78
28	IERAICPGE	202	1.6000	17.78
29	VVKTAGFDS	410	1.6000	17.78
30	MREMLAITG	462	1.6000	17.78
31	LVSSAAVGA	563	1.6000	17.78
32	VTIIDAFEA	177	1.5000	16.67
33	LLTDGRFSG	483	1.5000	16.67
34	VTGHTMAEN	362	1.4000	15.56
35	VIRYEGPKG	450	1.3000	14.44
36	VLLAGCDKS	131	1.2000	13.33
37	ILHGSLAPE	399	1.2000	13.33
38	LDVAGRVLD	522	1.1000	12.22
39	VVMAFGGST	282	1.0000	11.11
40	IKGAGLGKD	472	1.0000	11.11
41	LCVGHIAPE	496	1.0000	11.11
42	VMAFGGSTN	283	0.9000	10.00
43	IKPRSRDVT	16	0.8000	8.89
44	LYAGSILPG	157	0.8000	8.89

45	VSREVIADS	109	0.7000	7.78
46	VGACSRGLM	186	0.7000	7.78
47	VELLRRGIT	258	0.7000	7.78
48	LLRRGITAR	260	0.7000	7.78
49	VKLVSSAAV	561	0.7000	7.78
50	ITPCNLSLD	60	0.6000	6.67
51	VFLYAGSIL	155	0.6000	6.67
52	LLDAGLLHG	349	0.6000	6.67
53	ILPGRAKLS	162	0.5000	5.56
54	IAVVMAFGG	280	0.5000	5.56
55	YVKLVSSAA	560	0.5000	5.56
56	LANAVKEGV	70	0.4000	4.44
57	VPVVMKALL	342	0.4000	4.44

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	VVMKALLDA	344	3.7000	42.53
2	MYTANTMAS	216	3.1000	35.63
3	VMQAERLDG	121	3.0000	34.48
4	VKPFGRHVM	325	2.7000	31.03
5	LMAAARLDL	144	2.5600	29.43
6	LHLLAIAHE	294	2.3000	26.44
7	FLYAGSILP	156	2.2000	25.29
8	VVELLRRGI	257	2.2000	25.29
9	LQDFSRIGS	309	2.2000	25.29
10	MREMLAITG	462	2.2000	25.29
11	LVSREVIAD	108	2.0000	22.99
12	LSKYVKLVS	557	1.9000	21.84
13	YVKLVSSAA	560	1.8000	20.69
14	LRNGDRIRL	514	1.7600	20.23
15	FGTISVSDG	88	1.7000	19.54
16	VKLVSSAAV	561	1.7000	19.54

17	VLHLLAIAH	293	1.6000	18.39
18	FSLVSREVI	106	1.4000	16.09
19	VELLRRGIT	258	1.3000	14.94
20	VGACSRGLM	186	1.2000	13.79
21	LRALANPIH	384	1.1500	13.22
22	FENAIAVVM	276	1.1000	12.64
23	LAITGAIKG	466	1.1000	12.64
24	VTIIDAFEA	177	1.0000	11.49
25	FEAVGACSR	183	1.0000	11.49
26	IRYEGPKGG	451	1.0000	11.49
27	VLSKYVKLV	556	1.0000	11.49
28	WNEITPCNL	57	0.9600	11.03
29	VVMAFGGST	282	0.9000	10.34
30	LYAGSILPG	157	0.8000	9.20
31	LLDAGLLHG	349	0.8000	9.20
32	MLRAVGMDD	35	0.7000	8.05
33	VPVVMKALL	342	0.6600	7.59
34	IALLRNGDR	511	0.6000	6.90
35	FSRIGSGVP	312	0.5000	5.75
36	IGGVPVVMK	339	0.5000	5.75
37	VVKTAGFDS	410	0.5000	5.75
38	VGDAVVIRY	445	0.5000	5.75
39	ITGAIKGAG	468	0.5000	5.75
40	MLMAAARLD	143	0.4000	4.60
41	LRRGITARD	261	0.4000	4.60
42	LLLTDGRFS	482	0.4000	4.60
43	IRLDVAGRV	520	0.4000	4.60
44	LGMSLPGSA	229	0.3000	3.45
45	ITARDILTK	265	0.3000	3.45
46	LLHGDCLTV	354	0.3000	3.45
47	VLRALANPI	383	0.3000	3.45
48	VEVVMQAER	118	0.2000	2.30
49	LPGRAKLSD	163	0.2000	2.30
50	VLLLTDGRF	481	0.2000	2.30

51	YAGSILPGR	158	0.1500	1.72
52	IHPSGGITI	391	0.1000	1.15
53	VGHIAPEAV	498	0.1000	1.15
54	LAAITPPDP	371	0.0500	0.57

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	VVMKALLDA	344	1.9000	27.94
2	YVKLVSSAA	560	1.8000	26.47
3	MYTANTMAS	216	1.1000	16.18
4	VVELLRRGI	257	1.1000	16.18
5	LHLLAIAHE	294	0.9000	13.24
6	VKLVSSAAV	561	0.7000	10.29
7	VLHLLAIAH	293	0.5800	8.53
8	LRALANPIH	384	0.5800	8.53
9	VTIIDAFEA	177	0.5000	7.35
10	VELLRRGIT	258	0.5000	7.35
11	VKPFGRHVM	325	0.5000	7.35
12	FGTISVSDG	88	0.3000	4.41
13	LGMSLPGSA	229	0.2000	2.94
14	LQDFSRIGS	309	0.2000	2.94
15	VVMAFGGST	282	0.1000	1.47
16	IGGVPVVMK	339	-0.1000	0
17	MLAITGAIK	465	-0.1000	0
18	VMQAERLDG	121	-0.2000	0
19	LMAAARLDL	144	-0.2000	0
20	LLLTDGRFS	482	-0.2000	0
21	VPVVMKALL	342	-0.3000	0
22	VVIRYEGPK	449	-0.3000	0
23	LSKYVKLVS	557	-0.3000	0
24	FLYAGSILP	156	-0.4000	0
25	VGACSRGLM	186	-0.4000	0

26	VDAIERAIC	199	-0.4000	0
27	ITILHGSLA	397	-0.4000	0
28	VVKTAGFDS	410	-0.4000	0
29	FEAVGACSR	183	-0.5000	0
30	LVSSAAVGA	563	-0.5000	0
31	FSLVSREVI	106	-0.6000	0
32	FSRIGSGVP	312	-0.6000	0
33	VLSKYVKLV	556	-0.6000	0
34	LVSREVIAD	108	-0.7000	0
35	VLLAGCDKS	131	-0.7000	0
36	LRRGITARD	261	-0.7000	0
37	IRLDVAGRV	520	-0.7000	0
38	MREMLAITG	462	-0.8000	0
39	LRNGDRIRL	514	-0.8000	0
40	VSREVIADS	109	-0.9000	0
41	MLMAAARLD	143	-0.9000	0
42	YTANTMASA	217	-0.9000	0
43	FENAIAVVM	276	-0.9000	0
44	VLRALANPI	383	-0.9000	0
45	IRYEGPKGG	451	-1.0000	0
46	ITGAIKGAG	468	-1.0000	0
47	IALLRNGDR	511	-1.0000	0
48	VSSAAVGAV	564	-1.1000	0
49	LPGMLMAAA	140	-1.2000	0
50	VEVVMQAER	118	-1.3000	0
51	LDRLANAVK	67	-1.4000	0
52	FAKPQIGVA	46	-1.5000	0
53	ILPGRAKLS	162	-1.5000	0
54	FSGGTTGLC	489	-1.5000	0
55	VVMQAERLD	120	-1.6000	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	VVMKALLDA	344	4.7000	56.63
2	MYTANTMAS	216	3.7000	44.58
3	VLHLLAIAH	293	3.1800	38.31
4	LQDFSRIGS	309	2.8000	33.73
5	LRALANPIH	384	2.7300	32.89
6	VMQAERLDG	121	2.6000	31.33
7	LMAAARLDL	144	2.6000	31.33
8	LSKYVKLVS	557	2.5000	30.12
9	VVELLRRGI	257	2.3000	27.71
10	VKPFGRHVM	325	2.2000	26.51
11	VTIIDAFEA	177	2.0000	24.10
12	LVSREVIAD	108	1.9000	22.89
13	LHLLAIAHE	294	1.9000	22.89
14	MREMLAITG	462	1.8000	21.69
15	LRNGDRIRL	514	1.8000	21.69
16	VKLVSSAAV	561	1.7000	20.48
17	VELLRRGIT	258	1.6000	19.28
18	IGGVPVVMK	339	1.4000	16.87
19	LGMSLPGSA	229	1.3000	15.66
20	ITARDILTK	265	1.2000	14.46
21	VVMAFGGST	282	1.2000	14.46
22	VVKTAGFDS	410	1.1000	13.25
23	LLLTDGRFS	482	1.0000	12.05
24	VLSKYVKLV	556	1.0000	12.05
25	LVSSAAVGA	563	1.0000	12.05
26	MLAITGAIK	465	0.9000	10.84
27	VVIRYEGPK	449	0.8000	9.64
28	YVKLVSSAA	560	0.8000	9.64
29	VGACSRGLM	186	0.7000	8.43
30	VPVVMKALL	342	0.7000	8.43
31	LAITGAIKG	466	0.7000	8.43
32	MLRAVGMDD	35	0.6000	7.23
33	VDAIERAIC	199	0.6000	7.23

34	ITILHGSLA	397	0.6000	7.23
35	IRYEGPKGG	451	0.6000	7.23
36	LYAGSILPG	157	0.4000	4.82
37	LLDAGLLHG	349	0.4000	4.82
38	VLRALANPI	383	0.4000	4.82
39	IRLDVAGRV	520	0.4000	4.82
40	MLMAAARLD	143	0.3000	3.61
41	LRRGITARD	261	0.3000	3.61
42	LLHGDCLTV	354	0.3000	3.61
43	FLYAGSILP	156	0.2000	2.41
44	IHPSGGITI	391	0.2000	2.41
45	VGDAVVIRY	445	0.2000	2.41
46	VSREVIADS	109	0.1000	1.20
47	ILPGRAKLS	162	0.1000	1.20
48	LPGRAKLSD	163	0.1000	1.20
49	ITGAIKGAG	468	0.1000	1.20
50	VGHIAPEAV	498	0.1000	1.20
51	IALLRNGDR	511	0.1000	1.20
52	LAAITPPDP	371	0.0500	0.60
53	LANAVKEGV	70	-0.2000	0
54	LPGMLMAAA	140	-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	LHLLAIAHE	294	3.9000	43.82
2	VVMKALLDA	344	3.7000	41.57
3	LVSREVIAD	108	3.6000	40.45
4	VLHLLAIAH	293	3.4000	38.20
5	LRALANPIH	384	2.9500	33.15
6	VMQAERLDG	121	2.9000	32.58
7	MYTANTMAS	216	2.7000	30.34
8	LMAAARLDL	144	2.6000	29.21

9	MLRAVGMDD	35	2.3000	25.84
10	VKPFGRHVM	325	2.3000	25.84
11	MREMLAITG	462	2.1000	23.60
12	MLMAAARLD	143	2.0000	22.47
13	LRRGITARD	261	2.0000	22.47
14	LPGRAKLSD	163	1.8000	20.22
15	LQDFSRIGS	309	1.8000	20.22
16	LRNGDRIRL	514	1.8000	20.22
17	YVKLVSSAA	560	1.8000	20.22
18	FGTISVSDG	88	1.6000	17.98
19	FLYAGSILP	156	1.6000	17.98
20	VVELLRRGI	257	1.5000	16.85
21	VELLRRGIT	258	1.5000	16.85
22	LSKYVKLVS	557	1.5000	16.85
23	VVMQAERLD	120	1.3000	14.61
24	MHFSLVSRE	104	1.1000	12.36
25	VVMAFGGST	282	1.1000	12.36
26	FEGTARVFD	421	1.1000	12.36
27	IKGAGLGKD	472	1.1000	12.36
28	IERAICPGE	202	1.0500	11.80
29	WNEITPCNL	57	1.0000	11.24
30	VTIIDAFEA	177	1.0000	11.24
31	LAITGAIKG	466	1.0000	11.24
32	VKLVSSAAV	561	1.0000	11.24
33	IRYEGPKGG	451	0.9000	10.11
34	IGVASSWNE	51	0.8000	8.99
35	VGACSRGLM	186	0.8000	8.99
36	FSLVSREVI	106	0.7000	7.87
37	LYAGSILPG	157	0.7000	7.87
38	FENAIAVVM	276	0.7000	7.87
39	VPVVMKALL	342	0.7000	7.87
40	LLDAGLLHG	349	0.7000	7.87
41	ITGAIKGAG	468	0.4000	4.49
42	LGMSLPGSA	229	0.3000	3.37

43	VGDAVVIRY	445	0.3000	3.37
44	VLSKYVKLV	556	0.3000	3.37
45	LLAIAHEAN	296	0.1000	1.12
46	VVKTAGFDS	410	0.1000	1.12
47	FSRIGSGVP	312	-0.1000	0
48	IAVVMAFGG	280	-0.2000	0
49	LCVGHIAPE	496	-0.2000	0
50	ILTKEAFEN	270	-0.3000	0
51	IGGVPVVMK	339	-0.3000	0
52	IRLDVAGRV	520	-0.3000	0
53	VIRYEGPKG	450	-0.3500	0

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	VVMKALLDA	344	4.9000	58.33
2	VVELLRRGI	257	3.2000	38.10
3	VKPFGRHVM	325	3.1000	36.90
4	VLSKYVKLV	556	2.5000	29.76
5	LSKYVKLVS	557	2.5000	29.76
6	MYTANTMAS	216	2.4000	28.57
7	VVMQAERLD	120	2.2000	26.19
8	LLLTDGRFS	482	2.1000	25.00
9	MLMAAARLD	143	1.9000	22.62
10	LQDFSRIGS	309	1.9000	22.62
11	VVKTAGFDS	410	1.6000	19.05
12	LVSSAAVGA	563	1.6000	19.05
13	LRALANPIH	384	1.5800	18.81
14	LVSREVIAD	108	1.5000	17.86
15	VMQAERLDG	121	1.5000	17.86
16	LMAAARLDL	144	1.5000	17.86
17	VTIIDAFEA	177	1.5000	17.86
18	VLRALANPI	383	1.5000	17.86

19	IRYEGPKGG	451	1.4000	16.67
20	VLLAGCDKS	131	1.2000	14.29
21	LHLLAIAHE	294	1.2000	14.29
22	VLHLLAIAH	293	1.1800	14.05
23	ITARDILTK	265	1.0000	11.90
24	ILTKEAFEN	270	1.0000	11.90
25	LEKAAARGM	27	0.9000	10.71
26	VSREVIADS	109	0.7000	8.33
27	LLRRGITAR	260	0.7000	8.33
28	LRNGDRIRL	514	0.7000	8.33
29	IGGVPVVMK	339	0.6000	7.14
30	VVIRYEGPK	449	0.6000	7.14
31	LDLAAVFLY	150	0.5000	5.95
32	ILPGRAKLS	162	0.5000	5.95
33	LRRGITARD	261	0.5000	5.95
34	YVKLVSSAA	560	0.5000	5.95
35	VKLVSSAAV	561	0.4000	4.76
36	LGMSLPGSA	229	0.3000	3.57
37	ITILHGSLA	397	0.3000	3.57
38	MREMLAITG	462	0.3000	3.57
39	LLTDGRFSG	483	0.2000	2.38
40	LANAVKEGV	70	0.1000	1.19
41	VVMAFGGST	282	0.1000	1.19
42	IKPRSRDVT	16	-0.1000	0
43	LEFGTISVS	86	-0.1000	0
44	LPGRAKLSD	163	-0.1000	0
45	MSRADVDAI	194	-0.2000	0
46	VELLRRGIT	258	-0.2000	0
47	MGHEGMHFS	99	-0.3000	0
48	IGVASSWNE	51	-0.4000	0
49	MHFSLVSRE	104	-0.4000	0
50	LPGMLMAAA	140	-0.4000	0
51	VFLYAGSIL	155	-0.4000	0
52	VGACSRGLM	186	-0.4000	0

53	LLRNGDRIR	513	-0.4000	0
54	IRLDVAGRV	520	-0.4000	0

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	VVMKALLDA	344	3.9000	46.43
2	VVELLRRGI	257	2.2000	26.19
3	VKPFGRHVM	325	2.1000	25.00
4	VLSKYVKLV	556	1.5000	17.86
5	LSKYVKLVS	557	1.5000	17.86
6	YVKLVSSAA	560	1.5000	17.86
7	MYTANTMAS	216	1.4000	16.67
8	VVMQAERLD	120	1.2000	14.29
9	LLLTDGRFS	482	1.1000	13.10
10	MLMAAARLD	143	0.9000	10.71
11	LQDFSRIGS	309	0.9000	10.71
12	VVKTAGFDS	410	0.6000	7.14
13	LVSSAAVGA	563	0.6000	7.14
14	LRALANPIH	384	0.5800	6.90
15	LVSREVIAD	108	0.5000	5.95
16	VMQAERLDG	121	0.5000	5.95
17	LMAAARLDL	144	0.5000	5.95
18	VTIIDAFEA	177	0.5000	5.95
19	VLRALANPI	383	0.5000	5.95
20	IRYEGPKGG	451	0.4000	4.76
21	VLLAGCDKS	131	0.2000	2.38
22	LHLLAIAHE	294	0.2000	2.38
23	FGRHVMSDV	328	0.2000	2.38
24	VLHLLAIAH	293	0.1800	2.14
25	FENAIAVVM	276	0.1000	1.19
26	LEKAAARGM	27	-0.1000	0
27	FLYAGSILP	156	-0.1000	0

28	VSREVIADS	109	-0.3000	0
29	LLRRGITAR	260	-0.3000	0
30	LRNGDRIRL	514	-0.3000	0
31	IGGVPVVMK	339	-0.4000	0
32	VVIRYEGPK	449	-0.4000	0
33	FSLVSREVI	106	-0.5000	0
34	LDLAAVFLY	150	-0.5000	0
35	ILPGRAKLS	162	-0.5000	0
36	LRRGITARD	261	-0.5000	0
37	VKLVSSAAV	561	-0.6000	0
38	LGMSLPGSA	229	-0.7000	0
39	ITILHGSLA	397	-0.7000	0
40	MREMLAITG	462	-0.7000	0
41	FASRQQDFS	538	-0.7000	0
42	FGTISVSDG	88	-0.8000	0
43	YTANTMASA	217	-0.8000	0
44	LLTDGRFSG	483	-0.8000	0
45	LANAVKEGV	70	-0.9000	0
46	FARRSGQAV	249	-0.9000	0
47	VVMAFGGST	282	-0.9000	0
48	IGSGVPHLA	315	-1.0000	0
49	VIRYEGPKG	450	-1.0000	0
50	FSPPPPRYT	545	-1.0000	0
51	IKPRSRDVT	16	-1.1000	0
52	LEFGTISVS	86	-1.1000	0
53	LPGRAKLSD	163	-1.1000	0
54	MSRADVDAI	194	-1.2000	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	VVMKALLDA	344	4.9000	55.68
2	VKPFGRHVM	325	4.6000	52.27

3	VVELLRRGI	257	4.1000	46.59
4	VLSKYVKLV	556	3.5000	39.77
5	VVMQAERLD	120	3.3000	37.50
6	MLMAAARLD	143	3.0000	34.09
7	VMQAERLDG	121	2.9000	32.95
8	LSKYVKLVS	557	2.9000	32.95
9	MYTANTMAS	216	2.8000	31.82
10	IRYEGPKGG	451	2.8000	31.82
11	LVSREVIAD	108	2.6000	29.55
12	LHLLAIAHE	294	2.6000	29.55
13	LLLTDGRFS	482	2.5000	28.41
14	LMAAARLDL	144	2.4600	27.95
15	LEKAAARGM	27	2.4000	27.27
16	VLRALANPI	383	2.4000	27.27
17	LQDFSRIGS	309	2.3000	26.14
18	LLRRGITAR	260	2.2000	25.00
19	VVKTAGFDS	410	2.0000	22.73
20	LDLAAVFLY	150	1.8000	20.45
21	ILTKEAFEN	270	1.8000	20.45
22	MREMLAITG	462	1.7000	19.32
23	LRNGDRIRL	514	1.6600	18.86
24	VLLAGCDKS	131	1.6000	18.18
25	LRRGITARD	261	1.6000	18.18
26	LLTDGRFSG	483	1.6000	18.18
27	LVSSAAVGA	563	1.6000	18.18
28	VTIIDAFEA	177	1.5000	17.05
29	VIRYEGPKG	450	1.4000	15.91
30	VKLVSSAAV	561	1.4000	15.91
31	LANAVKEGV	70	1.1000	12.50
32	VSREVIADS	109	1.1000	12.50
33	VGACSRGLM	186	1.1000	12.50
34	ITARDILTK	265	1.1000	12.50
35	LLRNGDRIR	513	1.1000	12.50
36	IGVASSWNE	51	1.0000	11.36

37	MHFSLVSRE	104	1.0000	11.36
38	LPGRAKLSD	163	1.0000	11.36
39	LRALANPIH	384	1.0000	11.36
40	LYAGSILPG	157	0.9000	10.23
41	ILPGRAKLS	162	0.9000	10.23
42	VVMAFGGST	282	0.8000	9.09
43	MSRADVDAI	194	0.7000	7.95
44	IGGVPVVMK	339	0.7000	7.95
45	LLDAGLLHG	349	0.7000	7.95
46	VVIRYEGPK	449	0.7000	7.95
47	IKPRSRDVT	16	0.6000	6.82
48	FENAIAVVM	276	0.6000	6.82
49	IAVVMAFGG	280	0.6000	6.82
50	VLHLLAIAH	293	0.6000	6.82
51	IRLDVAGRV	520	0.6000	6.82
52	VFLYAGSIL	155	0.5600	6.36
53	VELLRRGIT	258	0.5000	5.68
54	YVKLVSSAA	560	0.5000	5.68
55	MLRAVGMDD	35	0.4000	4.55
56	LAIAHEANV	297	0.4000	4.55
57	LLHGDCLTV	354	0.4000	4.55

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	VVMKALLDA	344	4.9000	55.68
2	VKPFGRHVM	325	4.6000	52.27
3	VVELLRRGI	257	4.1000	46.59
4	VLSKYVKLV	556	3.5000	39.77
5	VVMQAERLD	120	3.3000	37.50
6	MLMAAARLD	143	3.0000	34.09
7	VMQAERLDG	121	2.9000	32.95
8	LSKYVKLVS	557	2.9000	32.95

9	MYTANTMAS	216	2.8000	31.82
10	IRYEGPKGG	451	2.8000	31.82
11	LVSREVIAD	108	2.6000	29.55
12	LHLLAIAHE	294	2.6000	29.55
13	LLLTDGRFS	482	2.5000	28.41
14	LMAAARLDL	144	2.4600	27.95
15	LEKAAARGM	27	2.4000	27.27
16	VLRALANPI	383	2.4000	27.27
17	LQDFSRIGS	309	2.3000	26.14
18	LLRRGITAR	260	2.2000	25.00
19	VVKTAGFDS	410	2.0000	22.73
20	LDLAAVFLY	150	1.8000	20.45
21	ILTKEAFEN	270	1.8000	20.45
22	MREMLAITG	462	1.7000	19.32
23	LRNGDRIRL	514	1.6600	18.86
24	VLLAGCDKS	131	1.6000	18.18
25	LRRGITARD	261	1.6000	18.18
26	LLTDGRFSG	483	1.6000	18.18
27	LVSSAAVGA	563	1.6000	18.18
28	VTIIDAFEA	177	1.5000	17.05
29	VIRYEGPKG	450	1.4000	15.91
30	VKLVSSAAV	561	1.4000	15.91
31	LANAVKEGV	70	1.1000	12.50
32	VSREVIADS	109	1.1000	12.50
33	VGACSRGLM	186	1.1000	12.50
34	ITARDILTK	265	1.1000	12.50
35	LLRNGDRIR	513	1.1000	12.50
36	IGVASSWNE	51	1.0000	11.36
37	MHFSLVSRE	104	1.0000	11.36
38	LPGRAKLSD	163	1.0000	11.36
39	LRALANPIH	384	1.0000	11.36
40	LYAGSILPG	157	0.9000	10.23
41	ILPGRAKLS	162	0.9000	10.23
42	VVMAFGGST	282	0.8000	9.09

43	MSRADVDAI	194	0.7000	7.95
44	IGGVPVVMK	339	0.7000	7.95
45	LLDAGLLHG	349	0.7000	7.95
46	VVIRYEGPK	449	0.7000	7.95
47	IKPRSRDVT	16	0.6000	6.82
48	FENAIAVVM	276	0.6000	6.82
49	IAVVMAFGG	280	0.6000	6.82
50	VLHLLAIAH	293	0.6000	6.82
51	IRLDVAGRV	520	0.6000	6.82
52	VFLYAGSIL	155	0.5600	6.36
53	VELLRRGIT	258	0.5000	5.68
54	YVKLVSSAA	560	0.5000	5.68
55	MLRAVGMDD	35	0.4000	4.55
56	LAIAHEANV	297	0.4000	4.55
57	LLHGDCLTV	354	0.4000	4.55

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	LRNGDRIRL	514	5.7000	58.16
2	VFLYAGSIL	155	5.6000	57.14
3	VKPFGRHVM	325	5.4800	55.92
4	VVMKALLDA	344	4.9000	50.00
5	LMAAARLDL	144	4.5000	45.92
6	LQDFSRIGS	309	4.5000	45.92
7	VIRYEGPKG	450	4.3000	43.88
8	VVMAFGGST	282	3.8000	38.78
9	VTIIDAFEA	177	3.5000	35.71
10	IHPSGGITI	391	3.5000	35.71
11	LSKYVKLVS	557	3.5000	35.71
12	LLHGDCLTV	354	3.4000	34.69
13	VVKTAGFDS	410	3.4000	34.69
14	VMQAERLDG	121	3.2000	32.65

15	VKLVSSAAV	561	3.2000	32.65
16	VMAFGGSTN	283	3.1000	31.63
17	VLRALANPI	383	3.1000	31.63
18	IRLDVAGRV	520	3.1000	31.63
19	ITILHGSLA	397	2.8000	28.57
20	VFSAGGYPL	78	2.7000	27.55
21	MREMLAITG	462	2.7000	27.55
22	VVELLRRGI	257	2.6000	26.53
23	LRALANPIH	384	2.6000	26.53
24	YVKLVSSAA	560	2.5000	25.51
25	VELLRRGIT	258	2.4000	24.49
26	LVSSAAVGA	563	2.3000	23.47
27	MYTANTMAS	216	2.2600	23.06
28	LLTDGRFSG	483	2.2000	22.45
29	VLHLLAIAH	293	2.1000	21.43
30	LYAGSILPG	157	2.0500	20.92
31	MLRAVGMDD	35	2.0000	20.41
32	FGRHVMSDV	328	2.0000	20.41
33	LGKDVLLLT	477	2.0000	20.41
34	ISVSDGISM	91	1.9800	20.20
35	LAITGAIKG	466	1.9000	19.39
36	LVSREVIAD	108	1.8000	18.37
37	FLYAGSILP	156	1.8000	18.37
38	IKPRSRDVT	16	1.7000	17.35
39	MKALLDAGL	346	1.7000	17.35
40	VLLLTDGRF	481	1.7000	17.35
41	MAFGGSTNA	284	1.6000	16.33
42	VGACSRGLM	186	1.5800	16.12
43	ITVGDAVVI	443	1.5000	15.31
44	IDAFEAVGA	180	1.4000	14.29
45	LMSRADVDA	193	1.4000	14.29
46	LGMSLPGSA	229	1.4000	14.29
47	LLLTDGRFS	482	1.4000	14.29
48	IAVVMAFGG	280	1.3000	13.27

49	IALLRNGDR	511	1.2000	12.24
50	LLRRGITAR	260	1.1500	11.73
51	IAHEANVAL	299	1.1000	11.22
52	IGSGVPHLA	315	1.1000	11.22
53	VVIRYEGPK	449	1.1000	11.22
54	IRYEGPKGG	451	1.1000	11.22
55	VLLAGCDKS	131	1.0000	10.20
56	LLDAGLLHG	349	1.0000	10.20
57	VFDGERAAL	427	1.0000	10.20

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	LRNGDRIRL	514	4.7000	47.96
2	VFLYAGSIL	155	4.6000	46.94
3	VKPFGRHVM	325	4.4800	45.71
4	VVMKALLDA	344	3.9000	39.80
5	LMAAARLDL	144	3.5000	35.71
6	LQDFSRIGS	309	3.5000	35.71
7	YVKLVSSAA	560	3.5000	35.71
8	VIRYEGPKG	450	3.3000	33.67
9	FGRHVMSDV	328	3.0000	30.61
10	FLYAGSILP	156	2.8000	28.57
11	VVMAFGGST	282	2.8000	28.57
12	VTIIDAFEA	177	2.5000	25.51
13	IHPSGGITI	391	2.5000	25.51
14	LSKYVKLVS	557	2.5000	25.51
15	LLHGDCLTV	354	2.4000	24.49
16	VVKTAGFDS	410	2.4000	24.49
17	VMQAERLDG	121	2.2000	22.45
18	VKLVSSAAV	561	2.2000	22.45
19	VMAFGGSTN	283	2.1000	21.43
20	VLRALANPI	383	2.1000	21.43

21	IRLDVAGRV	520	2.1000	21.43
22	FSLVSREVI	106	1.9000	19.39
23	ITILHGSLA	397	1.8000	18.37
24	VFSAGGYPL	78	1.7000	17.35
25	MREMLAITG	462	1.7000	17.35
26	VVELLRRGI	257	1.6000	16.33
27	FGGSTNAVL	286	1.6000	16.33
28	LRALANPIH	384	1.6000	16.33
29	FARRSGQAV	249	1.4000	14.29
30	VELLRRGIT	258	1.4000	14.29
31	LVSSAAVGA	563	1.3000	13.27
32	MYTANTMAS	216	1.2600	12.86
33	LLTDGRFSG	483	1.2000	12.24
34	VLHLLAIAH	293	1.1000	11.22
35	LYAGSILPG	157	1.0500	10.71
36	MLRAVGMDD	35	1.0000	10.20
37	LGKDVLLLT	477	1.0000	10.20
38	ISVSDGISM	91	0.9800	10.00
39	FENAIAVVM	276	0.9800	10.00
40	LAITGAIKG	466	0.9000	9.18
41	LVSREVIAD	108	0.8000	8.16
42	IKPRSRDVT	16	0.7000	7.14
43	MKALLDAGL	346	0.7000	7.14
44	VLLLTDGRF	481	0.7000	7.14
45	MAFGGSTNA	284	0.6000	6.12
46	VGACSRGLM	186	0.5800	5.92
47	WNEITPCNL	57	0.5000	5.10
48	FSRIGSGVP	312	0.5000	5.10
49	ITVGDAVVI	443	0.5000	5.10
50	IDAFEAVGA	180	0.4000	4.08
51	LMSRADVDA	193	0.4000	4.08
52	LGMSLPGSA	229	0.4000	4.08
53	LLLTDGRFS	482	0.4000	4.08
54	YPLEFGTIS	84	0.3000	3.06

55	FGTISVSDG	88	0.3000	3.06
56	IAVVMAFGG	280	0.3000	3.06
57	IALLRNGDR	511	0.2000	2.04

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	LRNGDRIRL	514	5.7000	58.16
2	VFLYAGSIL	155	5.6000	57.14
3	VKPFGRHVM	325	5.4800	55.92
4	VVMKALLDA	344	4.9000	50.00
5	LMAAARLDL	144	4.5000	45.92
6	LQDFSRIGS	309	4.5000	45.92
7	VIRYEGPKG	450	4.3000	43.88
8	VVMAFGGST	282	3.8000	38.78
9	VTIIDAFEA	177	3.5000	35.71
10	IHPSGGITI	391	3.5000	35.71
11	LSKYVKLVS	557	3.5000	35.71
12	LLHGDCLTV	354	3.4000	34.69
13	VVKTAGFDS	410	3.4000	34.69
14	VMQAERLDG	121	3.2000	32.65
15	VKLVSSAAV	561	3.2000	32.65
16	VMAFGGSTN	283	3.1000	31.63
17	VLRALANPI	383	3.1000	31.63
18	IRLDVAGRV	520	3.1000	31.63
19	ITILHGSLA	397	2.8000	28.57
20	VFSAGGYPL	78	2.7000	27.55
21	MREMLAITG	462	2.7000	27.55
22	VVELLRRGI	257	2.6000	26.53
23	LRALANPIH	384	2.6000	26.53
24	YVKLVSSAA	560	2.5000	25.51
25	VELLRRGIT	258	2.4000	24.49
26	LVSSAAVGA	563	2.3000	23.47

27	MYTANTMAS	216	2.2600	23.06
28	LLTDGRFSG	483	2.2000	22.45
29	VLHLLAIAH	293	2.1000	21.43
30	LYAGSILPG	157	2.0500	20.92
31	MLRAVGMDD	35	2.0000	20.41
32	FGRHVMSDV	328	2.0000	20.41
33	LGKDVLLLT	477	2.0000	20.41
34	ISVSDGISM	91	1.9800	20.20
35	LAITGAIKG	466	1.9000	19.39
36	LVSREVIAD	108	1.8000	18.37
37	FLYAGSILP	156	1.8000	18.37
38	IKPRSRDVT	16	1.7000	17.35
39	MKALLDAGL	346	1.7000	17.35
40	VLLLTDGRF	481	1.7000	17.35
41	MAFGGSTNA	284	1.6000	16.33
42	VGACSRGLM	186	1.5800	16.12
43	ITVGDAVVI	443	1.5000	15.31
44	IDAFEAVGA	180	1.4000	14.29
45	LMSRADVDA	193	1.4000	14.29
46	LGMSLPGSA	229	1.4000	14.29
47	LLLTDGRFS	482	1.4000	14.29
48	IAVVMAFGG	280	1.3000	13.27
49	IALLRNGDR	511	1.2000	12.24
50	LLRRGITAR	260	1.1500	11.73
51	IAHEANVAL	299	1.1000	11.22
52	IGSGVPHLA	315	1.1000	11.22
53	VVIRYEGPK	449	1.1000	11.22
54	IRYEGPKGG	451	1.1000	11.22
55	VLLAGCDKS	131	1.0000	10.20
56	LLDAGLLHG	349	1.0000	10.20
57	VFDGERAAL	427	1.0000	10.20

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

	2.3	9.8

Rank	Sequence	At Position	Score	% of Highest Score
1	FEAVGACSR	183	3.7000	37.76
2	MLAITGAIK	465	3.7000	37.76
3	VTIIDAFEA	177	3.3000	33.67
4	VVKTAGFDS	410	3.3000	33.67
5	MREMLAITG	462	3.3000	33.67
6	VADIKPRSR	13	3.0000	30.61
7	VLHLLAIAH	293	3.0000	30.61
8	LADVKPFGR	322	3.0000	30.61
9	LLLTDGRFS	482	3.0000	30.61
10	VVMAFGGST	282	2.6000	26.53
11	IAVVMAFGG	280	2.5000	25.51
12	WNEITPCNL	57	2.4000	24.49
13	VLRALANPI	383	2.4000	24.49
14	LAITGAIKG	466	2.4000	24.49
15	IALLRNGDR	511	2.4000	24.49
16	VFSAGGYPL	78	2.2000	22.45
17	VVIRYEGPK	449	2.2000	22.45
18	IRYEGPKGG	451	2.2000	22.45
19	YVKLVSSAA	560	2.0000	20.41
20	IGGVPVVMK	339	1.9000	19.39
21	VEVVMQAER	118	1.8000	18.37
22	FLYAGSILP	156	1.7000	17.35
23	VVELLRRGI	257	1.7000	17.35
24	IHPSGGITI	391	1.7000	17.35
25	VKLVSSAAV	561	1.5000	15.31
26	VLLLTDGRF	481	1.4000	14.29
27	LRNGDRIRL	514	1.3000	13.27
28	MLMAAARLD	143	1.2000	12.24
29	LGMSLPGSA	229	1.2000	12.24
30	VFLYAGSIL	155	1.0000	10.20
31	FSRIGSGVP	312	1.0000	10.20
32	LEKAAARGM	27	0.9000	9.18

33	LRALANPIH	384	0.9000	9.18
34	FSLVSREVI	106	0.8000	8.16
35	FENAIAVVM	276	0.8000	8.16
36	LLRNGDRIR	513	0.8000	8.16
37	FGTISVSDG	88	0.7000	7.14
38	LMAAARLDL	144	0.7000	7.14
39	LAAVFLYAG	152	0.7000	7.14
40	IRLDVAGRV	520	0.7000	7.14
41	YAGSILPGR	158	0.6000	6.12
42	ITILHGSLA	397	0.6000	6.12
43	LVSSAAVGA	563	0.5000	5.10
44	LDRLANAVK	67	0.4000	4.08
45	LLRRGITAR	260	0.4000	4.08
46	VVMKALLDA	344	0.4000	4.08
47	LAPEGAVVK	404	0.4000	4.08
48	ILPGRAKLS	162	0.3000	3.06
49	VLLAGCDKS	131	0.2000	2.04
50	LDLAAVFLY	150	0.2000	2.04
51	MYTANTMAS	216	0.2000	2.04
52	FGGSTNAVL	286	0.2000	2.04
53	VKPFGRHVM	325	0.2000	2.04
54	ISVSDGISM	91	0.1000	1.02
55	VGHIAPEAV	498	0.1000	1.02

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	FEAVGACSR	183	3.7000	37.76
2	MLAITGAIK	465	3.7000	37.76
3	VTIIDAFEA	177	3.3000	33.67
4	VVKTAGFDS	410	3.3000	33.67
5	MREMLAITG	462	3.3000	33.67
6	VADIKPRSR	13	3.0000	30.61

7	VLHLLAIAH	293	3.0000	30.61
8	LADVKPFGR	322	3.0000	30.61
9	LLLTDGRFS	482	3.0000	30.61
10	VVMAFGGST	282	2.6000	26.53
11	IAVVMAFGG	280	2.5000	25.51
12	WNEITPCNL	57	2.4000	24.49
13	VLRALANPI	383	2.4000	24.49
14	LAITGAIKG	466	2.4000	24.49
15	IALLRNGDR	511	2.4000	24.49
16	VFSAGGYPL	78	2.2000	22.45
17	VVIRYEGPK	449	2.2000	22.45
18	IRYEGPKGG	451	2.2000	22.45
19	YVKLVSSAA	560	2.0000	20.41
20	IGGVPVVMK	339	1.9000	19.39
21	VEVVMQAER	118	1.8000	18.37
22	FLYAGSILP	156	1.7000	17.35
23	VVELLRRGI	257	1.7000	17.35
24	IHPSGGITI	391	1.7000	17.35
25	VKLVSSAAV	561	1.5000	15.31
26	VLLLTDGRF	481	1.4000	14.29
27	LRNGDRIRL	514	1.3000	13.27
28	MLMAAARLD	143	1.2000	12.24
29	LGMSLPGSA	229	1.2000	12.24
30	VFLYAGSIL	155	1.0000	10.20
31	FSRIGSGVP	312	1.0000	10.20
32	LEKAAARGM	27	0.9000	9.18
33	LRALANPIH	384	0.9000	9.18
34	FSLVSREVI	106	0.8000	8.16
35	FENAIAVVM	276	0.8000	8.16
36	LLRNGDRIR	513	0.8000	8.16
37	FGTISVSDG	88	0.7000	7.14
38	LMAAARLDL	144	0.7000	7.14
39	LAAVFLYAG	152	0.7000	7.14
40	IRLDVAGRV	520	0.7000	7.14

41	YAGSILPGR	158	0.6000	6.12
42	ITILHGSLA	397	0.6000	6.12
43	LVSSAAVGA	563	0.5000	5.10
44	LDRLANAVK	67	0.4000	4.08
45	LLRRGITAR	260	0.4000	4.08
46	VVMKALLDA	344	0.4000	4.08
47	LAPEGAVVK	404	0.4000	4.08
48	ILPGRAKLS	162	0.3000	3.06
49	VLLAGCDKS	131	0.2000	2.04
50	LDLAAVFLY	150	0.2000	2.04
51	MYTANTMAS	216	0.2000	2.04
52	FGGSTNAVL	286	0.2000	2.04
53	VKPFGRHVM	325	0.2000	2.04
54	ISVSDGISM	91	0.1000	1.02
55	VGHIAPEAV	498	0.1000	1.02