MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Mon Mar 29 00:10:13 2010
Length of input sequence	941 amino acids
Number of nanomers from input sequence	933
Number of nanomers with obligatory P1 anchor residue	286
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	94

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	IRMMGAEGL	750	3.3000	55.00
2	LVLITGYDA	539	2.8000	46.67
3	YIRMMGAEG	749	1.5000	25.00
4	MRYLRALAD	472	1.3000	21.67
5	VRRIDGAYG	917	1.3000	21.67
6	MKLNAAAEM	497	1.2200	20.33
7	VRAHLAPFL	709	1.0700	17.83
8	YHGAGGLTA	350	1.0000	16.67

9	FGVAAAAPA	437	1.0000	16.67
10	LEIANASML	140	0.9000	15.00
11	MIPLGSCTM	489	0.7800	13.00
12	YLAVHAKHA	285	0.7500	12.50
13	LARAKANGI	399	0.5000	8.33
14	ITKLTGITV	802	0.5000	8.33
15	LAVLAAMYA	340	0.4900	8.17
16	VVVVDCHDN	602	0.4500	7.50
17	VFTQTAAVL	178	0.4000	6.67
18	FGRQHPFAP	513	0.3000	5.00
19	MMGAEGLRA	752	0.3000	5.00
20	YRTETSMMR	465	0.2900	4.83
21	YGFHAPTMS	820	0.1900	3.17
22	MLAVIGVDS	21	0.0500	0.83
23	FFGVIAQLP	211	0.0500	0.83
24	LRAASLTAI	758	-0.0100	0
25	LRNIIENPA	99	-0.1000	0
26	LRALADKDI	475	-0.1000	0
27	LAGMRVVVV	597	-0.1000	0
28	LNLHKTFCI	687	-0.1000	0
29	YAGLLAIHE	560	-0.2000	0
30	YGSASILPI	737	-0.2000	0
31	VATMLAVIG	18	-0.3000	0
32	YQPEISQGR	115	-0.3000	0
33	FTQTAAVLA	179	-0.3000	0
34	LNALVGLAR	668	-0.3000	0
35	VCSCPPVEA	930	-0.3000	0
36	LIPSSAHGT	582	-0.4000	0
37	FLPGHPFAP	716	-0.4000	0
38	YRLALQTRE	313	-0.4100	0
39	WAYIRMMGA	747	-0.4100	0
40	YTGENGMVA	784	-0.4100	0
41	LVAVGADLL	241	-0.4500	0
42	LLNFQTLVT	127	-0.5200	0

43	VKAVPAGIL	35	-0.5500	0
44	LRGITKLTG	799	-0.6000	0
45	FPVAGTLMV	829	-0.6000	0
46	VTDLTGLEI	134	-0.7000	0
47	VLATRAKPL	185	-0.7000	0
48	ITGYDAVSL	542	-0.7000	0
49	YVDGANLNA	662	-0.7000	0
50	LQPNAGSQG	550	-0.7600	0
51	LRALADANT	71	-0.8000	0
52	FGVIAQLPG	212	-0.8000	0
53	YTREQAAYP	896	-0.8000	0
54	VLDAFGVAA	433	-0.9000	0
55	LMITYPSTH	632	-0.9000	0
56	ILPITWAYI	742	-0.9000	0
57	MVAHECILD	790	-0.9000	0
58	VLLAVLAAM	338	-0.9200	0
59	LLAVLAAMY	339	-0.9500	0
60	LEALLNFQT	124	-1.0000	0
61	FLTHPAFTQ	456	-1.0000	0
62	YPLGTAFRP	903	-1.0000	0
63	IAQLPGASG	215	-1.2000	0
64	VGLARPGKF	672	-1.2000	0
65	LVGLARPGK	671	-1.2300	0
66	MIGQGYYDT	84	-1.3000	0
67	FQTLVTDLT	130	-1.3000	0
68	MGFGGPHAG	276	-1.3000	0
69	IIENPAWYT	102	-1.3400	0
70	VIAQLPGAS	214	-1.4000	0
71	VAAAAPAHT	439	-1.4000	0
72	LLAIHEYHA	563	-1.4000	0
73	ICLIPSSAH	580	-1.4000	0
74	FAPELPKGY	722	-1.4000	0
75	YPVSSAPYG	730	-1.4300	0
76	LAAMYASYH	343	-1.5000	0

77	LRQLVADLQ	528	-1.5000	0
78	LPITWAYIR	743	-1.5000	0
79	LTLIAPPGE	251	-1.5300	0
80	LLALTLIAP	248	-1.6000	0
81	VSLQPNAGS	548	-1.6000	0
82	IVTADLRAG	197	-1.6100	0
83	IRRDKATSN	324	-1.6100	0
84	YDTHTPPVL	90	-1.6300	0
85	FRPKVWPAV	909	-1.6300	0
86	LVCSCPPVE	929	-1.6300	0
87	LDSLPPAAS	55	-1.7000	0
88	FGTTQRFGV	266	-1.7000	0
89	FGVPMGFGG	272	-1.7000	0
90	LHKTFCIPH	689	-1.7000	0
91	MIGIRAEID	855	-1.7000	0
92	LPGASGRIT	218	-1.7100	0
93	VHAKHARQL	288	-1.7100	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	IRMMGAEGL	750	4.3000	71.67
2	LVLITGYDA	539	3.8000	63.33
3	MRYLRALAD	472	2.3000	38.33
4	VRRIDGAYG	917	2.3000	38.33
5	MKLNAAAEM	497	2.2200	37.00
6	VRAHLAPFL	709	2.0700	34.50
7	LEIANASML	140	1.9000	31.67
8	MIPLGSCTM	489	1.7800	29.67
9	LARAKANGI	399	1.5000	25.00
10	ITKLTGITV	802	1.5000	25.00
11	LAVLAAMYA	340	1.4900	24.83
12	VVVVDCHDN	602	1.4500	24.17

13	VFTQTAAVL	178	1.4000	23.33
14	MMGAEGLRA	752	1.3000	21.67
15	MLAVIGVDS	21	1.0500	17.50
16	FGVAAAAPA	437	1.0000	16.67
17	LRAASLTAI	758	0.9900	16.50
18	LRNIIENPA	99	0.9000	15.00
19	LRALADKDI	475	0.9000	15.00
20	LAGMRVVVV	597	0.9000	15.00
21	LNLHKTFCI	687	0.9000	15.00
22	VATMLAVIG	18	0.7000	11.67
23	LNALVGLAR	668	0.7000	11.67
24	VCSCPPVEA	930	0.7000	11.67
25	LIPSSAHGT	582	0.6000	10.00
26	LVAVGADLL	241	0.5500	9.17
27	YIRMMGAEG	749	0.5000	8.33
28	LLNFQTLVT	127	0.4800	8.00
29	VKAVPAGIL	35	0.4500	7.50
30	LRGITKLTG	799	0.4000	6.67
31	VTDLTGLEI	134	0.3000	5.00
32	VLATRAKPL	185	0.3000	5.00
33	FGRQHPFAP	513	0.3000	5.00
34	ITGYDAVSL	542	0.3000	5.00
35	LQPNAGSQG	550	0.2400	4.00
36	LRALADANT	71	0.2000	3.33
37	VLDAFGVAA	433	0.1000	1.67
38	LMITYPSTH	632	0.1000	1.67
39	ILPITWAYI	742	0.1000	1.67
40	MVAHECILD	790	0.1000	1.67
41	VLLAVLAAM	338	0.0800	1.33
42	FFGVIAQLP	211	0.0500	0.83
43	LLAVLAAMY	339	0.0500	0.83
44	IAQLPGASG	215	-0.2000	0
45	VGLARPGKF	672	-0.2000	0
46	LVGLARPGK	671	-0.2300	0

47	YLAVHAKHA	285	-0.2500	0
48	MIGQGYYDT	84	-0.3000	0
49	FTQTAAVLA	179	-0.3000	0
50	MGFGGPHAG	276	-0.3000	0
51	IIENPAWYT	102	-0.3400	0
52	VIAQLPGAS	214	-0.4000	0
53	VAAAAPAHT	439	-0.4000	0
54	LLAIHEYHA	563	-0.4000	0
55	ICLIPSSAH	580	-0.4000	0
56	FLPGHPFAP	716	-0.4000	0
57	LAAMYASYH	343	-0.5000	0
58	LRQLVADLQ	528	-0.5000	0
59	LPITWAYIR	743	-0.5000	0
60	LTLIAPPGE	251	-0.5300	0
61	LLALTLIAP	248	-0.6000	0
62	VSLQPNAGS	548	-0.6000	0
63	FPVAGTLMV	829	-0.6000	0
64	IVTADLRAG	197	-0.6100	0
65	IRRDKATSN	324	-0.6100	0
66	LVCSCPPVE	929	-0.6300	0
67	LDSLPPAAS	55	-0.7000	0
68	LHKTFCIPH	689	-0.7000	0
69	MIGIRAEID	855	-0.7000	0
70	LPGASGRIT	218	-0.7100	0
71	VHAKHARQL	288	-0.7100	0
72	YRTETSMMR	465	-0.7100	0
73	VADLQSWLV	532	-0.7800	0
74	LTGLEIANA	137	-0.8000	0
75	FGVIAQLPG	212	-0.8000	0
76	ICTAQVLLA	333	-0.8000	0
77	LRAKVGEHA	618	-0.8000	0
78	ILDLRGITK	796	-0.8000	0
79	YGFHAPTMS	820	-0.8100	0
80	LGTAFRPKV	905	-0.9300	0

81	VIGVDSLDD	24	-0.9500	0
82	MTLMHRAAR	158	-1.0000	0
83	FLTHPAFTQ	456	-1.0000	0
84	LPKGYPVSS	726	-1.0000	0
85	LTAITSANY	763	-1.0000	0
86	MHRAARGPV	161	-1.1000	0
87	MMRYLRALA	471	-1.1000	0
88	LWRVDADHV	409	-1.1500	0
89	YAGLLAIHE	560	-1.2000	0
90	YGSASILPI	737	-1.2000	0
91	YQPEISQGR	115	-1.3000	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	LVTDLTGLE	133	5.0000	52.63
2	LRGITKLTG	799	4.8000	50.53
3	VVVDCHDNG	603	4.6000	48.42
4	IRRDKATSN	324	4.5000	47.37
5	ITVDDVAKR	808	4.5000	47.37
6	LVADLQSWL	531	4.1300	43.47
7	VVLDAFGVA	432	4.1000	43.16
8	IALDRSMIP	483	4.0000	42.11
9	LVGLARPGK	671	3.8000	40.00
10	LNLHKTFCI	687	3.7000	38.95
11	LVCSCPPVE	929	3.7000	38.95
12	IGLDSQAVA	11	3.5000	36.84
13	MKLNAAAEM	497	3.4000	35.79
14	IRMMGAEGL	750	3.3600	35.37
15	VLLAVLAAM	338	3.3000	34.74
16	VTADLRAGL	198	3.2600	34.32
17	LVHDKYFDT	378	3.2000	33.68
18	VRRIDGAYG	917	3.1000	32.63

19	VYVDGANLN	661	3.0100	31.68
20	VDSDGTPAY	305	3.0000	31.58
21	VGLARPGKF	672	3.0000	31.58
22	MHRAARGPV	161	2.9000	30.53
23	VAFGTTQRF	264	2.9000	30.53
24	LRAASLTAI	758	2.9000	30.53
25	IGVDSLDDL	25	2.8600	30.11
26	VRAHLAPFL	709	2.8600	30.11
27	LVLITGYDA	539	2.8500	30.00
28	VIAQLPGAS	214	2.8000	29.47
29	IGADVAFGT	260	2.8000	29.47
30	MRVVVVDCH	600	2.8000	29.47
31	MRYLRALAD	472	2.6000	27.37
32	MTLMHRAAR	158	2.5000	26.32
33	VGADLLALT	244	2.5000	26.32
34	LGTAFRPKV	905	2.5000	26.32
35	VAVSMIGQG	80	2.4000	25.26
36	LTLIAPPGE	251	2.4000	25.26
37	MIPLGSCTM	489	2.4000	25.26
38	VVDADVFTQ	173	2.3000	24.21
39	LRAGLPDGE	202	2.3000	24.21
40	LVGVSVDSD	300	2.3000	24.21
41	VDADHVSVA	412	2.2700	23.89
42	VVVDADVFT	172	2.2000	23.16
43	LLRNIIENP	98	2.1000	22.11
44	MYASYHGAG	346	2.0000	21.05
45	LRGAPHTAQ	877	2.0000	21.05
46	MGFGGPHAG	276	1.9000	20.00
47	WRVDADHVS	410	1.9000	20.00
48	LDRSMIPLG	485	1.9000	20.00
49	LAGMRVVVV	597	1.9000	20.00
50	LARPGKFGG	674	1.9000	20.00
51	MVAHECILD	790	1.9000	20.00
52	WPVDDNPLR	870	1.9000	20.00

53	LAVKAVPAG	33	1.8000	18.95
54	VKRVVVDAD	169	1.8000	18.95
55	IVTADLRAG	197	1.8000	18.95
56	LVQQAHDRG	231	1.8000	18.95
57	MMRYLRALA	471	1.8000	18.95
58	LPKGYPVSS	726	1.8000	18.95
59	YGFHAPTMS	820	1.8000	18.95
60	LRNIIENPA	99	1.7100	18.00
61	VSMIGQGYY	82	1.7000	17.89
62	VLARAKANG	398	1.7000	17.89
63	YRTETSMMR	465	1.7000	17.89
64	LMITYPSTH	632	1.6700	17.58
65	LEIANASML	140	1.6300	17.16
66	MLAVIGVDS	21	1.6000	16.84
67	LAVLAAMYA	340	1.6000	16.84
68	VACDEATTD	419	1.6000	16.84
69	LNAAAEMES	499	1.6000	16.84
70	LTGITVDDV	805	1.6000	16.84
71	LAVIGVDSL	22	1.5600	16.42
72	VLLRNIIEN	97	1.5000	15.79
73	LGIEIVTAD	193	1.5000	15.79
74	IEIVTADLR	195	1.5000	15.79
75	LAVHAKHAR	286	1.5000	15.79
76	YRLALQTRE	313	1.5000	15.79
77	FLPGHPFAP	716	1.5000	15.79
78	LQPNAGSQG	550	1.4700	15.47
79	LVAVGADLL	241	1.4600	15.37
80	LNFQTLVTD	128	1.4000	14.74
81	LATRAKPLG	186	1.4000	14.74
82	ICTAQVLLA	333	1.4000	14.74
83	LRQLVADLQ	528	1.4000	14.74
84	YEHDIAEIC	643	1.4000	14.74
85	LLALTLIAP	248	1.3000	13.68
86	LALQTREQH	315	1.3000	13.68

87	LLAVLAAMY	339	1.3000	13.68
88	LQSWLVLIT	535	1.3000	13.68
89	LARAKANGI	399	1.2100	12.74
90	LDSQAVATM	13	1.2000	12.63
91	WYTAYTPYQ	108	1.2000	12.63
92	VSLQPNAGS	548	1.2000	12.63
93	VVVVDCHDN	602	1.2000	12.63
94	YGSASILPI	737	1.2000	12.63

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	VVLDAFGVA	432	3.1000	34.07
2	WYTAYTPYQ	108	2.9000	31.87
3	IRRDKATSN	324	2.7000	29.67
4	LVGLARPGK	671	2.7000	29.67
5	LVTDLTGLE	133	2.6000	28.57
6	IGLDSQAVA	11	2.5000	27.47
7	WRVDADHVS	410	2.5000	27.47
8	YEHDIAEIC	643	2.4000	26.37
9	LRGITKLTG	799	2.4000	26.37
10	YGFHAPTMS	820	2.4000	26.37
11	MRVVVVDCH	600	2.3800	26.15
12	VVVDCHDNG	603	2.2000	24.18
13	LVADLQSWL	531	2.1700	23.85
14	VVDADVFTQ	173	2.0000	21.98
15	FLTHPAFTQ	456	2.0000	21.98
16	IALDRSMIP	483	2.0000	21.98
17	ITVDDVAKR	808	2.0000	21.98
18	LVLITGYDA	539	1.8500	20.33
19	LNLHKTFCI	687	1.8000	19.78
20	LRGAPHTAQ	877	1.7000	18.68
21	LVHDKYFDT	378	1.5000	16.48

22	FLPGHPFAP	716	1.5000	16.48
23	WAYIRMMGA	747	1.5000	16.48
24	VIAQLPGAS	214	1.4000	15.38
25	IRMMGAEGL	750	1.4000	15.38
26	WPVDDNPLR	870	1.4000	15.38
27	VTADLRAGL	198	1.3000	14.29
28	YGSASILPI	737	1.3000	14.29
29	LVCSCPPVE	929	1.3000	14.29
30	VDADHVSVA	412	1.2700	13.96
31	LMITYPSTH	632	1.2500	13.74
32	VYVDGANLN	661	1.2100	13.30
33	YRTETSMMR	465	1.2000	13.19
34	IGADVAFGT	260	1.1000	12.09
35	YRLALQTRE	313	1.1000	12.09
36	LRQLVADLQ	528	1.1000	12.09
37	FGVAAAAPA	437	1.0000	10.99
38	LRAASLTAI	758	1.0000	10.99
39	IGVDSLDDL	25	0.9000	9.89
40	MHRAARGPV	161	0.9000	9.89
41	MKLNAAAEM	497	0.9000	9.89
42	FGRQHPFAP	513	0.9000	9.89
43	YVDGANLNA	662	0.9000	9.89
44	VRAHLAPFL	709	0.9000	9.89
45	LALQTREQH	315	0.8800	9.67
46	VGADLLALT	244	0.8000	8.79
47	VLLAVLAAM	338	0.8000	8.79
48	MMRYLRALA	471	0.8000	8.79
49	LRNIIENPA	99	0.7100	7.80
50	VDSDGTPAY	305	0.7000	7.69
51	WLVLITGYD	538	0.7000	7.69
52	FGGDVSHLN	680	0.7000	7.69
53	VRRIDGAYG	917	0.7000	7.69
54	YHASRGEPH	569	0.6800	7.47
55	LAVLAAMYA	340	0.6000	6.59

56	ICLIPSSAH	580	0.5500	6.04
57	VVVDADVFT	172	0.5000	5.49
58	YHGAGGLTA	350	0.5000	5.49
59	MRYLRALAD	472	0.5000	5.49
60	LGTAFRPKV	905	0.5000	5.49
61	FGVIAQLPG	212	0.4000	4.40
62	ICTAQVLLA	333	0.4000	4.40
63	LPKGYPVSS	726	0.4000	4.40
64	YPVSSAPYG	730	0.4000	4.40
65	YTPYQPEIS	112	0.3000	3.30
66	FGTTQRFGV	266	0.3000	3.30
67	FTQYRTETS	462	0.3000	3.30
68	FPVAGTLMV	829	0.3000	3.30
69	MLAVIGVDS	21	0.2000	2.20
70	FQTLVTDLT	130	0.2000	2.20
71	LVGVSVDSD	300	0.2000	2.20
72	LNAAAEMES	499	0.2000	2.20
73	YPLGTAFRP	903	0.2000	2.20
74	VGPVAVRAH	704	0.1800	1.98
75	LLRNIIENP	98	0.1000	1.10
76	YLAVHAKHA	285	0.1000	1.10
77	VGLARPGKF	672	0.1000	1.10
78	YIRMMGAEG	749	0.1000	1.10
79	FRPKVWPAV	909	0.1000	1.10
80	LTGLEIANA	137	-0.1000	0
81	LRAGLPDGE	202	-0.1000	0
82	MIPLGSCTM	489	-0.1000	0
83	LAGMRVVVV	597	-0.1000	0
84	WPAVRRIDG	914	-0.1000	0
85	VCSCPPVEA	930	-0.1000	0
86	VPMGFGGPH	274	-0.1200	0
87	VSLQPNAGS	548	-0.2000	0
88	MMGAEGLRA	752	-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	LRGITKLTG	799	3.9000	44.32
2	IRRDKATSN	324	3.7000	42.05
3	MRVVVVDCH	600	3.6800	41.82
4	IGLDSQAVA	11	3.5000	39.77
5	VVVDCHDNG	603	3.5000	39.77
6	ITVDDVAKR	808	3.0000	34.09
7	LVADLQSWL	531	2.9000	32.95
8	VYVDGANLN	661	2.9000	32.95
9	IRMMGAEGL	750	2.8000	31.82
10	VVLDAFGVA	432	2.7000	30.68
11	IALDRSMIP	483	2.7000	30.68
12	LRGAPHTAQ	877	2.7000	30.68
13	LRNIIENPA	99	2.4000	27.27
14	LRQLVADLQ	528	2.4000	27.27
15	VTADLRAGL	198	2.3000	26.14
16	WRVDADHVS	410	2.3000	26.14
17	LVGLARPGK	671	2.3000	26.14
18	LALQTREQH	315	2.2800	25.91
19	IGVDSLDDL	25	2.2000	25.00
20	LVTDLTGLE	133	2.2000	25.00
21	VDADHVSVA	412	2.0000	22.73
22	MRYLRALAD	472	2.0000	22.73
23	LRAASLTAI	758	2.0000	22.73
24	LMITYPSTH	632	1.9800	22.50
25	ICTAQVLLA	333	1.9000	21.59
26	MKLNAAAEM	497	1.9000	21.59
27	VGADLLALT	244	1.8000	20.45
28	VLLAVLAAM	338	1.8000	20.45
29	MMRYLRALA	471	1.8000	20.45
30	YEHDIAEIC	643	1.8000	20.45

31	LVLITGYDA	539	1.7000	19.32
32	VRRIDGAYG	917	1.7000	19.32
33	LLRNIIENP	98	1.5000	17.05
34	VVDADVFTQ	173	1.5000	17.05
35	LVGVSVDSD	300	1.5000	17.05
36	YGFHAPTMS	820	1.4000	15.91
37	VVVDADVFT	172	1.3800	15.68
38	MGFGGPHAG	276	1.3000	14.77
39	LAVLAAMYA	340	1.3000	14.77
40	LNLHKTFCI	687	1.3000	14.77
41	MMGAEGLRA	752	1.3000	14.77
42	ICLIPSSAH	580	1.2800	14.55
43	LPKGYPVSS	726	1.2800	14.55
44	LRAGLPDGE	202	1.2000	13.64
45	VVVVDCHDN	602	1.2000	13.64
46	VAFGTTQRF	264	1.1000	12.50
47	LQSWLVLIT	535	1.1000	12.50
48	MLAVIGVDS	21	1.0800	12.27
49	MTLMHRAAR	158	1.0000	11.36
50	VKRVVVDAD	169	1.0000	11.36
51	VIAQLPGAS	214	1.0000	11.36
52	LVHDKYFDT	378	1.0000	11.36
53	LARAKANGI	399	1.0000	11.36
54	LAVIGVDSL	22	0.9000	10.23
55	LTGLEIANA	137	0.9000	10.23
56	MIPLGSCTM	489	0.9000	10.23
57	LNAAAEMES	499	0.9000	10.23
58	LIPSSAHGT	582	0.9000	10.23
59	LTGITVDDV	805	0.9000	10.23
60	LVCSCPPVE	929	0.9000	10.23
61	VGPVAVRAH	704	0.8800	10.00
62	LLNFQTLVT	127	0.8000	9.09
63	LVAVGADLL	241	0.8000	9.09
64	LAVHAKHAR	286	0.8000	9.09

65	VSLQPNAGS	548	0.8000	9.09
66	LAIHEYHAS	564	0.8000	9.09
67	YGSASILPI	737	0.8000	9.09
68	LAGMRVVVV	597	0.7800	8.86
69	VCSCPPVEA	930	0.7800	8.86
70	LVQQAHDRG	231	0.7000	7.95
71	VDLDDLRAK	613	0.7000	7.95
72	LRAKVGEHA	618	0.7000	7.95
73	IGADVAFGT	260	0.6000	6.82
74	IPLGSCTMK	490	0.6000	6.82
75	WYTAYTPYQ	108	0.5000	5.68
76	MHRAARGPV	161	0.5000	5.68
77	VACDEATTD	419	0.5000	5.68
78	FGGDVSHLN	680	0.5000	5.68
79	VRAHLAPFL	709	0.5000	5.68
80	MVAHECILD	790	0.4800	5.45
81	LEIANASML	140	0.4000	4.55
82	LGIEIVTAD	193	0.4000	4.55
83	YVDGANLNA	662	0.4000	4.55
84	VLLRNIIEN	97	0.3800	4.32
85	LTAIARRVH	356	0.3800	4.32
86	IEIVTADLR	195	0.3000	3.41
87	VDSDGTPAY	305	0.3000	3.41
88	VLARAKANG	398	0.3000	3.41
89	MIGIRAEID	855	0.3000	3.41
90	VIGVDSLDD	24	0.2000	2.27
91	WAYIRMMGA	747	0.2000	2.27
92	LNFQTLVTD	128	0.1800	2.05
93	LDSLPPAAS	55	0.1000	1.14
94	IVTADLRAG	197	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	LRGITKLTG	799	3.9000	44.32
2	IRRDKATSN	324	3.7000	42.05
3	MRVVVVDCH	600	3.6800	41.82
4	IGLDSQAVA	11	3.5000	39.77
5	VVVDCHDNG	603	3.5000	39.77
6	ITVDDVAKR	808	3.0000	34.09
7	LVADLQSWL	531	2.9000	32.95
8	VYVDGANLN	661	2.9000	32.95
9	IRMMGAEGL	750	2.8000	31.82
10	VVLDAFGVA	432	2.7000	30.68
11	IALDRSMIP	483	2.7000	30.68
12	LRGAPHTAQ	877	2.7000	30.68
13	LRNIIENPA	99	2.4000	27.27
14	LRQLVADLQ	528	2.4000	27.27
15	VTADLRAGL	198	2.3000	26.14
16	WRVDADHVS	410	2.3000	26.14
17	LVGLARPGK	671	2.3000	26.14
18	LALQTREQH	315	2.2800	25.91
19	IGVDSLDDL	25	2.2000	25.00
20	LVTDLTGLE	133	2.2000	25.00
21	VDADHVSVA	412	2.0000	22.73
22	MRYLRALAD	472	2.0000	22.73
23	LRAASLTAI	758	2.0000	22.73
24	LMITYPSTH	632	1.9800	22.50
25	ICTAQVLLA	333	1.9000	21.59
26	MKLNAAAEM	497	1.9000	21.59
27	VGADLLALT	244	1.8000	20.45
28	VLLAVLAAM	338	1.8000	20.45
29	MMRYLRALA	471	1.8000	20.45
30	YEHDIAEIC	643	1.8000	20.45
31	LVLITGYDA	539	1.7000	19.32
32	VRRIDGAYG	917	1.7000	19.32
33	LLRNIIENP	98	1.5000	17.05

34	VVDADVFTQ	173	1.5000	17.05
35	LVGVSVDSD	300	1.5000	17.05
36	YGFHAPTMS	820	1.4000	15.91
37	VVVDADVFT	172	1.3800	15.68
38	MGFGGPHAG	276	1.3000	14.77
39	LAVLAAMYA	340	1.3000	14.77
40	LNLHKTFCI	687	1.3000	14.77
41	MMGAEGLRA	752	1.3000	14.77
42	ICLIPSSAH	580	1.2800	14.55
43	LPKGYPVSS	726	1.2800	14.55
44	LRAGLPDGE	202	1.2000	13.64
45	VVVVDCHDN	602	1.2000	13.64
46	VAFGTTQRF	264	1.1000	12.50
47	LQSWLVLIT	535	1.1000	12.50
48	MLAVIGVDS	21	1.0800	12.27
49	MTLMHRAAR	158	1.0000	11.36
50	VKRVVVDAD	169	1.0000	11.36
51	VIAQLPGAS	214	1.0000	11.36
52	LVHDKYFDT	378	1.0000	11.36
53	LARAKANGI	399	1.0000	11.36
54	LAVIGVDSL	22	0.9000	10.23
55	LTGLEIANA	137	0.9000	10.23
56	MIPLGSCTM	489	0.9000	10.23
57	LNAAAEMES	499	0.9000	10.23
58	LIPSSAHGT	582	0.9000	10.23
59	LTGITVDDV	805	0.9000	10.23
60	LVCSCPPVE	929	0.9000	10.23
61	VGPVAVRAH	704	0.8800	10.00
62	LLNFQTLVT	127	0.8000	9.09
63	LVAVGADLL	241	0.8000	9.09
64	LAVHAKHAR	286	0.8000	9.09
65	VSLQPNAGS	548	0.8000	9.09
66	LAIHEYHAS	564	0.8000	9.09
67	YGSASILPI	737	0.8000	9.09

68	LAGMRVVVV	597	0.7800	8.86
69	VCSCPPVEA	930	0.7800	8.86
70	LVQQAHDRG	231	0.7000	7.95
71	VDLDDLRAK	613	0.7000	7.95
72	LRAKVGEHA	618	0.7000	7.95
73	IGADVAFGT	260	0.6000	6.82
74	IPLGSCTMK	490	0.6000	6.82
75	WYTAYTPYQ	108	0.5000	5.68
76	MHRAARGPV	161	0.5000	5.68
77	VACDEATTD	419	0.5000	5.68
78	FGGDVSHLN	680	0.5000	5.68
79	VRAHLAPFL	709	0.5000	5.68
80	MVAHECILD	790	0.4800	5.45
81	LEIANASML	140	0.4000	4.55
82	LGIEIVTAD	193	0.4000	4.55
83	YVDGANLNA	662	0.4000	4.55
84	VLLRNIIEN	97	0.3800	4.32
85	LTAIARRVH	356	0.3800	4.32
86	IEIVTADLR	195	0.3000	3.41
87	VDSDGTPAY	305	0.3000	3.41
88	VLARAKANG	398	0.3000	3.41
89	MIGIRAEID	855	0.3000	3.41
90	VIGVDSLDD	24	0.2000	2.27
91	WAYIRMMGA	747	0.2000	2.27
92	LNFQTLVTD	128	0.1800	2.05
93	LDSLPPAAS	55	0.1000	1.14
94	IVTADLRAG	197	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	LRGITKLTG	799	3.9000	44.32
2	IRRDKATSN	324	3.7000	42.05

3	MRVVVVDCH	600	3.6800	41.82
4	IGLDSQAVA	11	3.5000	39.77
5	VVVDCHDNG	603	3.5000	39.77
6	ITVDDVAKR	808	3.0000	34.09
7	LVADLQSWL	531	2.9000	32.95
8	VYVDGANLN	661	2.9000	32.95
9	IRMMGAEGL	750	2.8000	31.82
10	VVLDAFGVA	432	2.7000	30.68
11	IALDRSMIP	483	2.7000	30.68
12	LRGAPHTAQ	877	2.7000	30.68
13	LRNIIENPA	99	2.4000	27.27
14	LRQLVADLQ	528	2.4000	27.27
15	VTADLRAGL	198	2.3000	26.14
16	WRVDADHVS	410	2.3000	26.14
17	LVGLARPGK	671	2.3000	26.14
18	LALQTREQH	315	2.2800	25.91
19	IGVDSLDDL	25	2.2000	25.00
20	LVTDLTGLE	133	2.2000	25.00
21	VDADHVSVA	412	2.0000	22.73
22	MRYLRALAD	472	2.0000	22.73
23	LRAASLTAI	758	2.0000	22.73
24	LMITYPSTH	632	1.9800	22.50
25	ICTAQVLLA	333	1.9000	21.59
26	MKLNAAAEM	497	1.9000	21.59
27	VGADLLALT	244	1.8000	20.45
28	VLLAVLAAM	338	1.8000	20.45
29	MMRYLRALA	471	1.8000	20.45
30	YEHDIAEIC	643	1.8000	20.45
31	LVLITGYDA	539	1.7000	19.32
32	VRRIDGAYG	917	1.7000	19.32
33	LLRNIIENP	98	1.5000	17.05
34	VVDADVFTQ	173	1.5000	17.05
35	LVGVSVDSD	300	1.5000	17.05
36	YGFHAPTMS	820	1.4000	15.91

37	VVVDADVFT	172	1.3800	15.68
38	MGFGGPHAG	276	1.3000	14.77
39	LAVLAAMYA	340	1.3000	14.77
40	LNLHKTFCI	687	1.3000	14.77
41	MMGAEGLRA	752	1.3000	14.77
42	ICLIPSSAH	580	1.2800	14.55
43	LPKGYPVSS	726	1.2800	14.55
44	LRAGLPDGE	202	1.2000	13.64
45	VVVVDCHDN	602	1.2000	13.64
46	VAFGTTQRF	264	1.1000	12.50
47	LQSWLVLIT	535	1.1000	12.50
48	MLAVIGVDS	21	1.0800	12.27
49	MTLMHRAAR	158	1.0000	11.36
50	VKRVVVDAD	169	1.0000	11.36
51	VIAQLPGAS	214	1.0000	11.36
52	LVHDKYFDT	378	1.0000	11.36
53	LARAKANGI	399	1.0000	11.36
54	LAVIGVDSL	22	0.9000	10.23
55	LTGLEIANA	137	0.9000	10.23
56	MIPLGSCTM	489	0.9000	10.23
57	LNAAAEMES	499	0.9000	10.23
58	LIPSSAHGT	582	0.9000	10.23
59	LTGITVDDV	805	0.9000	10.23
60	LVCSCPPVE	929	0.9000	10.23
61	VGPVAVRAH	704	0.8800	10.00
62	LLNFQTLVT	127	0.8000	9.09
63	LVAVGADLL	241	0.8000	9.09
64	LAVHAKHAR	286	0.8000	9.09
65	VSLQPNAGS	548	0.8000	9.09
66	LAIHEYHAS	564	0.8000	9.09
67	YGSASILPI	737	0.8000	9.09
68	LAGMRVVVV	597	0.7800	8.86
69	VCSCPPVEA	930	0.7800	8.86
70	LVQQAHDRG	231	0.7000	7.95

71	VDLDDLRAK	613	0.7000	7.95
72	LRAKVGEHA	618	0.7000	7.95
73	IGADVAFGT	260	0.6000	6.82
74	IPLGSCTMK	490	0.6000	6.82
75	WYTAYTPYQ	108	0.5000	5.68
76	MHRAARGPV	161	0.5000	5.68
77	VACDEATTD	419	0.5000	5.68
78	FGGDVSHLN	680	0.5000	5.68
79	VRAHLAPFL	709	0.5000	5.68
80	MVAHECILD	790	0.4800	5.45
81	LEIANASML	140	0.4000	4.55
82	LGIEIVTAD	193	0.4000	4.55
83	YVDGANLNA	662	0.4000	4.55
84	VLLRNIIEN	97	0.3800	4.32
85	LTAIARRVH	356	0.3800	4.32
86	IEIVTADLR	195	0.3000	3.41
87	VDSDGTPAY	305	0.3000	3.41
88	VLARAKANG	398	0.3000	3.41
89	MIGIRAEID	855	0.3000	3.41
90	VIGVDSLDD	24	0.2000	2.27
91	WAYIRMMGA	747	0.2000	2.27
92	LNFQTLVTD	128	0.1800	2.05
93	LDSLPPAAS	55	0.1000	1.14
94	IVTADLRAG	197	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	LVTDLTGLE	133	4.0000	42.11
2	LRGITKLTG	799	3.8000	40.00
3	VVVDCHDNG	603	3.6000	37.89
4	IRRDKATSN	324	3.5000	36.84
5	ITVDDVAKR	808	3.5000	36.84

6	LVADLQSWL	531	3.1300	32.95
7	VVLDAFGVA	432	3.1000	32.63
8	IALDRSMIP	483	3.0000	31.58
9	WRVDADHVS	410	2.9000	30.53
10	WPVDDNPLR	870	2.9000	30.53
11	LVGLARPGK	671	2.8000	29.47
12	YGFHAPTMS	820	2.8000	29.47
13	YRTETSMMR	465	2.7000	28.42
14	LNLHKTFCI	687	2.7000	28.42
15	LVCSCPPVE	929	2.7000	28.42
16	IGLDSQAVA	11	2.5000	26.32
17	YRLALQTRE	313	2.5000	26.32
18	FLPGHPFAP	716	2.5000	26.32
19	MKLNAAAEM	497	2.4000	25.26
20	YEHDIAEIC	643	2.4000	25.26
21	IRMMGAEGL	750	2.3600	24.84
22	VLLAVLAAM	338	2.3000	24.21
23	VTADLRAGL	198	2.2600	23.79
24	WYTAYTPYQ	108	2.2000	23.16
25	LVHDKYFDT	378	2.2000	23.16
26	YGSASILPI	737	2.2000	23.16
27	VRRIDGAYG	917	2.1000	22.11
28	VYVDGANLN	661	2.0100	21.16
29	VDSDGTPAY	305	2.0000	21.05
30	VGLARPGKF	672	2.0000	21.05
31	MHRAARGPV	161	1.9000	20.00
32	VAFGTTQRF	264	1.9000	20.00
33	FGRQHPFAP	513	1.9000	20.00
34	LRAASLTAI	758	1.9000	20.00
35	IGVDSLDDL	25	1.8600	19.58
36	VRAHLAPFL	709	1.8600	19.58
37	LVLITGYDA	539	1.8500	19.47
38	FGVIAQLPG	212	1.8000	18.95
39	VIAQLPGAS	214	1.8000	18.95

40	IGADVAFGT	260	1.8000	18.95
41	WLVLITGYD	538	1.8000	18.95
42	MRVVVVDCH	600	1.8000	18.95
43	YPVSSAPYG	730	1.8000	18.95
44	MRYLRALAD	472	1.6000	16.84
45	MTLMHRAAR	158	1.5000	15.79
46	VGADLLALT	244	1.5000	15.79
47	FGGDVSHLN	680	1.5000	15.79
48	WAYIRMMGA	747	1.5000	15.79
49	YIRMMGAEG	749	1.5000	15.79
50	LGTAFRPKV	905	1.5000	15.79
51	VAVSMIGQG	80	1.4000	14.74
52	LTLIAPPGE	251	1.4000	14.74
53	MIPLGSCTM	489	1.4000	14.74
54	VVDADVFTQ	173	1.3000	13.68
55	LRAGLPDGE	202	1.3000	13.68
56	FGTTQRFGV	266	1.3000	13.68
57	LVGVSVDSD	300	1.3000	13.68
58	FLTHPAFTQ	456	1.3000	13.68
59	FPVAGTLMV	829	1.3000	13.68
60	WPAVRRIDG	914	1.3000	13.68
61	VDADHVSVA	412	1.2700	13.37
62	VVVDADVFT	172	1.2000	12.63
63	YPLGTAFRP	903	1.2000	12.63
64	LLRNIIENP	98	1.1000	11.58
65	FRPKVWPAV	909	1.1000	11.58
66	MYASYHGAG	346	1.0000	10.53
67	FGVAAAAPA	437	1.0000	10.53
68	LRGAPHTAQ	877	1.0000	10.53
69	FQTLVTDLT	130	0.9000	9.47
70	MGFGGPHAG	276	0.9000	9.47
71	LDRSMIPLG	485	0.9000	9.47
72	LAGMRVVVV	597	0.9000	9.47
73	YVDGANLNA	662	0.9000	9.47

74	LARPGKFGG	674	0.9000	9.47
75	MVAHECILD	790	0.9000	9.47
76	LAVKAVPAG	33	0.8000	8.42
77	YQPEISQGR	115	0.8000	8.42
78	VKRVVVDAD	169	0.8000	8.42
79	IVTADLRAG	197	0.8000	8.42
80	LVQQAHDRG	231	0.8000	8.42
81	MMRYLRALA	471	0.8000	8.42
82	LPKGYPVSS	726	0.8000	8.42
83	LRNIIENPA	99	0.7100	7.47
84	VSMIGQGYY	82	0.7000	7.37
85	YTPYQPEIS	112	0.7000	7.37
86	VLARAKANG	398	0.7000	7.37
87	FTQYRTETS	462	0.7000	7.37
88	LMITYPSTH	632	0.6700	7.05
89	LEIANASML	140	0.6300	6.63
90	MLAVIGVDS	21	0.6000	6.32
91	FFGVIAQLP	211	0.6000	6.32
92	LAVLAAMYA	340	0.6000	6.32
93	VACDEATTD	419	0.6000	6.32
94	LNAAAEMES	499	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	LRGITKLTG	799	3.9000	44.32
2	IRRDKATSN	324	3.7000	42.05
3	MRVVVVDCH	600	3.6800	41.82
4	IGLDSQAVA	11	3.5000	39.77
5	VVVDCHDNG	603	3.5000	39.77
6	ITVDDVAKR	808	3.0000	34.09
7	LVADLQSWL	531	2.9000	32.95
8	VYVDGANLN	661	2.9000	32.95

9	IRMMGAEGL	750	2.8000	31.82
10	VVLDAFGVA	432	2.7000	30.68
11	IALDRSMIP	483	2.7000	30.68
12	LRGAPHTAQ	877	2.7000	30.68
13	LRNIIENPA	99	2.4000	27.27
14	LRQLVADLQ	528	2.4000	27.27
15	VTADLRAGL	198	2.3000	26.14
16	WRVDADHVS	410	2.3000	26.14
17	LVGLARPGK	671	2.3000	26.14
18	LALQTREQH	315	2.2800	25.91
19	IGVDSLDDL	25	2.2000	25.00
20	LVTDLTGLE	133	2.2000	25.00
21	VDADHVSVA	412	2.0000	22.73
22	MRYLRALAD	472	2.0000	22.73
23	LRAASLTAI	758	2.0000	22.73
24	LMITYPSTH	632	1.9800	22.50
25	ICTAQVLLA	333	1.9000	21.59
26	MKLNAAAEM	497	1.9000	21.59
27	VGADLLALT	244	1.8000	20.45
28	VLLAVLAAM	338	1.8000	20.45
29	MMRYLRALA	471	1.8000	20.45
30	YEHDIAEIC	643	1.8000	20.45
31	LVLITGYDA	539	1.7000	19.32
32	VRRIDGAYG	917	1.7000	19.32
33	LLRNIIENP	98	1.5000	17.05
34	VVDADVFTQ	173	1.5000	17.05
35	LVGVSVDSD	300	1.5000	17.05
36	YGFHAPTMS	820	1.4000	15.91
37	VVVDADVFT	172	1.3800	15.68
38	MGFGGPHAG	276	1.3000	14.77
39	LAVLAAMYA	340	1.3000	14.77
40	LNLHKTFCI	687	1.3000	14.77
41	MMGAEGLRA	752	1.3000	14.77
42	ICLIPSSAH	580	1.2800	14.55

43	LPKGYPVSS	726	1.2800	14.55
44	LRAGLPDGE	202	1.2000	13.64
45	VVVVDCHDN	602	1.2000	13.64
46	VAFGTTQRF	264	1.1000	12.50
47	LQSWLVLIT	535	1.1000	12.50
48	MLAVIGVDS	21	1.0800	12.27
49	MTLMHRAAR	158	1.0000	11.36
50	VKRVVVDAD	169	1.0000	11.36
51	VIAQLPGAS	214	1.0000	11.36
52	LVHDKYFDT	378	1.0000	11.36
53	LARAKANGI	399	1.0000	11.36
54	LAVIGVDSL	22	0.9000	10.23
55	LTGLEIANA	137	0.9000	10.23
56	MIPLGSCTM	489	0.9000	10.23
57	LNAAAEMES	499	0.9000	10.23
58	LIPSSAHGT	582	0.9000	10.23
59	LTGITVDDV	805	0.9000	10.23
60	LVCSCPPVE	929	0.9000	10.23
61	VGPVAVRAH	704	0.8800	10.00
62	LLNFQTLVT	127	0.8000	9.09
63	LVAVGADLL	241	0.8000	9.09
64	LAVHAKHAR	286	0.8000	9.09
65	VSLQPNAGS	548	0.8000	9.09
66	LAIHEYHAS	564	0.8000	9.09
67	YGSASILPI	737	0.8000	9.09
68	LAGMRVVVV	597	0.7800	8.86
69	VCSCPPVEA	930	0.7800	8.86
70	LVQQAHDRG	231	0.7000	7.95
71	VDLDDLRAK	613	0.7000	7.95
72	LRAKVGEHA	618	0.7000	7.95
73	IGADVAFGT	260	0.6000	6.82
74	IPLGSCTMK	490	0.6000	6.82
75	WYTAYTPYQ	108	0.5000	5.68
76	MHRAARGPV	161	0.5000	5.68

77	VACDEATTD	419	0.5000	5.68
78	FGGDVSHLN	680	0.5000	5.68
79	VRAHLAPFL	709	0.5000	5.68
80	MVAHECILD	790	0.4800	5.45
81	LEIANASML	140	0.4000	4.55
82	LGIEIVTAD	193	0.4000	4.55
83	YVDGANLNA	662	0.4000	4.55
84	VLLRNIIEN	97	0.3800	4.32
85	LTAIARRVH	356	0.3800	4.32
86	IEIVTADLR	195	0.3000	3.41
87	VDSDGTPAY	305	0.3000	3.41
88	VLARAKANG	398	0.3000	3.41
89	MIGIRAEID	855	0.3000	3.41
90	VIGVDSLDD	24	0.2000	2.27
91	WAYIRMMGA	747	0.2000	2.27
92	LNFQTLVTD	128	0.1800	2.05
93	LDSLPPAAS	55	0.1000	1.14
94	IVTADLRAG	197	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	YRTETSMMR	465	4.5000	52.33
2	WRVDADHVS	410	3.7000	43.02
3	YQPEISQGR	115	3.0000	34.88
4	YGFHAPTMS	820	3.0000	34.88
5	IRMMGAEGL	750	2.7000	31.40
6	WYTAYTPYQ	108	2.6000	30.23
7	VSLQPNAGS	548	2.5000	29.07
8	LNLHKTFCI	687	2.5000	29.07
9	LMVEPTESE	835	2.5000	29.07
10	FQTLVTDLT	130	2.4000	27.91
11	LRQLVADLQ	528	2.2000	25.58

12	LMITYPSTH	632	2.1800	25.35
13	MLDEGTAAA	147	2.1000	24.42
14	IALDRSMIP	483	1.9000	22.09
15	YEHDIAEIC	643	1.9000	22.09
16	FPVAGTLMV	829	1.9000	22.09
17	IRRDKATSN	324	1.8000	20.93
18	MRYLRALAD	472	1.8000	20.93
19	MIPLGSCTM	489	1.8000	20.93
20	FGGDVSHLN	680	1.7000	19.77
21	ICLIPSSAH	580	1.6800	19.53
22	LGIEIVTAD	193	1.6000	18.60
23	FLTHPAFTQ	456	1.6000	18.60
24	MKLNAAAEM	497	1.6000	18.60
25	MRVVVVDCH	600	1.4800	17.21
26	LVTDLTGLE	133	1.4000	16.28
27	WAYIRMMGA	747	1.3000	15.12
28	FTQYRTETS	462	1.2000	13.95
29	WLVLITGYD	538	1.2000	13.95
30	YVDGANLNA	662	1.2000	13.95
31	LAVLAAMYA	340	1.1000	12.79
32	VVLDAFGVA	432	1.1000	12.79
33	LLNFQTLVT	127	1.0000	11.63
34	FGVAAAAPA	437	1.0000	11.63
35	VYVDGANLN	661	1.0000	11.63
36	YGSASILPI	737	1.0000	11.63
37	YTGENGMVA	784	1.0000	11.63
38	WPVDDNPLR	870	1.0000	11.63
39	YTREQAAYP	896	0.9000	10.47
40	YYDTHTPPV	89	0.8000	9.30
41	LAIHEYHAS	564	0.8000	9.30
42	ITVDDVAKR	808	0.8000	9.30
43	VVVDADVFT	172	0.7800	9.07
44	FTQTAAVLA	179	0.7800	9.07
45	LRNIIENPA	99	0.7000	8.14

46	LHKTFCIPH	689	0.6600	7.67
47	ICTAQVLLA	333	0.6000	6.98
48	VRAHLAPFL	709	0.6000	6.98
49	MVAHECILD	790	0.5800	6.74
50	FAPELPKGY	722	0.5000	5.81
51	IGLDSQAVA	11	0.4000	4.65
52	LLRNIIENP	98	0.4000	4.65
53	LRGAPHTAQ	877	0.4000	4.65
54	YHASRGEPH	569	0.3800	4.42
55	LAGMRVVVV	597	0.3800	4.42
56	VIAQLPGAS	214	0.3000	3.49
57	LRALADKDI	475	0.3000	3.49
58	VVVDCHDNG	603	0.3000	3.49
59	VAHECILDL	791	0.3000	3.49
60	VEPTESESL	837	0.3000	3.49
61	IRAEIDKVG	858	0.3000	3.49
62	VVDADVFTQ	173	0.2000	2.33
63	YHGAGGLTA	350	0.2000	2.33
64	LVLITGYDA	539	0.2000	2.33
65	YIRMMGAEG	749	0.2000	2.33
66	VRRIDGAYG	917	0.2000	2.33
67	LAVIGVDSL	22	-0.1000	0
68	LTGLEIANA	137	-0.1000	0
69	YRLALQTRE	313	-0.1000	0
70	LTGITVDDV	805	-0.1000	0
71	YLAVHAKHA	285	-0.2000	0
72	VDADHVSVA	412	-0.2000	0
73	LVADLQSWL	531	-0.2000	0
74	ILPITWAYI	742	-0.2000	0
75	LTAITSANY	763	-0.2000	0
76	LAAMYASYH	343	-0.2200	0
77	LRALADANT	71	-0.3000	0
78	YLRALADKD	474	-0.3000	0
79	FGRQHPFAP	513	-0.3000	0

80	VLITGYDAV	540	-0.3000	0
81	LRAASLTAI	758	-0.3000	0
82	YTPYQPEIS	112	-0.4000	0
83	VFTQTAAVL	178	-0.4000	0
84	LQSWLVLIT	535	-0.4000	0
85	MIGIRAEID	855	-0.4000	0
86	VDSDGTPAY	305	-0.5000	0
87	VLLAVLAAM	338	-0.5000	0
88	MMGAEGLRA	752	-0.5000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LNLHKTFCI	687	5.1000	53.12
2	LQSWLVLIT	535	3.7000	38.54
3	LLNFQTLVT	127	3.5000	36.46
4	VGPVAVRAH	704	2.7800	28.96
5	LMHRAARGP	160	2.7000	28.13
6	VVDADVFTQ	173	2.7000	28.13
7	LVLITGYDA	539	2.5800	26.88
8	LAIHEYHAS	564	2.4000	25.00
9	VSLQPNAGS	548	2.3000	23.96
10	YGFHAPTMS	820	2.3000	23.96
11	FLTHPAFTQ	456	2.2000	22.92
12	VAFGTTQRF	264	2.1000	21.88
13	MVAHECILD	790	2.1000	21.88
14	VLLRNIIEN	97	2.0000	20.83
15	IRMMGAEGL	750	2.0000	20.83
16	ICTAQVLLA	333	1.9000	19.79
17	ITDWSALVQ	225	1.8000	18.75
18	VQQAHDRGA	232	1.8000	18.75
19	LMITYPSTH	632	1.7800	18.54
20	ICLIPSSAH	580	1.7600	18.33

21	IVTADLRAG	197	1.7000	17.71
22	MRYLRALAD	472	1.7000	17.71
23	VHAKHARQL	288	1.6000	16.67
24	LRGAPHTAQ	877	1.6000	16.67
25	MIPLGSCTM	489	1.4000	14.58
26	YVDGANLNA	662	1.4000	14.58
27	VRAHLAPFL	709	1.4000	14.58
28	WYTAYTPYQ	108	1.3000	13.54
29	MKLNAAAEM	497	1.3000	13.54
30	LAGMRVVVV	597	1.2000	12.50
31	ITYPSTHGV	634	1.2000	12.50
32	ITWAYIRMM	745	1.2000	12.50
33	FPVAGTLMV	829	1.2000	12.50
34	LARAKANGI	399	1.0000	10.42
35	VVVVDCHDN	602	1.0000	10.42
36	LRNIIENPA	99	0.9800	10.21
37	VIGVDSLDD	24	0.9000	9.38
38	LRAASLTAI	758	0.9000	9.38
39	MRVVVVDCH	600	0.8800	9.17
40	LHKTFCIPH	689	0.8800	9.17
41	MITYPSTHG	633	0.8000	8.33
42	MMGAEGLRA	752	0.8000	8.33
43	IGIRAEIDK	856	0.8000	8.33
44	LAVLAAMYA	340	0.7000	7.29
45	WDHPYTREQ	892	0.7000	7.29
46	VLLAVLAAM	338	0.5000	5.21
47	INLWRVDAD	407	0.5000	5.21
48	VGEHAERLS	622	0.5000	5.21
49	VYEHDIAEI	642	0.5000	5.21
50	VRRIDGAYG	917	0.4800	5.00
51	LPITWAYIR	743	0.4000	4.17
52	VCSCPPVEA	930	0.4000	4.17
53	VSDHSTFAD	0	0.3000	3.12
54	IARRVHAHA	359	0.3000	3.12

55	LGDALVHDK	374	0.3000	3.12
56	YGSASILPI	737	0.3000	3.12
57	LAAMYASYH	343	0.2800	2.92
58	LEIANASML	140	0.2000	2.08
59	LPGRLVGVS	296	0.2000	2.08
60	LQTREQHIR	317	0.2000	2.08
61	LRALADKDI	475	0.2000	2.08
62	LADANTVAV	74	0.1000	1.04
63	LEALLNFQT	124	0.1000	1.04
64	MGFGGPHAG	276	0.1000	1.04
65	ILPITWAYI	742	0.0800	0.83
66	LTAITSANY	763	0.0800	0.83
67	LRGITKLTG	799	0.0800	0.83
68	VLARVPGRA	387	-0.1000	0
69	LDAFGVAAA	434	-0.1000	0
70	LNAAAEMES	499	-0.1000	0
71	VATMLAVIG	18	-0.2000	0
72	IATRTSEFL	449	-0.2000	0
73	VADLQSWLV	532	-0.2000	0
74	VAVRAHLAP	707	-0.2000	0
75	MLAVIGVDS	21	-0.3000	0
76	IIENPAWYT	102	-0.3000	0
77	VAVGADLLA	242	-0.3000	0
78	YRTETSMMR	465	-0.3000	0
79	LIPSSAHGT	582	-0.3000	0
80	LPKGYPVSS	726	-0.3000	0
81	LDLRGITKL	797	-0.3000	0
82	VHAHAEAIA	363	-0.4000	0
83	IPLGSCTMK	490	-0.4000	0
84	LRAKVGEHA	618	-0.4000	0
85	LLAIHEYHA	563	-0.4200	0
86	WAYIRMMGA	747	-0.4200	0
87	LAVKAVPAG	33	-0.5000	0
88	LTGLEIANA	137	-0.5000	0

89	VLATRAKPL	185	-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	IRMMGAEGL	750	3.7000	42.05
2	ICLIPSSAH	580	3.6800	41.82
3	LLNFQTLVT	127	3.5000	39.77
4	MIPLGSCTM	489	3.0000	34.09
5	MRVVVVDCH	600	2.9800	33.86
6	VSLQPNAGS	548	2.7000	30.68
7	MRYLRALAD	472	2.6000	29.55
8	LRQLVADLQ	528	2.5000	28.41
9	LVLITGYDA	539	2.5000	28.41
10	LAAMYASYH	343	2.3800	27.05
11	LNLHKTFCI	687	2.3500	26.70
12	LMITYPSTH	632	2.2800	25.91
13	LAVLAAMYA	340	2.2000	25.00
14	VVDADVFTQ	173	2.1500	24.43
15	LRNIIENPA	99	2.1000	23.86
16	LAGMRVVVV	597	2.1000	23.86
17	LRGAPHTAQ	877	1.9000	21.59
18	VRRIDGAYG	917	1.5000	17.05
19	VIGVDSLDD	24	1.4000	15.91
20	VGPVAVRAH	704	1.3800	15.68
21	LQSWLVLIT	535	1.3500	15.34
22	WYTAYTPYQ	108	1.3000	14.77
23	VVVVDCHDN	602	1.3000	14.77
24	ICTAQVLLA	333	1.2000	13.64
25	LRAASLTAI	758	1.2000	13.64
26	LEALLNFQT	124	1.1500	13.07
27	LTGLEIANA	137	1.1000	12.50
28	LEIANASML	140	1.1000	12.50

29	LARAKANGI	399	1.1000	12.50
30	MITYPSTHG	633	1.1000	12.50
31	ILPITWAYI	742	1.1000	12.50
32	LTAITSANY	763	1.1000	12.50
33	MKLNAAAEM	497	1.0000	11.36
34	LRALADANT	71	0.9000	10.23
35	LVGVSVDSD	300	0.8000	9.09
36	IRRDKATSN	324	0.8000	9.09
37	YRTETSMMR	465	0.8000	9.09
38	VATMLAVIG	18	0.7000	7.95
39	FQTLVTDLT	130	0.7000	7.95
40	MLAVIGVDS	21	0.6000	6.82
41	LDSLPPAAS	55	0.6000	6.82
42	VIAQLPGAS	214	0.6000	6.82
43	LDAFGVAAA	434	0.6000	6.82
44	MLDEGTAAA	147	0.5000	5.68
45	LGIEIVTAD	193	0.5000	5.68
46	VLLAVLAAM	338	0.5000	5.68
47	LLAVLAAMY	339	0.5000	5.68
48	FTQYRTETS	462	0.5000	5.68
49	LRALADKDI	475	0.5000	5.68
50	WLVLITGYD	538	0.5000	5.68
51	WAYIRMMGA	747	0.5000	5.68
52	FPVAGTLMV	829	0.5000	5.68
53	LVAVGADLL	241	0.4000	4.55
54	LRGITKLTG	799	0.4000	4.55
55	YGFHAPTMS	820	0.4000	4.55
56	LAVIGVDSL	22	0.3000	3.41
57	VKRVVVDAD	169	0.3000	3.41
58	IALDRSMIP	483	0.3000	3.41
59	ITYPSTHGV	634	0.3000	3.41
60	LTGITVDDV	805	0.3000	3.41
61	YIRMMGAEG	749	0.1000	1.14
62	MMGAEGLRA	752	0.1000	1.14

63	VCSCPPVEA	930	0.1000	1.14
64	LHKTFCIPH	689	0.0600	0.68
65	IAEICAAVH	647	-0.0200	0
66	IEIVTADLR	195	-0.1000	0
67	LADANTVAV	74	-0.2000	0
68	VFTQTAAVL	178	-0.2000	0
69	WRVDADHVS	410	-0.2000	0
70	LNAAAEMES	499	-0.2000	0
71	INLWRVDAD	407	-0.2500	0
72	VVLDAFGVA	432	-0.3000	0
73	LSALMITYP	629	-0.3000	0
74	LLALTLIAP	248	-0.3200	0
75	VYVDGANLN	661	-0.4000	0
76	LNALVGLAR	668	-0.4000	0
77	LVGLARPGK	671	-0.4000	0
78	YGSASILPI	737	-0.4000	0
79	LLAIHEYHA	563	-0.5000	0
80	MVAHECILD	790	-0.5200	0
81	ITDWSALVQ	225	-0.5500	0
82	FLTHPAFTQ	456	-0.5500	0
83	LDSQAVATM	13	-0.6000	0
84	VKAVPAGIL	35	-0.6000	0
85	MTLMHRAAR	158	-0.6000	0
86	LTLIAPPGE	251	-0.6000	0
87	YRLALQTRE	313	-0.6000	0
88	LGDALVHDK	374	-0.6000	0
89	VADLQSWLV	532	-0.7000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	MRYLRALAD	472	4.3000	45.74
2	WLVLITGYD	538	4.2000	44.68

3	ICLIPSSAH	580	3.9000	41.49
4	IRMMGAEGL	750	3.7000	39.36
5	LLNFQTLVT	127	3.4000	36.17
6	YRLALQTRE	313	3.4000	36.17
7	MRVVVVDCH	600	3.2000	34.04
8	VIGVDSLDD	24	3.1000	32.98
9	WYTAYTPYQ	108	3.1000	32.98
10	MIPLGSCTM	489	3.1000	32.98
11	FQTLVTDLT	130	2.6000	27.66
12	LAAMYASYH	343	2.6000	27.66
13	YAGLLAIHE	560	2.5800	27.45
14	LVGVSVDSD	300	2.5000	26.60
15	LMITYPSTH	632	2.5000	26.60
16	YIRMMGAEG	749	2.4000	25.53
17	LRQLVADLQ	528	2.3000	24.47
18	VVVVDCHDN	602	2.3000	24.47
19	YPVLYTGEN	780	2.3000	24.47
20	LGIEIVTAD	193	2.2000	23.40
21	LVTDLTGLE	133	2.0000	21.28
22	VKRVVVDAD	169	2.0000	21.28
23	LMVEPTESE	835	2.0000	21.28
24	VVDADVFTQ	173	1.9500	20.74
25	YYPVLYTGE	779	1.9000	20.21
26	IRRDKATSN	324	1.8000	19.15
27	YRTETSMMR	465	1.8000	19.15
28	FPVAGTLMV	829	1.8000	19.15
29	VRRIDGAYG	917	1.8000	19.15
30	VSLQPNAGS	548	1.7000	18.09
31	MIGIRAEID	855	1.7000	18.09
32	LRGAPHTAQ	877	1.7000	18.09
33	VGPVAVRAH	704	1.6000	17.02
34	LNLHKTFCI	687	1.5500	16.49
35	FTQYRTETS	462	1.5000	15.96
36	YLRALADKD	474	1.5000	15.96

37	LVLITGYDA	539	1.5000	15.96
38	WAYIRMMGA	747	1.5000	15.96
39	INLWRVDAD	407	1.4500	15.43
40	LTLIAPPGE	251	1.4000	14.89
41	LAGMRVVVV	597	1.4000	14.89
42	MITYPSTHG	633	1.4000	14.89
43	YGFHAPTMS	820	1.4000	14.89
44	FLTHPAFTQ	456	1.2500	13.30
45	LQSWLVLIT	535	1.2500	13.30
46	FGVIAQLPG	212	1.2000	12.77
47	LAVLAAMYA	340	1.2000	12.77
48	LTAITSANY	763	1.2000	12.77
49	MVAHECILD	790	1.1800	12.55
50	LRNIIENPA	99	1.1000	11.70
51	LEIANASML	140	1.1000	11.70
52	MKLNAAAEM	497	1.1000	11.70
53	LEALLNFQT	124	1.0500	11.17
54	VATMLAVIG	18	1.0000	10.64
55	FGVAAAAPA	437	1.0000	10.64
56	LRALADANT	71	0.8000	8.51
57	WRVDADHVS	410	0.8000	8.51
58	FGGDVSHLN	680	0.8000	8.51
59	YGSASILPI	737	0.8000	8.51
60	LRGITKLTG	799	0.7000	7.45
61	LVCSCPPVE	929	0.7000	7.45
62	VLLAVLAAM	338	0.6000	6.38
63	LLAVLAAMY	339	0.6000	6.38
64	VYVDGANLN	661	0.6000	6.38
65	LPPAASEAE	58	0.4000	4.26
66	LNFQTLVTD	128	0.4000	4.26
67	FFGVIAQLP	211	0.4000	4.26
68	LVAVGADLL	241	0.4000	4.26
69	VVDCHDNGD	604	0.4000	4.26
70	LRAASLTAI	758	0.4000	4.26

71	LAVIGVDSL	22	0.3000	3.19
72	WSALVQQAH	228	0.3000	3.19
73	LARAKANGI	399	0.3000	3.19
74	ILPITWAYI	742	0.3000	3.19
75	LHKTFCIPH	689	0.2800	2.98
76	FGRQHPFAP	513	0.2500	2.66
77	YQPEISQGR	115	0.2000	2.13
78	YLAVHAKHA	285	0.2000	2.13
79	ICTAQVLLA	333	0.2000	2.13
80	IAEICAAVH	647	0.2000	2.13
81	LAELRALAD	68	0.1000	1.06
82	LTGLEIANA	137	0.1000	1.06
83	YTPYQPEIS	112	-0.1000	0
84	FAPASDTAG	519	-0.1000	0
85	WDHPYTREQ	892	-0.1000	0
86	VFTQTAAVL	178	-0.2000	0
87	YHGAGGLTA	350	-0.2000	0
88	LRALADKDI	475	-0.3000	0
89	IALDRSMIP	483	-0.3000	0
90	MLAVIGVDS	21	-0.4000	0
91	LDSLPPAAS	55	-0.4000	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	IRMMGAEGL	750	2.7000	30.68
2	ICLIPSSAH	580	2.6800	30.45
3	LLNFQTLVT	127	2.5000	28.41
4	WYTAYTPYQ	108	2.3000	26.14
5	MIPLGSCTM	489	2.0000	22.73
6	MRVVVVDCH	600	1.9800	22.50
7	YRTETSMMR	465	1.8000	20.45
8	FQTLVTDLT	130	1.7000	19.32

9	VSLQPNAGS	548	1.7000	19.32
10	MRYLRALAD	472	1.6000	18.18
11	FTQYRTETS	462	1.5000	17.05
12	LRQLVADLQ	528	1.5000	17.05
13	WLVLITGYD	538	1.5000	17.05
14	LVLITGYDA	539	1.5000	17.05
15	WAYIRMMGA	747	1.5000	17.05
16	FPVAGTLMV	829	1.5000	17.05
17	YGFHAPTMS	820	1.4000	15.91
18	LAAMYASYH	343	1.3800	15.68
19	LNLHKTFCI	687	1.3500	15.34
20	LMITYPSTH	632	1.2800	14.55
21	LAVLAAMYA	340	1.2000	13.64
22	VVDADVFTQ	173	1.1500	13.07
23	LRNIIENPA	99	1.1000	12.50
24	LAGMRVVVV	597	1.1000	12.50
25	YIRMMGAEG	749	1.1000	12.50
26	FGVAAAAPA	437	1.0000	11.36
27	LRGAPHTAQ	877	0.9000	10.23
28	WRVDADHVS	410	0.8000	9.09
29	YGSASILPI	737	0.6000	6.82
30	VRRIDGAYG	917	0.5000	5.68
31	FLTHPAFTQ	456	0.4500	5.11
32	VIGVDSLDD	24	0.4000	4.55
33	YRLALQTRE	313	0.4000	4.55
34	VGPVAVRAH	704	0.3800	4.32
35	LQSWLVLIT	535	0.3500	3.98
36	VVVVDCHDN	602	0.3000	3.41
37	YPVLYTGEN	780	0.3000	3.41
38	YQPEISQGR	115	0.2000	2.27
39	YLAVHAKHA	285	0.2000	2.27
40	ICTAQVLLA	333	0.2000	2.27
41	LRAASLTAI	758	0.2000	2.27
42	LEALLNFQT	124	0.1500	1.70

43	LTGLEIANA	137	0.1000	1.14
44	LEIANASML	140	0.1000	1.14
45	LARAKANGI	399	0.1000	1.14
46	MITYPSTHG	633	0.1000	1.14
47	ILPITWAYI	742	0.1000	1.14
48	LTAITSANY	763	0.1000	1.14
49	LRALADANT	71	-0.1000	0
50	YTPYQPEIS	112	-0.1000	0
51	FGVIAQLPG	212	-0.1000	0
52	FGRQHPFAP	513	-0.1500	0
53	LVGVSVDSD	300	-0.2000	0
54	IRRDKATSN	324	-0.2000	0
55	YHGAGGLTA	350	-0.2000	0
56	VATMLAVIG	18	-0.3000	0
57	MLAVIGVDS	21	-0.4000	0
58	LDSLPPAAS	55	-0.4000	0
59	VIAQLPGAS	214	-0.4000	0
60	LDAFGVAAA	434	-0.4000	0
61	YAGLLAIHE	560	-0.4200	0
62	MLDEGTAAA	147	-0.5000	0
63	LGIEIVTAD	193	-0.5000	0
64	VLLAVLAAM	338	-0.5000	0
65	LLAVLAAMY	339	-0.5000	0
66	LRALADKDI	475	-0.5000	0
67	LVAVGADLL	241	-0.6000	0
68	LRGITKLTG	799	-0.6000	0
69	LAVIGVDSL	22	-0.7000	0
70	VKRVVVDAD	169	-0.7000	0
71	IALDRSMIP	483	-0.7000	0
72	ITYPSTHGV	634	-0.7000	0
73	LTGITVDDV	805	-0.7000	0
74	MMGAEGLRA	752	-0.9000	0
75	WDHPYTREQ	892	-0.9000	0
76	VCSCPPVEA	930	-0.9000	0

77	WSALVQQAH	228	-0.9200	0
78	LHKTFCIPH	689	-0.9400	0
79	LVTDLTGLE	133	-1.0000	0
80	FTQTAAVLA	179	-1.0000	0
81	LMVEPTESE	835	-1.0000	0
82	MIGIRAEID	855	-1.0000	0
83	IAEICAAVH	647	-1.0200	0
84	YYDTHTPPV	89	-1.1000	0
85	IEIVTADLR	195	-1.1000	0
86	YYPVLYTGE	779	-1.1000	0
87	LADANTVAV	74	-1.2000	0
88	VFTQTAAVL	178	-1.2000	0
89	YLRALADKD	474	-1.2000	0
90	LNAAAEMES	499	-1.2000	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	MRYLRALAD	472	5.3000	56.38
2	ICLIPSSAH	580	4.9000	52.13
3	IRMMGAEGL	750	4.7000	50.00
4	LLNFQTLVT	127	4.4000	46.81
5	MRVVVVDCH	600	4.2000	44.68
6	VIGVDSLDD	24	4.1000	43.62
7	MIPLGSCTM	489	4.1000	43.62
8	LAAMYASYH	343	3.6000	38.30
9	LVGVSVDSD	300	3.5000	37.23
10	LMITYPSTH	632	3.5000	37.23
11	LRQLVADLQ	528	3.3000	35.11
12	VVVVDCHDN	602	3.3000	35.11
13	LGIEIVTAD	193	3.2000	34.04
14	WLVLITGYD	538	3.2000	34.04
15	LVTDLTGLE	133	3.0000	31.91

16	VKRVVVDAD	169	3.0000	31.91
17	LMVEPTESE	835	3.0000	31.91
18	VVDADVFTQ	173	2.9500	31.38
19	IRRDKATSN	324	2.8000	29.79
20	VRRIDGAYG	917	2.8000	29.79
21	VSLQPNAGS	548	2.7000	28.72
22	MIGIRAEID	855	2.7000	28.72
23	LRGAPHTAQ	877	2.7000	28.72
24	VGPVAVRAH	704	2.6000	27.66
25	LNLHKTFCI	687	2.5500	27.13
26	LVLITGYDA	539	2.5000	26.60
27	INLWRVDAD	407	2.4500	26.06
28	LTLIAPPGE	251	2.4000	25.53
29	YRLALQTRE	313	2.4000	25.53
30	LAGMRVVVV	597	2.4000	25.53
31	MITYPSTHG	633	2.4000	25.53
32	LQSWLVLIT	535	2.2500	23.94
33	LAVLAAMYA	340	2.2000	23.40
34	LTAITSANY	763	2.2000	23.40
35	MVAHECILD	790	2.1800	23.19
36	LRNIIENPA	99	2.1000	22.34
37	WYTAYTPYQ	108	2.1000	22.34
38	LEIANASML	140	2.1000	22.34
39	MKLNAAAEM	497	2.1000	22.34
40	LEALLNFQT	124	2.0500	21.81
41	VATMLAVIG	18	2.0000	21.28
42	LRALADANT	71	1.8000	19.15
43	LRGITKLTG	799	1.7000	18.09
44	LVCSCPPVE	929	1.7000	18.09
45	FQTLVTDLT	130	1.6000	17.02
46	VLLAVLAAM	338	1.6000	17.02
47	LLAVLAAMY	339	1.6000	17.02
48	VYVDGANLN	661	1.6000	17.02
49	YAGLLAIHE	560	1.5800	16.81

50	LPPAASEAE	58	1.4000	14.89
51	LNFQTLVTD	128	1.4000	14.89
52	LVAVGADLL	241	1.4000	14.89
53	VVDCHDNGD	604	1.4000	14.89
54	YIRMMGAEG	749	1.4000	14.89
55	LRAASLTAI	758	1.4000	14.89
56	LAVIGVDSL	22	1.3000	13.83
57	LARAKANGI	399	1.3000	13.83
58	ILPITWAYI	742	1.3000	13.83
59	YPVLYTGEN	780	1.3000	13.83
60	LHKTFCIPH	689	1.2800	13.62
61	ICTAQVLLA	333	1.2000	12.77
62	IAEICAAVH	647	1.2000	12.77
63	LAELRALAD	68	1.1000	11.70
64	LTGLEIANA	137	1.1000	11.70
65	IANASMLDE	142	1.0000	10.64
66	YYPVLYTGE	779	0.9000	9.57
67	VFTQTAAVL	178	0.8000	8.51
68	YRTETSMMR	465	0.8000	8.51
69	FPVAGTLMV	829	0.8000	8.51
70	LRALADKDI	475	0.7000	7.45
71	IALDRSMIP	483	0.7000	7.45
72	MLAVIGVDS	21	0.6000	6.38
73	LDSLPPAAS	55	0.6000	6.38
74	VIAQLPGAS	214	0.6000	6.38
75	LDAFGVAAA	434	0.6000	6.38
76	ITYPSTHGV	634	0.6000	6.38
77	LTGITVDDV	805	0.6000	6.38
78	LAEVDAFCE	845	0.5500	5.85
79	LDSQAVATM	13	0.5000	5.32
80	MLDEGTAAA	147	0.5000	5.32
81	FTQYRTETS	462	0.5000	5.32
82	YLRALADKD	474	0.5000	5.32
83	WAYIRMMGA	747	0.5000	5.32

84	VKAVPAGIL	35	0.4000	4.26
85	IVTADLRAG	197	0.4000	4.26
86	YGFHAPTMS	820	0.4000	4.26
87	VACDEATTD	419	0.3000	3.19
88	VSDHSTFAD	0	0.2500	2.66
89	ITDWSALVQ	225	0.2500	2.66
90	FLTHPAFTQ	456	0.2500	2.66
91	FGVIAQLPG	212	0.2000	2.13
92	VAVVLDAFG	430	0.2000	2.13
93	VGLARPGKF	672	0.2000	2.13
94	VRAHLAPFL	709	0.2000	2.13

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

Rank	Sequence	At Position	Score	% of Highest Score
1	YRTETSMMR	465	6.0000	66.67
2	YQPEISQGR	115	4.5000	50.00
3	WRVDADHVS	410	4.1000	45.56
4	LMVEPTESE	835	3.9000	43.33
5	IRMMGAEGL	750	3.6600	40.67
6	LNLHKTFCI	687	3.4000	37.78
7	YGFHAPTMS	820	3.4000	37.78
8	MIPLGSCTM	489	3.3000	36.67
9	FQTLVTDLT	130	3.1000	34.44
10	MKLNAAAEM	497	3.1000	34.44
11	MRYLRALAD	472	2.9000	32.22
12	IALDRSMIP	483	2.9000	32.22
13	VSLQPNAGS	548	2.9000	32.22
14	FPVAGTLMV	829	2.9000	32.22
15	LVTDLTGLE	133	2.8000	31.11
16	LGIEIVTAD	193	2.7000	30.00
17	IRRDKATSN	324	2.6000	28.89
18	FGGDVSHLN	680	2.5000	27.78

19	WPVDDNPLR	870	2.5000	27.78
20	WLVLITGYD	538	2.3000	25.56
21	ITVDDVAKR	808	2.3000	25.56
22	MLDEGTAAA	147	2.1000	23.33
23	WYTAYTPYQ	108	1.9000	21.11
24	YEHDIAEIC	643	1.9000	21.11
25	YGSASILPI	737	1.9000	21.11
26	YTREQAAYP	896	1.9000	21.11
27	YYDTHTPPV	89	1.8000	20.00
28	VYVDGANLN	661	1.8000	20.00
29	FAPELPKGY	722	1.8000	20.00
30	LLNFQTLVT	127	1.7000	18.89
31	VVVDCHDNG	603	1.7000	18.89
32	IRAEIDKVG	858	1.7000	18.89
33	MVAHECILD	790	1.6800	18.67
34	FTQYRTETS	462	1.6000	17.78
35	LMITYPSTH	632	1.6000	17.78
36	YIRMMGAEG	749	1.6000	17.78
37	VRRIDGAYG	917	1.6000	17.78
38	VRAHLAPFL	709	1.5600	17.33
39	LRQLVADLQ	528	1.5000	16.67
40	VVVDADVFT	172	1.4800	16.44
41	ILDTLTDTG	42	1.4000	15.56
42	LLRNIIENP	98	1.4000	15.56
43	FGVIAQLPG	212	1.4000	15.56
44	LAGMRVVVV	597	1.3800	15.33
45	YRLALQTRE	313	1.3000	14.44
46	WAYIRMMGA	747	1.3000	14.44
47	VAHECILDL	791	1.2600	14.00
48	VEPTESESL	837	1.2600	14.00
49	LRALADKDI	475	1.2000	13.33
50	LAIHEYHAS	564	1.2000	13.33
51	YVDGANLNA	662	1.2000	13.33
52	LAVLAAMYA	340	1.1000	12.22

53	VVLDAFGVA	432	1.1000	12.22
54	ICLIPSSAH	580	1.1000	12.22
55	LTAITSANY	763	1.1000	12.22
56	VAFGTTQRF	264	1.0000	11.11
57	VLLAVLAAM	338	1.0000	11.11
58	FGVAAAAPA	437	1.0000	11.11
59	YTGENGMVA	784	1.0000	11.11
60	LARAKANGI	399	0.9000	10.00
61	FLTHPAFTQ	456	0.9000	10.00
62	MRVVVVDCH	600	0.9000	10.00
63	LRGITKLTG	799	0.9000	10.00
64	LTGITVDDV	805	0.9000	10.00
65	LVCSCPPVE	929	0.9000	10.00
66	LAVIGVDSL	22	0.8600	9.56
67	VDSDGTPAY	305	0.8000	8.89
68	YLRALADKD	474	0.8000	8.89
69	YPVLYTGEN	780	0.8000	8.89
70	VLYTGENGM	782	0.8000	8.89
71	FTQTAAVLA	179	0.7800	8.67
72	YAGLLAIHE	560	0.7800	8.67
73	LVADLQSWL	531	0.7600	8.44
74	LDSQAVATM	13	0.7000	7.78
75	LRNIIENPA	99	0.7000	7.78
76	VIAQLPGAS	214	0.7000	7.78
77	FGRQHPFAP	513	0.7000	7.78
78	VLITGYDAV	540	0.7000	7.78
79	LIPSSAHGT	582	0.7000	7.78
80	ILPITWAYI	742	0.7000	7.78
81	MIGIRAEID	855	0.7000	7.78
82	LVQQAHDRG	231	0.6000	6.67
83	ICTAQVLLA	333	0.6000	6.67
84	LRAASLTAI	758	0.6000	6.67
85	VFTQTAAVL	178	0.5600	6.22
86	VIGVDSLDD	24	0.5000	5.56

87	YPVSSAPYG	730	0.5000	5.56
88	IGLDSQAVA	11	0.4000	4.44
89	LRALADANT	71	0.4000	4.44
90	LVGVSVDSD	300	0.4000	4.44
91	ITYPSTHGV	634	0.4000	4.44
92	VATMLAVIG	18	0.3800	4.22
93	LEIANASML	140	0.3600	4.00
94	VLATRAKPL	185	0.3600	4.00

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	IRMMGAEGL	750	3.7000	42.05
2	ICLIPSSAH	580	3.6800	41.82
3	LLNFQTLVT	127	3.5000	39.77
4	MIPLGSCTM	489	3.0000	34.09
5	MRVVVVDCH	600	2.9800	33.86
6	VSLQPNAGS	548	2.7000	30.68
7	MRYLRALAD	472	2.6000	29.55
8	LRQLVADLQ	528	2.5000	28.41
9	LVLITGYDA	539	2.5000	28.41
10	LAAMYASYH	343	2.3800	27.05
11	LNLHKTFCI	687	2.3500	26.70
12	LMITYPSTH	632	2.2800	25.91
13	LAVLAAMYA	340	2.2000	25.00
14	VVDADVFTQ	173	2.1500	24.43
15	LRNIIENPA	99	2.1000	23.86
16	LAGMRVVVV	597	2.1000	23.86
17	LRGAPHTAQ	877	1.9000	21.59
18	VRRIDGAYG	917	1.5000	17.05
19	VIGVDSLDD	24	1.4000	15.91
20	VGPVAVRAH	704	1.3800	15.68
21	LQSWLVLIT	535	1.3500	15.34

22	WYTAYTPYQ	108	1.3000	14.77
23	VVVVDCHDN	602	1.3000	14.77
24	ICTAQVLLA	333	1.2000	13.64
25	LRAASLTAI	758	1.2000	13.64
26	LEALLNFQT	124	1.1500	13.07
27	LTGLEIANA	137	1.1000	12.50
28	LEIANASML	140	1.1000	12.50
29	LARAKANGI	399	1.1000	12.50
30	MITYPSTHG	633	1.1000	12.50
31	ILPITWAYI	742	1.1000	12.50
32	LTAITSANY	763	1.1000	12.50
33	MKLNAAAEM	497	1.0000	11.36
34	LRALADANT	71	0.9000	10.23
35	LVGVSVDSD	300	0.8000	9.09
36	IRRDKATSN	324	0.8000	9.09
37	YRTETSMMR	465	0.8000	9.09
38	VATMLAVIG	18	0.7000	7.95
39	FQTLVTDLT	130	0.7000	7.95
40	MLAVIGVDS	21	0.6000	6.82
41	LDSLPPAAS	55	0.6000	6.82
42	VIAQLPGAS	214	0.6000	6.82
43	LDAFGVAAA	434	0.6000	6.82
44	MLDEGTAAA	147	0.5000	5.68
45	LGIEIVTAD	193	0.5000	5.68
46	VLLAVLAAM	338	0.5000	5.68
47	LLAVLAAMY	339	0.5000	5.68
48	FTQYRTETS	462	0.5000	5.68
49	LRALADKDI	475	0.5000	5.68
50	WLVLITGYD	538	0.5000	5.68
51	WAYIRMMGA	747	0.5000	5.68
52	FPVAGTLMV	829	0.5000	5.68
53	LVAVGADLL	241	0.4000	4.55
54	LRGITKLTG	799	0.4000	4.55
55	YGFHAPTMS	820	0.4000	4.55

56	LAVIGVDSL	22	0.3000	3.41
57	VKRVVVDAD	169	0.3000	3.41
58	IALDRSMIP	483	0.3000	3.41
59	ITYPSTHGV	634	0.3000	3.41
60	LTGITVDDV	805	0.3000	3.41
61	YIRMMGAEG	749	0.1000	1.14
62	MMGAEGLRA	752	0.1000	1.14
63	VCSCPPVEA	930	0.1000	1.14
64	LHKTFCIPH	689	0.0600	0.68
65	IAEICAAVH	647	-0.0200	0
66	IEIVTADLR	195	-0.1000	0
67	LADANTVAV	74	-0.2000	0
68	VFTQTAAVL	178	-0.2000	0
69	WRVDADHVS	410	-0.2000	0
70	LNAAAEMES	499	-0.2000	0
71	INLWRVDAD	407	-0.2500	0
72	VVLDAFGVA	432	-0.3000	0
73	LSALMITYP	629	-0.3000	0
74	LLALTLIAP	248	-0.3200	0
75	VYVDGANLN	661	-0.4000	0
76	LNALVGLAR	668	-0.4000	0
77	LVGLARPGK	671	-0.4000	0
78	YGSASILPI	737	-0.4000	0
79	LLAIHEYHA	563	-0.5000	0
80	MVAHECILD	790	-0.5200	0
81	ITDWSALVQ	225	-0.5500	0
82	FLTHPAFTQ	456	-0.5500	0
83	LDSQAVATM	13	-0.6000	0
84	VKAVPAGIL	35	-0.6000	0
85	MTLMHRAAR	158	-0.6000	0
86	LTLIAPPGE	251	-0.6000	0
87	YRLALQTRE	313	-0.6000	0
88	LGDALVHDK	374	-0.6000	0
89	VADLQSWLV	532	-0.7000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	YRTETSMMR	465	4.5000	52.33
2	WRVDADHVS	410	3.7000	43.02
3	YQPEISQGR	115	3.0000	34.88
4	YGFHAPTMS	820	3.0000	34.88
5	IRMMGAEGL	750	2.7000	31.40
6	WYTAYTPYQ	108	2.6000	30.23
7	VSLQPNAGS	548	2.5000	29.07
8	LNLHKTFCI	687	2.5000	29.07
9	LMVEPTESE	835	2.5000	29.07
10	FQTLVTDLT	130	2.4000	27.91
11	LRQLVADLQ	528	2.2000	25.58
12	LMITYPSTH	632	2.1800	25.35
13	MLDEGTAAA	147	2.1000	24.42
14	IALDRSMIP	483	1.9000	22.09
15	YEHDIAEIC	643	1.9000	22.09
16	FPVAGTLMV	829	1.9000	22.09
17	IRRDKATSN	324	1.8000	20.93
18	MRYLRALAD	472	1.8000	20.93
19	MIPLGSCTM	489	1.8000	20.93
20	FGGDVSHLN	680	1.7000	19.77
21	ICLIPSSAH	580	1.6800	19.53
22	LGIEIVTAD	193	1.6000	18.60
23	FLTHPAFTQ	456	1.6000	18.60
24	MKLNAAAEM	497	1.6000	18.60
25	MRVVVVDCH	600	1.4800	17.21
26	LVTDLTGLE	133	1.4000	16.28
27	WAYIRMMGA	747	1.3000	15.12
28	FTQYRTETS	462	1.2000	13.95
29	WLVLITGYD	538	1.2000	13.95
30	YVDGANLNA	662	1.2000	13.95

31	LAVLAAMYA	340	1.1000	12.79
32	VVLDAFGVA	432	1.1000	12.79
33	LLNFQTLVT	127	1.0000	11.63
34	FGVAAAAPA	437	1.0000	11.63
35	VYVDGANLN	661	1.0000	11.63
36	YGSASILPI	737	1.0000	11.63
37	YTGENGMVA	784	1.0000	11.63
38	WPVDDNPLR	870	1.0000	11.63
39	YTREQAAYP	896	0.9000	10.47
40	YYDTHTPPV	89	0.8000	9.30
41	LAIHEYHAS	564	0.8000	9.30
42	ITVDDVAKR	808	0.8000	9.30
43	VVVDADVFT	172	0.7800	9.07
44	FTQTAAVLA	179	0.7800	9.07
45	LRNIIENPA	99	0.7000	8.14
46	LHKTFCIPH	689	0.6600	7.67
47	ICTAQVLLA	333	0.6000	6.98
48	VRAHLAPFL	709	0.6000	6.98
49	MVAHECILD	790	0.5800	6.74
50	FAPELPKGY	722	0.5000	5.81
51	IGLDSQAVA	11	0.4000	4.65
52	LLRNIIENP	98	0.4000	4.65
53	LRGAPHTAQ	877	0.4000	4.65
54	YHASRGEPH	569	0.3800	4.42
55	LAGMRVVVV	597	0.3800	4.42
56	VIAQLPGAS	214	0.3000	3.49
57	LRALADKDI	475	0.3000	3.49
58	VVVDCHDNG	603	0.3000	3.49
59	VAHECILDL	791	0.3000	3.49
60	VEPTESESL	837	0.3000	3.49
61	IRAEIDKVG	858	0.3000	3.49
62	VVDADVFTQ	173	0.2000	2.33
63	YHGAGGLTA	350	0.2000	2.33
64	LVLITGYDA	539	0.2000	2.33

65	YIRMMGAEG	749	0.2000	2.33
66	VRRIDGAYG	917	0.2000	2.33
67	LAVIGVDSL	22	-0.1000	0
68	LTGLEIANA	137	-0.1000	0
69	YRLALQTRE	313	-0.1000	0
70	LTGITVDDV	805	-0.1000	0
71	YLAVHAKHA	285	-0.2000	0
72	VDADHVSVA	412	-0.2000	0
73	LVADLQSWL	531	-0.2000	0
74	ILPITWAYI	742	-0.2000	0
75	LTAITSANY	763	-0.2000	0
76	LAAMYASYH	343	-0.2200	0
77	LRALADANT	71	-0.3000	0
78	YLRALADKD	474	-0.3000	0
79	FGRQHPFAP	513	-0.3000	0
80	VLITGYDAV	540	-0.3000	0
81	LRAASLTAI	758	-0.3000	0
82	YTPYQPEIS	112	-0.4000	0
83	VFTQTAAVL	178	-0.4000	0
84	LQSWLVLIT	535	-0.4000	0
85	MIGIRAEID	855	-0.4000	0
86	VDSDGTPAY	305	-0.5000	0
87	VLLAVLAAM	338	-0.5000	0
88	MMGAEGLRA	752	-0.5000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IRMMGAEGL	750	6.5000	56.03
2	LNLHKTFCI	687	6.3200	54.48
3	YGSASILPI	737	5.8000	50.00
4	VEPTESESL	837	5.7000	49.14
5	VLATRAKPL	185	5.3000	45.69

6	FGTTQRFGV	266	4.9000	42.24
7	LRAASLTAI	758	4.6000	39.66
8	LARAKANGI	399	4.5000	38.79
9	VRAHLAPFL	709	4.5000	38.79
10	VKAVPAGIL	35	4.4000	37.93
11	LEIANASML	140	4.4000	37.93
12	LVLITGYDA	539	4.3000	37.07
13	FPVAGTLMV	829	4.1200	35.52
14	LVAVGADLL	241	4.1000	35.34
15	ILPITWAYI	742	3.9000	33.62
16	LHKTFCIPH	689	3.4000	29.31
17	ITGYDAVSL	542	3.3000	28.45
18	LLNFQTLVT	127	3.2200	27.76
19	LIPSSAHGT	582	3.2000	27.59
20	VLYTGENGM	782	3.1000	26.72
21	FTQTAAVLA	179	3.0000	25.86
22	LRGITKLTG	799	3.0000	25.86
23	FGGPHAGYL	278	2.9000	25.00
24	VVVVDCHDN	602	2.9000	25.00
25	WAYIRMMGA	747	2.9000	25.00
26	VAHECILDL	791	2.9000	25.00
27	LAVIGVDSL	22	2.8000	24.14
28	VIGVDSLDD	24	2.8000	24.14
29	IATRTSEFL	449	2.8000	24.14
30	YYDTHTPPV	89	2.7200	23.45
31	YRLALQTRE	313	2.7000	23.28
32	LMITYPSTH	632	2.7000	23.28
33	FGVIAQLPG	212	2.6000	22.41
34	VHAKHARQL	288	2.6000	22.41
35	YHGAGGLTA	350	2.6000	22.41
36	VLITGYDAV	540	2.6000	22.41
37	LAGMRVVVV	597	2.5000	21.55
38	FFGVIAQLP	211	2.4000	20.69
39	YLAVHAKHA	285	2.4000	20.69

40	YRTETSMMR	465	2.4000	20.69
41	YHASRGEPH	569	2.4000	20.69
42	MVAHECILD	790	2.4000	20.69
43	FLTHPAFTQ	456	2.3000	19.83
44	LPITWAYIR	743	2.3000	19.83
45	MRYLRALAD	472	2.2000	18.97
46	MIPLGSCTM	489	2.2000	18.97
47	LVADLQSWL	531	2.2000	18.97
48	VLLAVLAAM	338	2.1000	18.10
49	VGLARPGKF	672	2.1000	18.10
50	FRPKVWPAV	909	2.1000	18.10
51	LLAVLAAMY	339	2.0000	17.24
52	YFDTVLARV	383	2.0000	17.24
53	MKLNAAAEM	497	2.0000	17.24
54	LQSWLVLIT	535	2.0000	17.24
55	ITKLTGITV	802	2.0000	17.24
56	VTDLTGLEI	134	1.9000	16.38
57	ICLIPSSAH	580	1.9000	16.38
58	MMGAEGLRA	752	1.9000	16.38
59	VAFGTTQRF	264	1.8200	15.69
60	LRALADKDI	475	1.8000	15.52
61	YPSTHGVYE	636	1.8000	15.52
62	VDGANLNAL	663	1.8000	15.52
63	LTAITSANY	763	1.8000	15.52
64	VRRIDGAYG	917	1.8000	15.52
65	LRNIIENPA	99	1.7000	14.66
66	VFTQTAAVL	178	1.7000	14.66
67	VYEHDIAEI	642	1.7000	14.66
68	YYPVLYTGE	779	1.7000	14.66
69	MSFPVAGTL	827	1.7000	14.66
70	MLAVIGVDS	21	1.6000	13.79
71	LVCSCPPVE	929	1.6000	13.79
72	YDTHTPPVL	90	1.5000	12.93
73	YAGLLAIHE	560	1.5000	12.93

74	YGFHAPTMS	820	1.5000	12.93
75	ITYPSTHGV	634	1.4200	12.24
76	MHRAARGPV	161	1.4000	12.07
77	MESITWPEF	505	1.4000	12.07
78	LDLRGITKL	797	1.4000	12.07
79	VLLRNIIEN	97	1.3000	11.21
80	ICTAQVLLA	333	1.3000	11.21
81	YVDGANLNA	662	1.3000	11.21
82	VGPVAVRAH	704	1.3000	11.21
83	LADANTVAV	74	1.2200	10.52
84	VSMIGQGYY	82	1.2000	10.34
85	LVHDKYFDT	378	1.2000	10.34
86	LWRVDADHV	409	1.2000	10.34
87	MRVVVVDCH	600	1.2000	10.34
88	FLPGHPFAP	716	1.2000	10.34
89	ITWAYIRMM	745	1.2000	10.34
90	VVDADVFTQ	173	1.1000	9.48
91	LTGITVDDV	805	1.1000	9.48
92	MIGIRAEID	855	1.1000	9.48
93	WPAVRRIDG	914	1.1000	9.48
94	YQPEISQGR	115	1.0000	8.62

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	IRMMGAEGL	750	6.5000	56.03
2	LNLHKTFCI	687	6.3200	54.48
3	YGSASILPI	737	5.8000	50.00
4	VEPTESESL	837	5.7000	49.14
5	VLATRAKPL	185	5.3000	45.69
6	FGTTQRFGV	266	4.9000	42.24
7	LRAASLTAI	758	4.6000	39.66
8	LARAKANGI	399	4.5000	38.79

9	VRAHLAPFL	709	4.5000	38.79
10	VKAVPAGIL	35	4.4000	37.93
11	LEIANASML	140	4.4000	37.93
12	LVLITGYDA	539	4.3000	37.07
13	FPVAGTLMV	829	4.1200	35.52
14	LVAVGADLL	241	4.1000	35.34
15	ILPITWAYI	742	3.9000	33.62
16	LHKTFCIPH	689	3.4000	29.31
17	ITGYDAVSL	542	3.3000	28.45
18	LLNFQTLVT	127	3.2200	27.76
19	LIPSSAHGT	582	3.2000	27.59
20	VLYTGENGM	782	3.1000	26.72
21	FTQTAAVLA	179	3.0000	25.86
22	LRGITKLTG	799	3.0000	25.86
23	FGGPHAGYL	278	2.9000	25.00
24	VVVVDCHDN	602	2.9000	25.00
25	WAYIRMMGA	747	2.9000	25.00
26	VAHECILDL	791	2.9000	25.00
27	LAVIGVDSL	22	2.8000	24.14
28	VIGVDSLDD	24	2.8000	24.14
29	IATRTSEFL	449	2.8000	24.14
30	YYDTHTPPV	89	2.7200	23.45
31	YRLALQTRE	313	2.7000	23.28
32	LMITYPSTH	632	2.7000	23.28
33	FGVIAQLPG	212	2.6000	22.41
34	VHAKHARQL	288	2.6000	22.41
35	YHGAGGLTA	350	2.6000	22.41
36	VLITGYDAV	540	2.6000	22.41
37	LAGMRVVVV	597	2.5000	21.55
38	FFGVIAQLP	211	2.4000	20.69
39	YLAVHAKHA	285	2.4000	20.69
40	YRTETSMMR	465	2.4000	20.69
41	YHASRGEPH	569	2.4000	20.69
42	MVAHECILD	790	2.4000	20.69

43	FLTHPAFTQ	456	2.3000	19.83
44	LPITWAYIR	743	2.3000	19.83
45	MRYLRALAD	472	2.2000	18.97
46	MIPLGSCTM	489	2.2000	18.97
47	LVADLQSWL	531	2.2000	18.97
48	VLLAVLAAM	338	2.1000	18.10
49	VGLARPGKF	672	2.1000	18.10
50	FRPKVWPAV	909	2.1000	18.10
51	LLAVLAAMY	339	2.0000	17.24
52	YFDTVLARV	383	2.0000	17.24
53	MKLNAAAEM	497	2.0000	17.24
54	LQSWLVLIT	535	2.0000	17.24
55	ITKLTGITV	802	2.0000	17.24
56	VTDLTGLEI	134	1.9000	16.38
57	ICLIPSSAH	580	1.9000	16.38
58	MMGAEGLRA	752	1.9000	16.38
59	VAFGTTQRF	264	1.8200	15.69
60	LRALADKDI	475	1.8000	15.52
61	YPSTHGVYE	636	1.8000	15.52
62	VDGANLNAL	663	1.8000	15.52
63	LTAITSANY	763	1.8000	15.52
64	VRRIDGAYG	917	1.8000	15.52
65	LRNIIENPA	99	1.7000	14.66
66	VFTQTAAVL	178	1.7000	14.66
67	VYEHDIAEI	642	1.7000	14.66
68	YYPVLYTGE	779	1.7000	14.66
69	MSFPVAGTL	827	1.7000	14.66
70	MLAVIGVDS	21	1.6000	13.79
71	LVCSCPPVE	929	1.6000	13.79
72	YDTHTPPVL	90	1.5000	12.93
73	YAGLLAIHE	560	1.5000	12.93
74	YGFHAPTMS	820	1.5000	12.93
75	ITYPSTHGV	634	1.4200	12.24
76	MHRAARGPV	161	1.4000	12.07

77	MESITWPEF	505	1.4000	12.07
78	LDLRGITKL	797	1.4000	12.07
79	VLLRNIIEN	97	1.3000	11.21
80	ICTAQVLLA	333	1.3000	11.21
81	YVDGANLNA	662	1.3000	11.21
82	VGPVAVRAH	704	1.3000	11.21
83	LADANTVAV	74	1.2200	10.52
84	VSMIGQGYY	82	1.2000	10.34
85	LVHDKYFDT	378	1.2000	10.34
86	LWRVDADHV	409	1.2000	10.34
87	MRVVVVDCH	600	1.2000	10.34
88	FLPGHPFAP	716	1.2000	10.34
89	ITWAYIRMM	745	1.2000	10.34
90	VVDADVFTQ	173	1.1000	9.48
91	LTGITVDDV	805	1.1000	9.48
92	MIGIRAEID	855	1.1000	9.48
93	WPAVRRIDG	914	1.1000	9.48
94	YQPEISQGR	115	1.0000	8.62

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	MMRYLRALA	471	4.0000	46.51
2	VLARAKANG	398	3.9000	45.35
3	VLLRNIIEN	97	3.8000	44.19
4	WLVLITGYD	538	3.5000	40.70
5	MRYLRALAD	472	3.4000	39.53
6	LRGITKLTG	799	3.0000	34.88
7	YIRMMGAEG	749	2.8000	32.56
8	LPGRLVGVS	296	2.4000	27.91
9	VLARVPGRA	387	2.3000	26.74
10	FADRHIGLD	6	2.2000	25.58
11	LAVKAVPAG	33	2.1000	24.42

12	MRVVVVDCH	600	2.1000	24.42
13	YASYHGAGG	347	2.0000	23.26
14	VGPVAVRAH	704	2.0000	23.26
15	VLLAVLAAM	338	1.9000	22.09
16	IARRVHAHA	359	1.9000	22.09
17	WYTAYTPYQ	108	1.8000	20.93
18	YRLALQTRE	313	1.8000	20.93
19	MKLNAAAEM	497	1.8000	20.93
20	FRPKVWPAV	909	1.8000	20.93
21	VRRIDGAYG	917	1.8000	20.93
22	LVTDLTGLE	133	1.7000	19.77
23	LATRAKPLG	186	1.7000	19.77
24	LADKDIALD	478	1.7000	19.77
25	MIPLGSCTM	489	1.7000	19.77
26	VVVVDCHDN	602	1.6000	18.60
27	IRMMGAEGL	750	1.6000	18.60
28	YPVLYTGEN	780	1.6000	18.60
29	VHAKHARQL	288	1.5000	17.44
30	MTLMHRAAR	158	1.4000	16.28
31	VVDADVFTQ	173	1.4000	16.28
32	LVGVSVDSD	300	1.4000	16.28
33	YAGLLAIHE	560	1.4000	16.28
34	YTPYQPEIS	112	1.3000	15.12
35	FTQYRTETS	462	1.3000	15.12
36	YIARRLDEY	771	1.3000	15.12
37	YGDRNLVCS	924	1.3000	15.12
38	VIGVDSLDD	24	1.2000	13.95
39	LLNFQTLVT	127	1.2000	13.95
40	LMHRAARGP	160	1.1000	12.79
41	LMITYPSTH	632	1.1000	12.79
42	IVTADLRAG	197	1.0000	11.63
43	FGVIAQLPG	212	1.0000	11.63
44	LTAIARRVH	356	1.0000	11.63
45	FGVAAAAPA	437	1.0000	11.63

46	LQSWLVLIT	535	1.0000	11.63
47	YGSASILPI	737	1.0000	11.63
48	VKRVVVDAD	169	0.9000	10.47
49	LTLIAPPGE	251	0.9000	10.47
50	LRQLVADLQ	528	0.8000	9.30
51	LVGLARPGK	671	0.8000	9.30
52	YTAYTPYQP	109	0.7000	8.14
53	LVCSCPPVE	929	0.7000	8.14
54	LTGLEIANA	137	0.6000	6.98
55	MHRAARGPV	161	0.6000	6.98
56	INLWRVDAD	407	0.6000	6.98
57	LVLITGYDA	539	0.6000	6.98
58	VWPAVRRID	913	0.6000	6.98
59	YLAVHAKHA	285	0.5000	5.81
60	VAVRAHLAP	707	0.5000	5.81
61	LLAVLAAMY	339	0.4000	4.65
62	LAAMYASYH	343	0.4000	4.65
63	FLTHPAFTQ	456	0.4000	4.65
64	LRAKVGEHA	618	0.4000	4.65
65	VGLARPGKF	672	0.4000	4.65
66	LQTREQHIR	317	0.3000	3.49
67	YLRALADKD	474	0.3000	3.49
68	ITGYDAVSL	542	0.3000	3.49
69	LAGMRVVVV	597	0.3000	3.49
70	MVAHECILD	790	0.3000	3.49
71	WPAVRRIDG	914	0.3000	3.49
72	WSALVQQAH	228	0.2000	2.33
73	ICLIPSSAH	580	0.2000	2.33
74	LRGAPHTAQ	877	0.2000	2.33
75	MITYPSTHG	633	0.1000	1.16
76	FPVAGTLMV	829	0.1000	1.16
77	IGIRAEIDK	856	0.1000	1.16
78	VKAVPAGIL	35	-0.1000	0
79	ICTAQVLLA	333	-0.1000	0

80	LAVLAAMYA	340	-0.1000	0
81	WAYIRMMGA	747	-0.1000	0
82	LDSLPPAAS	55	-0.2000	0
83	LGIEIVTAD	193	-0.2000	0
84	VIAQLPGAS	214	-0.2000	0
85	YRTETSMMR	465	-0.2000	0
86	IHEYHASRG	566	-0.2000	0
87	ITWAYIRMM	745	-0.2000	0
88	VSMIGQGYY	82	-0.3000	0
89	LNFQTLVTD	128	-0.3000	0
90	LARVPGRAD	388	-0.3000	0
91	VATMLAVIG	18	-0.4000	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	MMRYLRALA	471	4.0000	50.00
2	VLARAKANG	398	2.6000	32.50
3	LPGRLVGVS	296	2.4000	30.00
4	VLARVPGRA	387	2.3000	28.75
5	IARRVHAHA	359	1.9000	23.75
6	VLLRNIIEN	97	1.8000	22.50
7	LRGITKLTG	799	1.7000	21.25
8	LVGLARPGK	671	1.5000	18.75
9	YIRMMGAEG	749	1.5000	18.75
10	FRPKVWPAV	909	1.5000	18.75
11	MTLMHRAAR	158	1.4000	17.50
12	YTPYQPEIS	112	1.3000	16.25
13	FTQYRTETS	462	1.3000	16.25
14	YGDRNLVCS	924	1.3000	16.25
15	WYTAYTPYQ	108	1.0000	12.50
16	FGVAAAAPA	437	1.0000	12.50
17	MRVVVVDCH	600	0.8800	11.00

18	LAVKAVPAG	33	0.8000	10.00
19	VLLAVLAAM	338	0.8000	10.00
20	WLVLITGYD	538	0.8000	10.00
21	YGSASILPI	737	0.8000	10.00
22	IGIRAEIDK	856	0.8000	10.00
23	VGPVAVRAH	704	0.7800	9.75
24	LMHRAARGP	160	0.7000	8.75
25	YASYHGAGG	347	0.7000	8.75
26	MRYLRALAD	472	0.7000	8.75
27	MKLNAAAEM	497	0.7000	8.75
28	LTGLEIANA	137	0.6000	7.50
29	VVDADVFTQ	173	0.6000	7.50
30	MIPLGSCTM	489	0.6000	7.50
31	LVLITGYDA	539	0.6000	7.50
32	IRMMGAEGL	750	0.6000	7.50
33	YLAVHAKHA	285	0.5000	6.25
34	VHAKHARQL	288	0.5000	6.25
35	VRRIDGAYG	917	0.5000	6.25
36	LATRAKPLG	186	0.4000	5.00
37	LRAKVGEHA	618	0.4000	5.00
38	YTAYTPYQP	109	0.3000	3.75
39	LLNFQTLVT	127	0.3000	3.75
40	MHRAARGPV	161	0.3000	3.75
41	LQTREQHIR	317	0.3000	3.75
42	YIARRLDEY	771	0.2000	2.50
43	LQSWLVLIT	535	0.1000	1.25
44	VAVRAHLAP	707	0.1000	1.25
45	ICTAQVLLA	333	-0.1000	0
46	LAVLAAMYA	340	-0.1000	0
47	WAYIRMMGA	747	-0.1000	0
48	LMITYPSTH	632	-0.1200	0
49	LDSLPPAAS	55	-0.2000	0
50	VIAQLPGAS	214	-0.2000	0
51	YRTETSMMR	465	-0.2000	0

52	FPVAGTLMV	829	-0.2000	0
53	LTAIARRVH	356	-0.2200	0
54	IVTADLRAG	197	-0.3000	0
55	FGVIAQLPG	212	-0.3000	0
56	FLTHPAFTQ	456	-0.4000	0
57	VVVVDCHDN	602	-0.4000	0
58	YPVLYTGEN	780	-0.4000	0
59	FADRHIGLD	6	-0.5000	0
60	VGLARPGKF	672	-0.5000	0
61	LDAFGVAAA	434	-0.6000	0
62	LNLHKTFCI	687	-0.6000	0
63	LRGAPHTAQ	877	-0.6000	0
64	LRNIIENPA	99	-0.7000	0
65	LLAVLAAMY	339	-0.7000	0
66	ITGYDAVSL	542	-0.7000	0
67	MMGAEGLRA	752	-0.7000	0
68	IGLDSQAVA	11	-0.8000	0
69	MLAVIGVDS	21	-0.8000	0
70	VVLDAFGVA	432	-0.8000	0
71	LAAMYASYH	343	-0.8200	0
72	FQTLVTDLT	130	-0.9000	0
73	WRVDADHVS	410	-0.9000	0
74	YGFHAPTMS	820	-0.9000	0
75	LADKDIALD	478	-1.0000	0
76	WPAVRRIDG	914	-1.0000	0
77	WSALVQQAH	228	-1.0200	0
78	ICLIPSSAH	580	-1.0200	0
79	VKAVPAGIL	35	-1.1000	0
80	FGTTQRFGV	266	-1.1000	0
81	YVDGANLNA	662	-1.1000	0
82	ILPITWAYI	742	-1.1000	0
83	FFGVIAQLP	211	-1.2000	0
84	LLALTLIAP	248	-1.2000	0
85	YRLALQTRE	313	-1.2000	0

86	LNAAAEMES	499	-1.2000	0
87	VSLQPNAGS	548	-1.2000	0
88	MITYPSTHG	633	-1.2000	0
89	LVTDLTGLE	133	-1.3000	0
90	LVGVSVDSD	300	-1.3000	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	MMRYLRALA	471	5.0000	62.50
2	VLARAKANG	398	3.6000	45.00
3	LPGRLVGVS	296	3.4000	42.50
4	VLARVPGRA	387	3.3000	41.25
5	IARRVHAHA	359	2.9000	36.25
6	VLLRNIIEN	97	2.8000	35.00
7	LRGITKLTG	799	2.7000	33.75
8	LVGLARPGK	671	2.5000	31.25
9	MTLMHRAAR	158	2.4000	30.00
10	MRVVVVDCH	600	1.8800	23.50
11	LAVKAVPAG	33	1.8000	22.50
12	VLLAVLAAM	338	1.8000	22.50
13	IGIRAEIDK	856	1.8000	22.50
14	VGPVAVRAH	704	1.7800	22.25
15	LMHRAARGP	160	1.7000	21.25
16	MRYLRALAD	472	1.7000	21.25
17	MKLNAAAEM	497	1.7000	21.25
18	LTGLEIANA	137	1.6000	20.00
19	VVDADVFTQ	173	1.6000	20.00
20	MIPLGSCTM	489	1.6000	20.00
21	LVLITGYDA	539	1.6000	20.00
22	IRMMGAEGL	750	1.6000	20.00
23	VHAKHARQL	288	1.5000	18.75
24	VRRIDGAYG	917	1.5000	18.75

25	LATRAKPLG	186	1.4000	17.50
26	LRAKVGEHA	618	1.4000	17.50
27	LLNFQTLVT	127	1.3000	16.25
28	MHRAARGPV	161	1.3000	16.25
29	LQTREQHIR	317	1.3000	16.25
30	LQSWLVLIT	535	1.1000	13.75
31	VAVRAHLAP	707	1.1000	13.75
32	LRQLVADLQ	528	1.0000	12.50
33	LAGMRVVVV	597	1.0000	12.50
34	ICTAQVLLA	333	0.9000	11.25
35	LAVLAAMYA	340	0.9000	11.25
36	LMITYPSTH	632	0.8800	11.00
37	LDSLPPAAS	55	0.8000	10.00
38	VIAQLPGAS	214	0.8000	10.00
39	LTAIARRVH	356	0.7800	9.75
40	IVTADLRAG	197	0.7000	8.75
41	VVVVDCHDN	602	0.6000	7.50
42	VGLARPGKF	672	0.5000	6.25
43	YIRMMGAEG	749	0.5000	6.25
44	FRPKVWPAV	909	0.5000	6.25
45	LDAFGVAAA	434	0.4000	5.00
46	LNLHKTFCI	687	0.4000	5.00
47	LRGAPHTAQ	877	0.4000	5.00
48	LRNIIENPA	99	0.3000	3.75
49	YTPYQPEIS	112	0.3000	3.75
50	LLAVLAAMY	339	0.3000	3.75
51	FTQYRTETS	462	0.3000	3.75
52	ITGYDAVSL	542	0.3000	3.75
53	MMGAEGLRA	752	0.3000	3.75
54	YGDRNLVCS	924	0.3000	3.75
55	IGLDSQAVA	11	0.2000	2.50
56	MLAVIGVDS	21	0.2000	2.50
57	VVLDAFGVA	432	0.2000	2.50
58	LAAMYASYH	343	0.1800	2.25

59	ICLIPSSAH	580	-0.0200	0
60	VKAVPAGIL	35	-0.1000	0
61	ILPITWAYI	742	-0.1000	0
62	LLALTLIAP	248	-0.2000	0
63	LNAAAEMES	499	-0.2000	0
64	WLVLITGYD	538	-0.2000	0
65	VSLQPNAGS	548	-0.2000	0
66	MITYPSTHG	633	-0.2000	0
67	YGSASILPI	737	-0.2000	0
68	LVTDLTGLE	133	-0.3000	0
69	LVGVSVDSD	300	-0.3000	0
70	YASYHGAGG	347	-0.3000	0
71	ITWAYIRMM	745	-0.3000	0
72	LRAASLTAI	758	-0.3000	0
73	ITVDDVAKR	808	-0.3000	0
74	VSMIGQGYY	82	-0.4000	0
75	LGTAFRPKV	905	-0.4000	0
76	VCSCPPVEA	930	-0.4000	0
77	VIGVDSLDD	24	-0.5000	0
78	MLDEGTAAA	147	-0.5000	0
79	YLAVHAKHA	285	-0.5000	0
80	IHEYHASRG	566	-0.5000	0
81	LNALVGLAR	668	-0.5000	0
82	LAPFLPGHP	713	-0.5000	0
83	LALTLIAPP	249	-0.6000	0
84	LRALADKDI	475	-0.6000	0
85	VATMLAVIG	18	-0.7000	0
86	LRALADANT	71	-0.7000	0
87	YTAYTPYQP	109	-0.7000	0
88	LEIANASML	140	-0.7000	0
89	VAAAAPAHT	439	-0.7000	0
90	LDLRGITKL	797	-0.7000	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	MMRYLRALA	471	5.0000	58.14
2	VLARAKANG	398	4.9000	56.98
3	VLLRNIIEN	97	4.8000	55.81
4	MRYLRALAD	472	4.4000	51.16
5	LRGITKLTG	799	4.0000	46.51
6	LPGRLVGVS	296	3.4000	39.53
7	VLARVPGRA	387	3.3000	38.37
8	LAVKAVPAG	33	3.1000	36.05
9	MRVVVVDCH	600	3.1000	36.05
10	VGPVAVRAH	704	3.0000	34.88
11	VLLAVLAAM	338	2.9000	33.72
12	IARRVHAHA	359	2.9000	33.72
13	MKLNAAAEM	497	2.8000	32.56
14	VRRIDGAYG	917	2.8000	32.56
15	LVTDLTGLE	133	2.7000	31.40
16	LATRAKPLG	186	2.7000	31.40
17	LADKDIALD	478	2.7000	31.40
18	MIPLGSCTM	489	2.7000	31.40
19	VVVVDCHDN	602	2.6000	30.23
20	IRMMGAEGL	750	2.6000	30.23
21	VHAKHARQL	288	2.5000	29.07
22	WLVLITGYD	538	2.5000	29.07
23	MTLMHRAAR	158	2.4000	27.91
24	VVDADVFTQ	173	2.4000	27.91
25	LVGVSVDSD	300	2.4000	27.91
26	VIGVDSLDD	24	2.2000	25.58
27	LLNFQTLVT	127	2.2000	25.58
28	LMHRAARGP	160	2.1000	24.42
29	LMITYPSTH	632	2.1000	24.42
30	IVTADLRAG	197	2.0000	23.26
31	LTAIARRVH	356	2.0000	23.26

32	LQSWLVLIT	535	2.0000	23.26
33	VKRVVVDAD	169	1.9000	22.09
34	LTLIAPPGE	251	1.9000	22.09
35	LRQLVADLQ	528	1.8000	20.93
36	LVGLARPGK	671	1.8000	20.93
37	YIRMMGAEG	749	1.8000	20.93
38	LVCSCPPVE	929	1.7000	19.77
39	LTGLEIANA	137	1.6000	18.60
40	MHRAARGPV	161	1.6000	18.60
41	INLWRVDAD	407	1.6000	18.60
42	LVLITGYDA	539	1.6000	18.60
43	VWPAVRRID	913	1.6000	18.60
44	VAVRAHLAP	707	1.5000	17.44
45	LLAVLAAMY	339	1.4000	16.28
46	LAAMYASYH	343	1.4000	16.28
47	LRAKVGEHA	618	1.4000	16.28
48	VGLARPGKF	672	1.4000	16.28
49	LQTREQHIR	317	1.3000	15.12
50	ITGYDAVSL	542	1.3000	15.12
51	LAGMRVVVV	597	1.3000	15.12
52	MVAHECILD	790	1.3000	15.12
53	FADRHIGLD	6	1.2000	13.95
54	ICLIPSSAH	580	1.2000	13.95
55	LRGAPHTAQ	877	1.2000	13.95
56	MITYPSTHG	633	1.1000	12.79
57	IGIRAEIDK	856	1.1000	12.79
58	YASYHGAGG	347	1.0000	11.63
59	VKAVPAGIL	35	0.9000	10.47
60	ICTAQVLLA	333	0.9000	10.47
61	LAVLAAMYA	340	0.9000	10.47
62	LDSLPPAAS	55	0.8000	9.30
63	WYTAYTPYQ	108	0.8000	9.30
64	LGIEIVTAD	193	0.8000	9.30
65	VIAQLPGAS	214	0.8000	9.30

66	YRLALQTRE	313	0.8000	9.30
67	IHEYHASRG	566	0.8000	9.30
68	ITWAYIRMM	745	0.8000	9.30
69	FRPKVWPAV	909	0.8000	9.30
70	VSMIGQGYY	82	0.7000	8.14
71	LNFQTLVTD	128	0.7000	8.14
72	LARVPGRAD	388	0.7000	8.14
73	VATMLAVIG	18	0.6000	6.98
74	IANASMLDE	142	0.6000	6.98
75	LRAGLPDGE	202	0.6000	6.98
76	LNLHKTFCI	687	0.6000	6.98
77	YPVLYTGEN	780	0.6000	6.98
78	LDAFGVAAA	434	0.4000	4.65
79	YAGLLAIHE	560	0.4000	4.65
80	IAEICAAVH	647	0.4000	4.65
81	LARPGKFGG	674	0.4000	4.65
82	LRNIIENPA	99	0.3000	3.49
83	YTPYQPEIS	112	0.3000	3.49
84	LEIANASML	140	0.3000	3.49
85	IAQLPGASG	215	0.3000	3.49
86	FTQYRTETS	462	0.3000	3.49
87	LHKTFCIPH	689	0.3000	3.49
88	MMGAEGLRA	752	0.3000	3.49
89	LTAITSANY	763	0.3000	3.49
90	YIARRLDEY	771	0.3000	3.49
91	LDLRGITKL	797	0.3000	3.49
92	LMVEPTESE	835	0.3000	3.49
93	YGDRNLVCS	924	0.3000	3.49
94	IGLDSQAVA	11	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	MMRYLRALA	471	4.0000	45.98
2	YTPYQPEIS	112	3.0000	34.48
3	FTQYRTETS	462	3.0000	34.48
4	VLLRNIIEN	97	2.6800	30.80
5	VLARAKANG	398	2.6000	29.89
6	IRMMGAEGL	750	2.3000	26.44
7	LRGITKLTG	799	2.3000	26.44
8	YGDRNLVCS	924	2.3000	26.44
9	LRGAPHTAQ	877	2.2000	25.29
10	LRAKVGEHA	618	2.1000	24.14
11	MRVVVVDCH	600	2.0800	23.91
12	IARRVHAHA	359	1.9000	21.84
13	YGFHAPTMS	820	1.9000	21.84
14	LPGRLVGVS	296	1.7000	19.54
15	LVGLARPGK	671	1.7000	19.54
16	FRPKVWPAV	909	1.7000	19.54
17	LMITYPSTH	632	1.6800	19.31
18	IGIRAEIDK	856	1.6800	19.31
19	YRLALQTRE	313	1.6000	18.39
20	VLARVPGRA	387	1.6000	18.39
21	MITYPSTHG	633	1.6000	18.39
22	LVLITGYDA	539	1.5000	17.24
23	YIRMMGAEG	749	1.5000	17.24
24	LRAASLTAI	758	1.5000	17.24
25	VVDADVFTQ	173	1.4500	16.67
26	MTLMHRAAR	158	1.4000	16.09
27	YGSASILPI	737	1.4000	16.09
28	YIARRLDEY	771	1.4000	16.09
29	LRNIIENPA	99	1.3000	14.94
30	MRYLRALAD	472	1.3000	14.94
31	WYTAYTPYQ	108	1.2000	13.79
32	YTAYTPYQP	109	1.2000	13.79
33	LRQLVADLQ	528	1.2000	13.79
34	LDLRGITKL	797	1.1000	12.64

35	LAVKAVPAG	33	1.0000	11.49
36	FGVAAAAPA	437	1.0000	11.49
37	LAGMRVVVV	597	1.0000	11.49
38	LAAMYASYH	343	0.9800	11.26
39	LLNFQTLVT	127	0.9000	10.34
40	LAVLAAMYA	340	0.9000	10.34
41	WAYIRMMGA	747	0.9000	10.34
42	LQTREQHIR	317	0.8000	9.20
43	VLLAVLAAM	338	0.8000	9.20
44	YRTETSMMR	465	0.8000	9.20
45	ICLIPSSAH	580	0.7800	8.97
46	YASYHGAGG	347	0.7000	8.05
47	MKLNAAAEM	497	0.7000	8.05
48	LQSWLVLIT	535	0.7000	8.05
49	VAVRAHLAP	707	0.7000	8.05
50	LTGLEIANA	137	0.6000	6.90
51	LATRAKPLG	186	0.6000	6.90
52	YHGAGGLTA	350	0.6000	6.90
53	MIPLGSCTM	489	0.6000	6.90
54	ICTAQVLLA	333	0.5000	5.75
55	VRRIDGAYG	917	0.5000	5.75
56	VGPVAVRAH	704	0.4800	5.52
57	FLTHPAFTQ	456	0.4500	5.17
58	LMHRAARGP	160	0.4000	4.60
59	FPVAGTLMV	829	0.4000	4.60
60	FQTLVTDLT	130	0.3000	3.45
61	FGVIAQLPG	212	0.3000	3.45
62	ITGYDAVSL	542	0.3000	3.45
63	IHEYHASRG	566	0.3000	3.45
64	LNLHKTFCI	687	0.2500	2.87
65	MLAVIGVDS	21	0.2000	2.30
66	VHAKHARQL	288	0.2000	2.30
67	LEIANASML	140	0.1000	1.15
68	LARAKANGI	399	0.1000	1.15

69	WLVLITGYD	538	0.1000	1.15
70	VVVVDCHDN	602	0.1000	1.15
71	WSALVQQAH	228	-0.0200	0
72	LGIEIVTAD	193	-0.1000	0
73	LVGVSVDSD	300	-0.1000	0
74	IRRDKATSN	324	-0.1000	0
75	MMGAEGLRA	752	-0.1000	0
76	WPAVRRIDG	914	-0.1200	0
77	LDSLPPAAS	55	-0.2000	0
78	FFGVIAQLP	211	-0.2000	0
79	LNAAAEMES	499	-0.2000	0
80	FGTTQRFGV	266	-0.2500	0
81	LLALTLIAP	248	-0.3200	0
82	MHRAARGPV	161	-0.4000	0
83	WRVDADHVS	410	-0.4000	0
84	VCSCPPVEA	930	-0.4000	0
85	IATRTSEFL	449	-0.5000	0
86	YVDGANLNA	662	-0.5000	0
87	LTAIARRVH	356	-0.5200	0
88	FLPGHPFAP	716	-0.5500	0
89	LLRNIIENP	98	-0.6000	0
90	VKRVVVDAD	169	-0.6000	0
91	IVTADLRAG	197	-0.6000	0
92	LDAFGVAAA	434	-0.6000	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	VLLRNIIEN	97	5.4000	53.47
2	MRYLRALAD	472	5.2000	51.49
3	LRGITKLTG	799	4.8000	47.52
4	MMRYLRALA	471	4.0000	39.60
5	VLARAKANG	398	3.9000	38.61

6	WLVLITGYD	538	3.6000	35.64
7	LAVKAVPAG	33	3.2500	32.18
8	VIGVDSLDD	24	3.0000	29.70
9	LLNFQTLVT	127	3.0000	29.70
10	YAGLLAIHE	560	3.0000	29.70
11	WYTAYTPYQ	108	2.9500	29.21
12	FRPKVWPAV	909	2.9500	29.21
13	YRLALQTRE	313	2.9000	28.71
14	LATRAKPLG	186	2.8500	28.22
15	FGVIAQLPG	212	2.8000	27.72
16	LQSWLVLIT	535	2.8000	27.72
17	YGSASILPI	737	2.8000	27.72
18	YIRMMGAEG	749	2.8000	27.72
19	IRMMGAEGL	750	2.7000	26.73
20	LPGRLVGVS	296	2.5000	24.75
21	YTPYQPEIS	112	2.4000	23.76
22	VLARVPGRA	387	2.4000	23.76
23	FTQYRTETS	462	2.4000	23.76
24	FADRHIGLD	6	2.3000	22.77
25	VVVVDCHDN	602	2.3000	22.77
26	VAVRAHLAP	707	2.3000	22.77
27	VGPVAVRAH	704	2.2000	21.78
28	LTLIAPPGE	251	2.0500	20.30
29	YASYHGAGG	347	2.0000	19.80
30	LVGLARPGK	671	1.9500	19.31
31	VVDADVFTQ	173	1.9000	18.81
32	VLLAVLAAM	338	1.9000	18.81
33	IARRVHAHA	359	1.9000	18.81
34	MVAHECILD	790	1.9000	18.81
35	FPVAGTLMV	829	1.9000	18.81
36	WPAVRRIDG	914	1.9000	18.81
37	LVCSCPPVE	929	1.8500	18.32
38	LVTDLTGLE	133	1.8000	17.82
39	YHGAGGLTA	350	1.8000	17.82

40	MKLNAAAEM	497	1.8000	17.82
41	MRVVVVDCH	600	1.8000	17.82
42	VRRIDGAYG	917	1.8000	17.82
43	YGDRNLVCS	924	1.8000	17.82
44	VHAKHARQL	288	1.7000	16.83
45	ICTAQVLLA	333	1.7000	16.83
46	LADKDIALD	478	1.7000	16.83
47	MIPLGSCTM	489	1.7000	16.83
48	YPVLYTGEN	780	1.7000	16.83
49	IGIRAEIDK	856	1.7000	16.83
50	LAVLAAMYA	340	1.5000	14.85
51	LRAKVGEHA	618	1.5000	14.85
52	WAYIRMMGA	747	1.5000	14.85
53	YTAYTPYQP	109	1.4000	13.86
54	IANASMLDE	142	1.4000	13.86
55	MTLMHRAAR	158	1.4000	13.86
56	YRTETSMMR	465	1.4000	13.86
57	LMHRAARGP	160	1.3000	12.87
58	LVLITGYDA	539	1.3000	12.87
59	LRGAPHTAQ	877	1.3000	12.87
60	IVTADLRAG	197	1.2000	11.88
61	LTAIARRVH	356	1.2000	11.88
62	MITYPSTHG	633	1.2000	11.88
63	YLAVHAKHA	285	1.1000	10.89
64	LVGVSVDSD	300	1.1000	10.89
65	LMITYPSTH	632	1.1000	10.89
66	MMGAEGLRA	752	1.1000	10.89
67	LAELRALAD	68	1.0000	9.90
68	LQTREQHIR	317	1.0000	9.90
69	FGVAAAAPA	437	1.0000	9.90
70	YIARRLDEY	771	1.0000	9.90
71	LGIEIVTAD	193	0.9000	8.91
72	FLTHPAFTQ	456	0.9000	8.91
73	LHKTFCIPH	689	0.9000	8.91

74	LLALTLIAP	248	0.8000	7.92
75	ITGYDAVSL	542	0.8000	7.92
76	LAGMRVVVV	597	0.8000	7.92
77	VWPAVRRID	913	0.8000	7.92
78	MHRAARGPV	161	0.7000	6.93
79	YVDGANLNA	662	0.7000	6.93
80	LTGLEIANA	137	0.6000	5.94
81	VKRVVVDAD	169	0.6000	5.94
82	ITDWSALVQ	225	0.5000	4.95
83	LRQLVADLQ	528	0.5000	4.95
84	VGLARPGKF	672	0.5000	4.95
85	LLAVLAAMY	339	0.4000	3.96
86	LAAMYASYH	343	0.4000	3.96
87	LNAAAEMES	499	0.4000	3.96
88	VAHECILDL	791	0.4000	3.96
89	LDLRGITKL	797	0.4000	3.96
90	LMVEPTESE	835	0.4000	3.96
91	WSALVQQAH	228	0.3000	2.97
92	INLWRVDAD	407	0.3000	2.97
93	LNALVGLAR	668	0.3000	2.97
94	MIGIRAEID	855	0.3000	2.97

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	LRGITKLTG	799	4.1000	49.40
2	LVGLARPGK	671	3.0500	36.75
3	MRYLRALAD	472	2.9000	34.94
4	YGSASILPI	737	2.6000	31.33
5	WYTAYTPYQ	108	2.1500	25.90
6	FGVIAQLPG	212	2.1000	25.30
7	WAYIRMMGA	747	2.1000	25.30
8	LLNFQTLVT	127	2.0000	24.10

9	LAVLAAMYA	340	1.9000	22.89
10	LVLITGYDA	539	1.9000	22.89
11	YHGAGGLTA	350	1.8000	21.69
12	LQSWLVLIT	535	1.8000	21.69
13	ICTAQVLLA	333	1.7000	20.48
14	FPVAGTLMV	829	1.6000	19.28
15	WLVLITGYD	538	1.3000	15.66
16	IRMMGAEGL	750	1.3000	15.66
17	YLAVHAKHA	285	1.2000	14.46
18	VVDADVFTQ	173	1.1000	13.25
19	MMRYLRALA	471	1.1000	13.25
20	YIRMMGAEG	749	1.1000	13.25
21	MMGAEGLRA	752	1.1000	13.25
22	VRRIDGAYG	917	1.1000	13.25
23	VGPVAVRAH	704	1.0800	13.01
24	LTGLEIANA	137	1.0000	12.05
25	MTLMHRAAR	158	1.0000	12.05
26	FGVAAAAPA	437	1.0000	12.05
27	MIPLGSCTM	489	1.0000	12.05
28	LLALTLIAP	248	0.8000	9.64
29	VLLAVLAAM	338	0.8000	9.64
30	YRTETSMMR	465	0.7000	8.43
31	MKLNAAAEM	497	0.7000	8.43
32	LNALVGLAR	668	0.7000	8.43
33	WPAVRRIDG	914	0.7000	8.43
34	MRVVVVDCH	600	0.6800	8.19
35	YGFHAPTMS	820	0.6000	7.23
36	LTAIARRVH	356	0.5800	6.99
37	VIAQLPGAS	214	0.5000	6.02
38	FLTHPAFTQ	456	0.5000	6.02
39	LRGAPHTAQ	877	0.5000	6.02
40	VIGVDSLDD	24	0.4000	4.82
41	VLLRNIIEN	97	0.4000	4.82
42	MHRAARGPV	161	0.4000	4.82

43	LNAAAEMES	499	0.4000	4.82
44	YAGLLAIHE	560	0.4000	4.82
45	VVVVDCHDN	602	0.4000	4.82
46	LNLHKTFCI	687	0.3000	3.61
47	LMITYPSTH	632	0.2800	3.37
48	LDSLPPAAS	55	0.2000	2.41
49	LRNIIENPA	99	0.2000	2.41
50	LRQLVADLQ	528	0.1000	1.20
51	LAGMRVVVV	597	0.1000	1.20
52	YPVLYTGEN	780	0.1000	1.20
53	LHKTFCIPH	689	0.0800	0.96
54	IVTADLRAG	197	-0.1000	0
55	YRLALQTRE	313	-0.1000	0
56	FRPKVWPAV	909	-0.1500	0
57	MLAVIGVDS	21	-0.2000	0
58	FGTTQRFGV	266	-0.2000	0
59	LRAASLTAI	758	-0.2000	0
60	LGTAFRPKV	905	-0.2500	0
61	LTLIAPPGE	251	-0.3500	0
62	ITDWSALVQ	225	-0.4000	0
63	VLARAKANG	398	-0.4000	0
64	FGRQHPFAP	513	-0.4000	0
65	VGLARPGKF	672	-0.4000	0
66	MVAHECILD	790	-0.4000	0
67	ILDLRGITK	796	-0.4000	0
68	ICLIPSSAH	580	-0.4200	0
69	VRAHLAPFL	709	-0.4500	0
70	YTPYQPEIS	112	-0.5000	0
71	LPGRLVGVS	296	-0.5000	0
72	FTQYRTETS	462	-0.5000	0
73	ILPITWAYI	742	-0.5000	0
74	ITKLTGITV	802	-0.5000	0
75	WSALVQQAH	228	-0.5200	0
76	LLAVLAAMY	339	-0.6000	0

77	VLARVPGRA	387	-0.6000	0
78	LRALADKDI	475	-0.6000	0
79	VSLQPNAGS	548	-0.6000	0
80	IGIRAEIDK	856	-0.6000	0
81	LALQTREQH	315	-0.6200	0
82	VSMIGQGYY	82	-0.7000	0
83	VTDLTGLEI	134	-0.7000	0
84	LDAFGVAAA	434	-0.7000	0
85	FQTLVTDLT	130	-0.8000	0
86	LAVKAVPAG	33	-0.8500	0
87	LVCSCPPVE	929	-0.8500	0
88	VKAVPAGIL	35	-0.9000	0
89	WRVDADHVS	410	-0.9000	0
90	LLAIHEYHA	563	-0.9000	0
91	YTGENGMVA	784	-0.9000	0
92	VCSCPPVEA	930	-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	LNLHKTFCI	687	4.4000	52.38
2	MMRYLRALA	471	3.2000	38.10
3	VVDADVFTQ	173	3.1000	36.90
4	LVGLARPGK	671	2.9000	34.52
5	LAVHAKHAR	286	2.6000	30.95
6	FLTHPAFTQ	456	2.6000	30.95
7	LAIHEYHAS	564	2.6000	30.95
8	IVTADLRAG	197	2.5000	29.76
9	LQSWLVLIT	535	2.5000	29.76
10	LRGITKLTG	799	2.5000	29.76
11	IRMMGAEGL	750	2.4000	28.57
12	VGPVAVRAH	704	2.3800	28.33
13	LLNFQTLVT	127	2.3000	27.38

14	VRAHLAPFL	709	2.2000	26.19
15	MRYLRALAD	472	2.1000	25.00
16	YGFHAPTMS	820	2.1000	25.00
17	LRGAPHTAQ	877	1.9000	22.62
18	MTLMHRAAR	158	1.8000	21.43
19	VHAKHARQL	288	1.8000	21.43
20	VLLAVLAAM	338	1.8000	21.43
21	MKLNAAAEM	497	1.8000	21.43
22	LALQTREQH	315	1.6800	20.00
23	LTAIARRVH	356	1.6800	20.00
24	ICTAQVLLA	333	1.6000	19.05
25	LRQLVADLQ	528	1.6000	19.05
26	LVLITGYDA	539	1.6000	19.05
27	VYEHDIAEI	642	1.6000	19.05
28	MRVVVVDCH	600	1.5800	18.81
29	VLARAKANG	398	1.5000	17.86
30	ITWAYIRMM	745	1.5000	17.86
31	LMHRAARGP	160	1.4000	16.67
32	VIAQLPGAS	214	1.4000	16.67
33	VSLQPNAGS	548	1.4000	16.67
34	LAGMRVVVV	597	1.4000	16.67
35	MVAHECILD	790	1.4000	16.67
36	LTGLEIANA	137	1.3000	15.48
37	MIPLGSCTM	489	1.3000	15.48
38	LRAKVGEHA	618	1.3000	15.48
39	VGEHAERLS	622	1.3000	15.48
40	LRAASLTAI	758	1.2000	14.29
41	LMITYPSTH	632	1.1800	14.05
42	LAVKAVPAG	33	1.0000	11.90
43	VLLRNIIEN	97	1.0000	11.90
44	MMGAEGLRA	752	1.0000	11.90
45	LAVLAAMYA	340	0.9000	10.71
46	VHAHAEAIA	363	0.9000	10.71
47	LRNIIENPA	99	0.8000	9.52

48	IARRVHAHA	359	0.8000	9.52
49	MGAEGLRAA	753	0.8000	9.52
50	WYTAYTPYQ	108	0.7000	8.33
51	LDAFGVAAA	434	0.7000	8.33
52	VWPAVRRID	913	0.7000	8.33
53	LNFQTLVTD	128	0.6000	7.14
54	FGRQHPFAP	513	0.6000	7.14
55	VVVVDCHDN	602	0.6000	7.14
56	VRRIDGAYG	917	0.6000	7.14
57	VCSCPPVEA	930	0.6000	7.14
58	LDSLPPAAS	55	0.5000	5.95
59	LARAKANGI	399	0.5000	5.95
60	INLWRVDAD	407	0.5000	5.95
61	YGSASILPI	737	0.5000	5.95
62	VFTQTAAVL	178	0.4000	4.76
63	LQTREQHIR	317	0.4000	4.76
64	LGDALVHDK	374	0.4000	4.76
65	LDSQAVATM	13	0.3000	3.57
66	MHRAARGPV	161	0.3000	3.57
67	ITDWSALVQ	225	0.3000	3.57
68	LPGRLVGVS	296	0.3000	3.57
69	LGTAFRPKV	905	0.3000	3.57
70	LLRNIIENP	98	0.2000	2.38
71	VLARVPGRA	387	0.2000	2.38
72	LVQQAHDRG	231	0.1000	1.19
73	LNAAAEMES	499	0.1000	1.19
74	LARPGKFGG	674	0.1000	1.19
75	LAAMYASYH	343	-0.0200	0
76	YTPYQPEIS	112	-0.1000	0
77	FTQYRTETS	462	-0.1000	0
78	LRALADKDI	475	-0.1000	0
79	LIPSSAHGT	582	-0.1000	0
80	LNALVGLAR	668	-0.1000	0
81	YIRMMGAEG	749	-0.1000	0

82	IGLDSQAVA	11	-0.2000	0
83	LLALTLIAP	248	-0.2000	0
84	LVCSCPPVE	929	-0.2000	0
85	VATMLAVIG	18	-0.3000	0
86	LEIANASML	140	-0.3000	0
87	YHGAGGLTA	350	-0.3000	0
88	ITYPSTHGV	634	-0.3000	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	LRGITKLTG	799	5.1000	61.45
2	LVGLARPGK	671	4.0500	48.80
3	MRYLRALAD	472	3.9000	46.99
4	LLNFQTLVT	127	3.0000	36.14
5	LAVLAAMYA	340	2.9000	34.94
6	LVLITGYDA	539	2.9000	34.94
7	LQSWLVLIT	535	2.8000	33.73
8	ICTAQVLLA	333	2.7000	32.53
9	IRMMGAEGL	750	2.3000	27.71
10	VVDADVFTQ	173	2.1000	25.30
11	MMRYLRALA	471	2.1000	25.30
12	MMGAEGLRA	752	2.1000	25.30
13	VRRIDGAYG	917	2.1000	25.30
14	VGPVAVRAH	704	2.0800	25.06
15	LTGLEIANA	137	2.0000	24.10
16	MTLMHRAAR	158	2.0000	24.10
17	MIPLGSCTM	489	2.0000	24.10
18	LLALTLIAP	248	1.8000	21.69
19	VLLAVLAAM	338	1.8000	21.69
20	MKLNAAAEM	497	1.7000	20.48
21	LNALVGLAR	668	1.7000	20.48
22	MRVVVVDCH	600	1.6800	20.24

23	YGSASILPI	737	1.6000	19.28
24	LTAIARRVH	356	1.5800	19.04
25	VIAQLPGAS	214	1.5000	18.07
26	LRGAPHTAQ	877	1.5000	18.07
27	VIGVDSLDD	24	1.4000	16.87
28	VLLRNIIEN	97	1.4000	16.87
29	MHRAARGPV	161	1.4000	16.87
30	LNAAAEMES	499	1.4000	16.87
31	VVVVDCHDN	602	1.4000	16.87
32	LNLHKTFCI	687	1.3000	15.66
33	LMITYPSTH	632	1.2800	15.42
34	LDSLPPAAS	55	1.2000	14.46
35	LRNIIENPA	99	1.2000	14.46
36	WYTAYTPYQ	108	1.1500	13.86
37	FGVIAQLPG	212	1.1000	13.25
38	LRQLVADLQ	528	1.1000	13.25
39	LAGMRVVVV	597	1.1000	13.25
40	WAYIRMMGA	747	1.1000	13.25
41	LHKTFCIPH	689	1.0800	13.01
42	IVTADLRAG	197	0.9000	10.84
43	MLAVIGVDS	21	0.8000	9.64
44	YHGAGGLTA	350	0.8000	9.64
45	LRAASLTAI	758	0.8000	9.64
46	LGTAFRPKV	905	0.7500	9.04
47	LTLIAPPGE	251	0.6500	7.83
48	ITDWSALVQ	225	0.6000	7.23
49	VLARAKANG	398	0.6000	7.23
50	VGLARPGKF	672	0.6000	7.23
51	MVAHECILD	790	0.6000	7.23
52	ILDLRGITK	796	0.6000	7.23
53	FPVAGTLMV	829	0.6000	7.23
54	ICLIPSSAH	580	0.5800	6.99
55	VRAHLAPFL	709	0.5500	6.63
56	LPGRLVGVS	296	0.5000	6.02

57	ILPITWAYI	742	0.5000	6.02
58	ITKLTGITV	802	0.5000	6.02
59	LLAVLAAMY	339	0.4000	4.82
60	VLARVPGRA	387	0.4000	4.82
61	LRALADKDI	475	0.4000	4.82
62	VSLQPNAGS	548	0.4000	4.82
63	IGIRAEIDK	856	0.4000	4.82
64	LALQTREQH	315	0.3800	4.58
65	VSMIGQGYY	82	0.3000	3.61
66	VTDLTGLEI	134	0.3000	3.61
67	LDAFGVAAA	434	0.3000	3.61
68	WLVLITGYD	538	0.3000	3.61
69	YLAVHAKHA	285	0.2000	2.41
70	LAVKAVPAG	33	0.1500	1.81
71	LVCSCPPVE	929	0.1500	1.81
72	VKAVPAGIL	35	0.1000	1.20
73	LLAIHEYHA	563	0.1000	1.20
74	YIRMMGAEG	749	0.1000	1.20
75	VCSCPPVEA	930	0.1000	1.20
76	IARRVHAHA	359	-0.1000	0
77	LGDALVHDK	374	-0.1000	0
78	VAVRAHLAP	707	-0.1000	0
79	ITWAYIRMM	745	-0.1000	0
80	LLRNIIENP	98	-0.2000	0
81	LALTLIAPP	249	-0.2000	0
82	VSHLNLHKT	684	-0.2000	0
83	LTAITSANY	763	-0.2000	0
84	LAAMYASYH	343	-0.2200	0
85	IAEICAAVH	647	-0.2200	0
86	LAELRALAD	68	-0.3000	0
87	LRALADANT	71	-0.3000	0
88	YRTETSMMR	465	-0.3000	0
89	LRAKVGEHA	618	-0.3000	0
90	VAHECILDL	791	-0.3000	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	LRGITKLTG	799	5.1000	61.45
2	LVGLARPGK	671	4.0500	48.80
3	MRYLRALAD	472	3.9000	46.99
4	LLNFQTLVT	127	3.0000	36.14
5	LAVLAAMYA	340	2.9000	34.94
6	LVLITGYDA	539	2.9000	34.94
7	LQSWLVLIT	535	2.8000	33.73
8	ICTAQVLLA	333	2.7000	32.53
9	IRMMGAEGL	750	2.3000	27.71
10	VVDADVFTQ	173	2.1000	25.30
11	MMRYLRALA	471	2.1000	25.30
12	MMGAEGLRA	752	2.1000	25.30
13	VRRIDGAYG	917	2.1000	25.30
14	VGPVAVRAH	704	2.0800	25.06
15	LTGLEIANA	137	2.0000	24.10
16	MTLMHRAAR	158	2.0000	24.10
17	MIPLGSCTM	489	2.0000	24.10
18	LLALTLIAP	248	1.8000	21.69
19	VLLAVLAAM	338	1.8000	21.69
20	MKLNAAAEM	497	1.7000	20.48
21	LNALVGLAR	668	1.7000	20.48
22	MRVVVVDCH	600	1.6800	20.24
23	YGSASILPI	737	1.6000	19.28
24	LTAIARRVH	356	1.5800	19.04
25	VIAQLPGAS	214	1.5000	18.07
26	LRGAPHTAQ	877	1.5000	18.07
27	VIGVDSLDD	24	1.4000	16.87
28	VLLRNIIEN	97	1.4000	16.87
29	MHRAARGPV	161	1.4000	16.87
30	LNAAAEMES	499	1.4000	16.87

31	VVVVDCHDN	602	1.4000	16.87
32	LNLHKTFCI	687	1.3000	15.66
33	LMITYPSTH	632	1.2800	15.42
34	LDSLPPAAS	55	1.2000	14.46
35	LRNIIENPA	99	1.2000	14.46
36	WYTAYTPYQ	108	1.1500	13.86
37	FGVIAQLPG	212	1.1000	13.25
38	LRQLVADLQ	528	1.1000	13.25
39	LAGMRVVVV	597	1.1000	13.25
40	WAYIRMMGA	747	1.1000	13.25
41	LHKTFCIPH	689	1.0800	13.01
42	IVTADLRAG	197	0.9000	10.84
43	MLAVIGVDS	21	0.8000	9.64
44	YHGAGGLTA	350	0.8000	9.64
45	LRAASLTAI	758	0.8000	9.64
46	LGTAFRPKV	905	0.7500	9.04
47	LTLIAPPGE	251	0.6500	7.83
48	ITDWSALVQ	225	0.6000	7.23
49	VLARAKANG	398	0.6000	7.23
50	VGLARPGKF	672	0.6000	7.23
51	MVAHECILD	790	0.6000	7.23
52	ILDLRGITK	796	0.6000	7.23
53	FPVAGTLMV	829	0.6000	7.23
54	ICLIPSSAH	580	0.5800	6.99
55	VRAHLAPFL	709	0.5500	6.63
56	LPGRLVGVS	296	0.5000	6.02
57	ILPITWAYI	742	0.5000	6.02
58	ITKLTGITV	802	0.5000	6.02
59	LLAVLAAMY	339	0.4000	4.82
60	VLARVPGRA	387	0.4000	4.82
61	LRALADKDI	475	0.4000	4.82
62	VSLQPNAGS	548	0.4000	4.82
63	IGIRAEIDK	856	0.4000	4.82
64	LALQTREQH	315	0.3800	4.58

65	VSMIGQGYY	82	0.3000	3.61
66	VTDLTGLEI	134	0.3000	3.61
67	LDAFGVAAA	434	0.3000	3.61
68	WLVLITGYD	538	0.3000	3.61
69	YLAVHAKHA	285	0.2000	2.41
70	LAVKAVPAG	33	0.1500	1.81
71	LVCSCPPVE	929	0.1500	1.81
72	VKAVPAGIL	35	0.1000	1.20
73	LLAIHEYHA	563	0.1000	1.20
74	YIRMMGAEG	749	0.1000	1.20
75	VCSCPPVEA	930	0.1000	1.20
76	IARRVHAHA	359	-0.1000	0
77	LGDALVHDK	374	-0.1000	0
78	VAVRAHLAP	707	-0.1000	0
79	ITWAYIRMM	745	-0.1000	0
80	LLRNIIENP	98	-0.2000	0
81	LALTLIAPP	249	-0.2000	0
82	VSHLNLHKT	684	-0.2000	0
83	LTAITSANY	763	-0.2000	0
84	LAAMYASYH	343	-0.2200	0
85	IAEICAAVH	647	-0.2200	0
86	LAELRALAD	68	-0.3000	0
87	LRALADANT	71	-0.3000	0
88	YRTETSMMR	465	-0.3000	0
89	LRAKVGEHA	618	-0.3000	0
90	VAHECILDL	791	-0.3000	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	VVLDAFGVA	432	4.1000	45.05
2	IRRDKATSN	324	3.7000	40.66
3	LVGLARPGK	671	3.7000	40.66

4	LVTDLTGLE	133	3.6000	39.56
5	IGLDSQAVA	11	3.5000	38.46
6	LRGITKLTG	799	3.4000	37.36
7	MRVVVVDCH	600	3.3800	37.14
8	VVVDCHDNG	603	3.2000	35.16
9	LVADLQSWL	531	3.1700	34.84
10	VVDADVFTQ	173	3.0000	32.97
11	IALDRSMIP	483	3.0000	32.97
12	ITVDDVAKR	808	3.0000	32.97
13	LVLITGYDA	539	2.8500	31.32
14	LNLHKTFCI	687	2.8000	30.77
15	LRGAPHTAQ	877	2.7000	29.67
16	LVHDKYFDT	378	2.5000	27.47
17	VIAQLPGAS	214	2.4000	26.37
18	IRMMGAEGL	750	2.4000	26.37
19	VTADLRAGL	198	2.3000	25.27
20	LVCSCPPVE	929	2.3000	25.27
21	VDADHVSVA	412	2.2700	24.95
22	LMITYPSTH	632	2.2500	24.73
23	VYVDGANLN	661	2.2100	24.29
24	IGADVAFGT	260	2.1000	23.08
25	LRQLVADLQ	528	2.1000	23.08
26	LRAASLTAI	758	2.0000	21.98
27	IGVDSLDDL	25	1.9000	20.88
28	WYTAYTPYQ	108	1.9000	20.88
29	MHRAARGPV	161	1.9000	20.88
30	MKLNAAAEM	497	1.9000	20.88
31	VRAHLAPFL	709	1.9000	20.88
32	LALQTREQH	315	1.8800	20.66
33	VGADLLALT	244	1.8000	19.78
34	VLLAVLAAM	338	1.8000	19.78
35	MMRYLRALA	471	1.8000	19.78
36	LRNIIENPA	99	1.7100	18.79
37	VDSDGTPAY	305	1.7000	18.68

38	VRRIDGAYG	917	1.7000	18.68
39	LAVLAAMYA	340	1.6000	17.58
40	ICLIPSSAH	580	1.5500	17.03
41	VVVDADVFT	172	1.5000	16.48
42	WRVDADHVS	410	1.5000	16.48
43	MRYLRALAD	472	1.5000	16.48
44	LGTAFRPKV	905	1.5000	16.48
45	ICTAQVLLA	333	1.4000	15.38
46	YEHDIAEIC	643	1.4000	15.38
47	LPKGYPVSS	726	1.4000	15.38
48	YGFHAPTMS	820	1.4000	15.38
49	MLAVIGVDS	21	1.2000	13.19
50	LVGVSVDSD	300	1.2000	13.19
51	LNAAAEMES	499	1.2000	13.19
52	VGPVAVRAH	704	1.1800	12.97
53	LLRNIIENP	98	1.1000	12.09
54	VGLARPGKF	672	1.1000	12.09
55	VAVSMIGQG	80	1.0000	10.99
56	MTLMHRAAR	158	1.0000	10.99
57	LTLIAPPGE	251	1.0000	10.99
58	VAFGTTQRF	264	1.0000	10.99
59	FLTHPAFTQ	456	1.0000	10.99
60	VDLDDLRAK	613	1.0000	10.99
61	LTGLEIANA	137	0.9000	9.89
62	LRAGLPDGE	202	0.9000	9.89
63	MIPLGSCTM	489	0.9000	9.89
64	LAGMRVVVV	597	0.9000	9.89
65	VCSCPPVEA	930	0.9000	9.89
66	VPMGFGGPH	274	0.8800	9.67
67	VSLQPNAGS	548	0.8000	8.79
68	MMGAEGLRA	752	0.8000	8.79
69	MVAHECILD	790	0.8000	8.79
70	VLLRNIIEN	97	0.7000	7.69
71	VKRVVVDAD	169	0.7000	7.69

72	LPGRLVGVS	296	0.7000	7.69
73	LTAIARRVH	356	0.6800	7.47
74	LEIANASML	140	0.6700	7.36
75	LAVIGVDSL	22	0.6000	6.59
76	MYASYHGAG	346	0.6000	6.59
77	VLARVPGRA	387	0.6000	6.59
78	IPLGSCTMK	490	0.6000	6.59
79	LQSWLVLIT	535	0.6000	6.59
80	LTGITVDDV	805	0.6000	6.59
81	LVAVGADLL	241	0.5000	5.49
82	MGFGGPHAG	276	0.5000	5.49
83	VACDEATTD	419	0.5000	5.49
84	LDRSMIPLG	485	0.5000	5.49
85	LARPGKFGG	674	0.5000	5.49
86	FLPGHPFAP	716	0.5000	5.49
87	WAYIRMMGA	747	0.5000	5.49
88	LAVKAVPAG	33	0.4000	4.40
89	VSMIGQGYY	82	0.4000	4.40
90	LGIEIVTAD	193	0.4000	4.40
91	IVTADLRAG	197	0.4000	4.40
92	LVQQAHDRG	231	0.4000	4.40
93	VVVVDCHDN	602	0.4000	4.40
94	WPVDDNPLR	870	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	FLTHPAFTQ	456	3.6000	42.86
2	LNLHKTFCI	687	3.4000	40.48
3	YGFHAPTMS	820	3.1000	36.90
4	MMRYLRALA	471	2.2000	26.19
5	VVDADVFTQ	173	2.1000	25.00
6	LVGLARPGK	671	1.9000	22.62

7	WYTAYTPYQ	108	1.7000	20.24
8	LAVHAKHAR	286	1.6000	19.05
9	FGRQHPFAP	513	1.6000	19.05
10	LAIHEYHAS	564	1.6000	19.05
11	IVTADLRAG	197	1.5000	17.86
12	LQSWLVLIT	535	1.5000	17.86
13	YGSASILPI	737	1.5000	17.86
14	LRGITKLTG	799	1.5000	17.86
15	IRMMGAEGL	750	1.4000	16.67
16	VGPVAVRAH	704	1.3800	16.43
17	LLNFQTLVT	127	1.3000	15.48
18	VRAHLAPFL	709	1.2000	14.29
19	MRYLRALAD	472	1.1000	13.10
20	FGVAAAAPA	437	1.0000	11.90
21	YTPYQPEIS	112	0.9000	10.71
22	FTQYRTETS	462	0.9000	10.71
23	YIRMMGAEG	749	0.9000	10.71
24	LRGAPHTAQ	877	0.9000	10.71
25	MTLMHRAAR	158	0.8000	9.52
26	VHAKHARQL	288	0.8000	9.52
27	VLLAVLAAM	338	0.8000	9.52
28	MKLNAAAEM	497	0.8000	9.52
29	YHGAGGLTA	350	0.7000	8.33
30	FRPKVWPAV	909	0.7000	8.33
31	LALQTREQH	315	0.6800	8.10
32	LTAIARRVH	356	0.6800	8.10
33	ICTAQVLLA	333	0.6000	7.14
34	LRQLVADLQ	528	0.6000	7.14
35	LVLITGYDA	539	0.6000	7.14
36	VYEHDIAEI	642	0.6000	7.14
37	MRVVVVDCH	600	0.5800	6.90
38	VLARAKANG	398	0.5000	5.95
39	ITWAYIRMM	745	0.5000	5.95
40	FPVAGTLMV	829	0.5000	5.95

41	LMHRAARGP	160	0.4000	4.76
42	VIAQLPGAS	214	0.4000	4.76
43	VSLQPNAGS	548	0.4000	4.76
44	LAGMRVVVV	597	0.4000	4.76
45	MVAHECILD	790	0.4000	4.76
46	LTGLEIANA	137	0.3000	3.57
47	FGTTQRFGV	266	0.3000	3.57
48	YRLALQTRE	313	0.3000	3.57
49	MIPLGSCTM	489	0.3000	3.57
50	LRAKVGEHA	618	0.3000	3.57
51	VGEHAERLS	622	0.3000	3.57
52	LRAASLTAI	758	0.2000	2.38
53	YGDRNLVCS	924	0.2000	2.38
54	LMITYPSTH	632	0.1800	2.14
55	YLAVHAKHA	285	0.1000	1.19
56	LAVLAAMYA	340	-0.1000	0
57	VHAHAEAIA	363	-0.1000	0
58	WRVDADHVS	410	-0.1000	0
59	WDHPYTREQ	892	-0.1000	0
60	LRNIIENPA	99	-0.2000	0
61	IARRVHAHA	359	-0.2000	0
62	MGAEGLRAA	753	-0.2000	0
63	FQTLVTDLT	130	-0.3000	0
64	LDAFGVAAA	434	-0.3000	0
65	VWPAVRRID	913	-0.3000	0
66	LNFQTLVTD	128	-0.4000	0
67	VVVVDCHDN	602	-0.4000	0
68	FLPGHPFAP	716	-0.4000	0
69	VRRIDGAYG	917	-0.4000	0
70	VCSCPPVEA	930	-0.4000	0
71	LDSLPPAAS	55	-0.5000	0
72	FGVIAQLPG	212	-0.5000	0
73	LARAKANGI	399	-0.5000	0
74	INLWRVDAD	407	-0.5000	0

75	WLVLITGYD	538	-0.5000	0
76	WSALVQQAH	228	-0.5200	0
77	YTAYTPYQP	109	-0.6000	0
78	VFTQTAAVL	178	-0.6000	0
79	LQTREQHIR	317	-0.6000	0
80	LGDALVHDK	374	-0.6000	0
81	LDSQAVATM	13	-0.7000	0
82	MHRAARGPV	161	-0.7000	0
83	ITDWSALVQ	225	-0.7000	0
84	LPGRLVGVS	296	-0.7000	0
85	WAYIRMMGA	747	-0.7000	0
86	LGTAFRPKV	905	-0.7000	0
87	YDTHTPPVL	90	-0.8000	0
88	LLRNIIENP	98	-0.8000	0
89	VLARVPGRA	387	-0.8000	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	LNLHKTFCI	687	4.3000	48.86
2	YGFHAPTMS	820	3.5000	39.77
3	LAVHAKHAR	286	3.1000	35.23
4	IVTADLRAG	197	2.9000	32.95
5	FLTHPAFTQ	456	2.9000	32.95
6	LRGITKLTG	799	2.9000	32.95
7	FGRQHPFAP	513	2.6000	29.55
8	YGSASILPI	737	2.4000	27.27
9	IRMMGAEGL	750	2.3600	26.82
10	MTLMHRAAR	158	2.3000	26.14
11	VLLAVLAAM	338	2.3000	26.14
12	MKLNAAAEM	497	2.3000	26.14
13	YIRMMGAEG	749	2.3000	26.14
14	MMRYLRALA	471	2.2000	25.00

15	MRYLRALAD	472	2.2000	25.00
16	LQSWLVLIT	535	2.2000	25.00
17	VRAHLAPFL	709	2.1600	24.55
18	LLNFQTLVT	127	2.0000	22.73
19	LAIHEYHAS	564	2.0000	22.73
20	LVGLARPGK	671	2.0000	22.73
21	ITWAYIRMM	745	2.0000	22.73
22	VLARAKANG	398	1.9000	21.59
23	MIPLGSCTM	489	1.8000	20.45
24	VHAKHARQL	288	1.7600	20.00
25	YRLALQTRE	313	1.7000	19.32
26	FRPKVWPAV	909	1.7000	19.32
27	YRTETSMMR	465	1.5000	17.05
28	VYEHDIAEI	642	1.5000	17.05
29	MVAHECILD	790	1.5000	17.05
30	FPVAGTLMV	829	1.5000	17.05
31	LAVKAVPAG	33	1.4000	15.91
32	LMHRAARGP	160	1.4000	15.91
33	VVDADVFTQ	173	1.4000	15.91
34	LAGMRVVVV	597	1.4000	15.91
35	YTPYQPEIS	112	1.3000	14.77
36	FGTTQRFGV	266	1.3000	14.77
37	FTQYRTETS	462	1.3000	14.77
38	LRAASLTAI	758	1.1000	12.50
39	WYTAYTPYQ	108	1.0000	11.36
40	FGVAAAAPA	437	1.0000	11.36
41	VRRIDGAYG	917	1.0000	11.36
42	FGVIAQLPG	212	0.9000	10.23
43	LQTREQHIR	317	0.9000	10.23
44	LDSQAVATM	13	0.8000	9.09
45	VLLRNIIEN	97	0.8000	9.09
46	VIAQLPGAS	214	0.8000	9.09
47	VSLQPNAGS	548	0.8000	9.09
48	VGPVAVRAH	704	0.8000	9.09

49	VWPAVRRID	913	0.8000	9.09
50	LNFQTLVTD	128	0.7000	7.95
51	YHGAGGLTA	350	0.7000	7.95
52	VGEHAERLS	622	0.7000	7.95
53	ICTAQVLLA	333	0.6000	6.82
54	INLWRVDAD	407	0.6000	6.82
55	WLVLITGYD	538	0.6000	6.82
56	LVLITGYDA	539	0.6000	6.82
57	FLPGHPFAP	716	0.6000	6.82
58	YGDRNLVCS	924	0.6000	6.82
59	LVQQAHDRG	231	0.5000	5.68
60	LARPGKFGG	674	0.5000	5.68
61	YTAYTPYQP	109	0.4000	4.55
62	YQPEISQGR	115	0.4000	4.55
63	FQTLVTDLT	130	0.4000	4.55
64	LATRAKPLG	186	0.4000	4.55
65	LARAKANGI	399	0.4000	4.55
66	VVVVDCHDN	602	0.4000	4.55
67	LNALVGLAR	668	0.4000	4.55
68	VGLARPGKF	672	0.4000	4.55
69	VFTQTAAVL	178	0.3600	4.09
70	LTGLEIANA	137	0.3000	3.41
71	MHRAARGPV	161	0.3000	3.41
72	YASYHGAGG	347	0.3000	3.41
73	WRVDADHVS	410	0.3000	3.41
74	LRAKVGEHA	618	0.3000	3.41
75	YIARRLDEY	771	0.3000	3.41
76	LGTAFRPKV	905	0.3000	3.41
77	LLRNIIENP	98	0.2000	2.27
78	LRGAPHTAQ	877	0.2000	2.27
79	LVCSCPPVE	929	0.2000	2.27
80	YDTHTPPVL	90	0.1600	1.82
81	VATMLAVIG	18	0.1000	1.14
82	YLAVHAKHA	285	0.1000	1.14

83	LALQTREQH	315	0.1000	1.14
84	LTAIARRVH	356	0.1000	1.14
85	LDSLPPAAS	55	-0.1000	0
86	LAVLAAMYA	340	-0.1000	0
87	VHAHAEAIA	363	-0.1000	0
88	LRQLVADLQ	528	-0.1000	0
89	MITYPSTHG	633	-0.1000	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	LNLHKTFCI	687	4.4000	52.38
2	MMRYLRALA	471	3.2000	38.10
3	VVDADVFTQ	173	3.1000	36.90
4	LVGLARPGK	671	2.9000	34.52
5	LAVHAKHAR	286	2.6000	30.95
6	FLTHPAFTQ	456	2.6000	30.95
7	LAIHEYHAS	564	2.6000	30.95
8	IVTADLRAG	197	2.5000	29.76
9	LQSWLVLIT	535	2.5000	29.76
10	LRGITKLTG	799	2.5000	29.76
11	IRMMGAEGL	750	2.4000	28.57
12	VGPVAVRAH	704	2.3800	28.33
13	LLNFQTLVT	127	2.3000	27.38
14	VRAHLAPFL	709	2.2000	26.19
15	MRYLRALAD	472	2.1000	25.00
16	YGFHAPTMS	820	2.1000	25.00
17	LRGAPHTAQ	877	1.9000	22.62
18	MTLMHRAAR	158	1.8000	21.43
19	VHAKHARQL	288	1.8000	21.43
20	VLLAVLAAM	338	1.8000	21.43
21	MKLNAAAEM	497	1.8000	21.43
22	LALQTREQH	315	1.6800	20.00

23	LTAIARRVH	356	1.6800	20.00
24	ICTAQVLLA	333	1.6000	19.05
25	LRQLVADLQ	528	1.6000	19.05
26	LVLITGYDA	539	1.6000	19.05
27	VYEHDIAEI	642	1.6000	19.05
28	MRVVVVDCH	600	1.5800	18.81
29	VLARAKANG	398	1.5000	17.86
30	ITWAYIRMM	745	1.5000	17.86
31	LMHRAARGP	160	1.4000	16.67
32	VIAQLPGAS	214	1.4000	16.67
33	VSLQPNAGS	548	1.4000	16.67
34	LAGMRVVVV	597	1.4000	16.67
35	MVAHECILD	790	1.4000	16.67
36	LTGLEIANA	137	1.3000	15.48
37	MIPLGSCTM	489	1.3000	15.48
38	LRAKVGEHA	618	1.3000	15.48
39	VGEHAERLS	622	1.3000	15.48
40	LRAASLTAI	758	1.2000	14.29
41	LMITYPSTH	632	1.1800	14.05
42	LAVKAVPAG	33	1.0000	11.90
43	VLLRNIIEN	97	1.0000	11.90
44	MMGAEGLRA	752	1.0000	11.90
45	LAVLAAMYA	340	0.9000	10.71
46	VHAHAEAIA	363	0.9000	10.71
47	LRNIIENPA	99	0.8000	9.52
48	IARRVHAHA	359	0.8000	9.52
49	MGAEGLRAA	753	0.8000	9.52
50	WYTAYTPYQ	108	0.7000	8.33
51	LDAFGVAAA	434	0.7000	8.33
52	VWPAVRRID	913	0.7000	8.33
53	LNFQTLVTD	128	0.6000	7.14
54	FGRQHPFAP	513	0.6000	7.14
55	VVVVDCHDN	602	0.6000	7.14
56	VRRIDGAYG	917	0.6000	7.14

57	VCSCPPVEA	930	0.6000	7.14
58	LDSLPPAAS	55	0.5000	5.95
59	LARAKANGI	399	0.5000	5.95
60	INLWRVDAD	407	0.5000	5.95
61	YGSASILPI	737	0.5000	5.95
62	VFTQTAAVL	178	0.4000	4.76
63	LQTREQHIR	317	0.4000	4.76
64	LGDALVHDK	374	0.4000	4.76
65	LDSQAVATM	13	0.3000	3.57
66	MHRAARGPV	161	0.3000	3.57
67	ITDWSALVQ	225	0.3000	3.57
68	LPGRLVGVS	296	0.3000	3.57
69	LGTAFRPKV	905	0.3000	3.57
70	LLRNIIENP	98	0.2000	2.38
71	VLARVPGRA	387	0.2000	2.38
72	LVQQAHDRG	231	0.1000	1.19
73	LNAAAEMES	499	0.1000	1.19
74	LARPGKFGG	674	0.1000	1.19
75	LAAMYASYH	343	-0.0200	0
76	YTPYQPEIS	112	-0.1000	0
77	FTQYRTETS	462	-0.1000	0
78	LRALADKDI	475	-0.1000	0
79	LIPSSAHGT	582	-0.1000	0
80	LNALVGLAR	668	-0.1000	0
81	YIRMMGAEG	749	-0.1000	0
82	IGLDSQAVA	11	-0.2000	0
83	LLALTLIAP	248	-0.2000	0
84	LVCSCPPVE	929	-0.2000	0
85	VATMLAVIG	18	-0.3000	0
86	LEIANASML	140	-0.3000	0
87	YHGAGGLTA	350	-0.3000	0
88	ITYPSTHGV	634	-0.3000	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	LRGITKLTG	799	5.5000	63.22
2	MRYLRALAD	472	4.0000	45.98
3	FGVIAQLPG	212	3.5000	40.23
4	YGSASILPI	737	3.5000	40.23
5	LVGLARPGK	671	3.1500	36.21
6	LLNFQTLVT	127	2.7000	31.03
7	FPVAGTLMV	829	2.6000	29.89
8	MTLMHRAAR	158	2.5000	28.74
9	MIPLGSCTM	489	2.5000	28.74
10	LQSWLVLIT	535	2.5000	28.74
11	YIRMMGAEG	749	2.5000	28.74
12	VRRIDGAYG	917	2.5000	28.74
13	WLVLITGYD	538	2.4000	27.59
14	VLLAVLAAM	338	2.3000	26.44
15	IRMMGAEGL	750	2.2600	25.98
16	YRTETSMMR	465	2.2000	25.29
17	MKLNAAAEM	497	2.2000	25.29
18	LNALVGLAR	668	2.2000	25.29
19	WAYIRMMGA	747	2.1000	24.14
20	WPAVRRIDG	914	2.1000	24.14
21	LAVLAAMYA	340	1.9000	21.84
22	LVLITGYDA	539	1.9000	21.84
23	LLALTLIAP	248	1.8000	20.69
24	YHGAGGLTA	350	1.8000	20.69
25	YAGLLAIHE	560	1.8000	20.69
26	ICTAQVLLA	333	1.7000	19.54
27	VIGVDSLDD	24	1.5000	17.24
28	VGLARPGKF	672	1.5000	17.24
29	WYTAYTPYQ	108	1.4500	16.67
30	MHRAARGPV	161	1.4000	16.09
31	IVTADLRAG	197	1.3000	14.94

32	YRLALQTRE	313	1.3000	14.94
33	VLLRNIIEN	97	1.2000	13.79
34	YLAVHAKHA	285	1.2000	13.79
35	VVVVDCHDN	602	1.2000	13.79
36	LNLHKTFCI	687	1.2000	13.79
37	MMRYLRALA	471	1.1000	12.64
38	LAGMRVVVV	597	1.1000	12.64
39	MMGAEGLRA	752	1.1000	12.64
40	LTLIAPPGE	251	1.0500	12.07
41	LTGLEIANA	137	1.0000	11.49
42	VLARAKANG	398	1.0000	11.49
43	FGVAAAAPA	437	1.0000	11.49
44	YGFHAPTMS	820	1.0000	11.49
45	VIAQLPGAS	214	0.9000	10.34
46	YPVLYTGEN	780	0.9000	10.34
47	FRPKVWPAV	909	0.8500	9.77
48	FGTTQRFGV	266	0.8000	9.20
49	LNAAAEMES	499	0.8000	9.20
50	LGTAFRPKV	905	0.7500	8.62
51	LLAVLAAMY	339	0.7000	8.05
52	LRAASLTAI	758	0.7000	8.05
53	MVAHECILD	790	0.7000	8.05
54	LDSLPPAAS	55	0.6000	6.90
55	VSMIGQGYY	82	0.6000	6.90
56	FGRQHPFAP	513	0.6000	6.90
57	LAVKAVPAG	33	0.5500	6.32
58	LVCSCPPVE	929	0.5500	6.32
59	VRAHLAPFL	709	0.5100	5.86
60	LAVHAKHAR	286	0.5000	5.75
61	VGPVAVRAH	704	0.5000	5.75
62	ITKLTGITV	802	0.5000	5.75
63	VVDADVFTQ	173	0.4000	4.60
64	ILPITWAYI	742	0.4000	4.60
65	ITWAYIRMM	745	0.4000	4.60

66	LRALADKDI	475	0.3000	3.45
67	MLAVIGVDS	21	0.2000	2.30
68	LRNIIENPA	99	0.2000	2.30
69	VTDLTGLEI	134	0.2000	2.30
70	MRVVVVDCH	600	0.1000	1.15
71	LTAITSANY	763	0.1000	1.15
72	VKAVPAGIL	35	0.0600	0.69
73	YYDTHTPPV	89	0.0500	0.57
74	LATRAKPLG	186	-0.0500	0
75	YTPYQPEIS	112	-0.1000	0
76	FQTLVTDLT	130	-0.1000	0
77	LPGRLVGVS	296	-0.1000	0
78	FTQYRTETS	462	-0.1000	0
79	VAVRAHLAP	707	-0.1000	0
80	LDSQAVATM	13	-0.2000	0
81	VATMLAVIG	18	-0.2000	0
82	LAELRALAD	68	-0.2000	0
83	LLRNIIENP	98	-0.2000	0
84	IANASMLDE	142	-0.2000	0
85	IAQLPGASG	215	-0.2000	0
86	LALTLIAPP	249	-0.2000	0
87	FLTHPAFTQ	456	-0.2000	0
88	VSLQPNAGS	548	-0.2000	0
89	LRGAPHTAQ	877	-0.2000	0
90	LMITYPSTH	632	-0.3000	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	LNLHKTFCI	687	5.3000	60.23
2	LAVHAKHAR	286	4.1000	46.59
3	IVTADLRAG	197	3.9000	44.32
4	LRGITKLTG	799	3.9000	44.32

5	IRMMGAEGL	750	3.3600	38.18
6	MTLMHRAAR	158	3.3000	37.50
7	VLLAVLAAM	338	3.3000	37.50
8	MKLNAAAEM	497	3.3000	37.50
9	MMRYLRALA	471	3.2000	36.36
10	MRYLRALAD	472	3.2000	36.36
11	LQSWLVLIT	535	3.2000	36.36
12	VRAHLAPFL	709	3.1600	35.91
13	LLNFQTLVT	127	3.0000	34.09
14	LAIHEYHAS	564	3.0000	34.09
15	LVGLARPGK	671	3.0000	34.09
16	ITWAYIRMM	745	3.0000	34.09
17	VLARAKANG	398	2.9000	32.95
18	MIPLGSCTM	489	2.8000	31.82
19	VHAKHARQL	288	2.7600	31.36
20	VYEHDIAEI	642	2.5000	28.41
21	MVAHECILD	790	2.5000	28.41
22	YGFHAPTMS	820	2.5000	28.41
23	LAVKAVPAG	33	2.4000	27.27
24	LMHRAARGP	160	2.4000	27.27
25	VVDADVFTQ	173	2.4000	27.27
26	LAGMRVVVV	597	2.4000	27.27
27	LRAASLTAI	758	2.1000	23.86
28	VRRIDGAYG	917	2.0000	22.73
29	LQTREQHIR	317	1.9000	21.59
30	FLTHPAFTQ	456	1.9000	21.59
31	LDSQAVATM	13	1.8000	20.45
32	VLLRNIIEN	97	1.8000	20.45
33	VIAQLPGAS	214	1.8000	20.45
34	VSLQPNAGS	548	1.8000	20.45
35	VGPVAVRAH	704	1.8000	20.45
36	VWPAVRRID	913	1.8000	20.45
37	LNFQTLVTD	128	1.7000	19.32
38	VGEHAERLS	622	1.7000	19.32

39	ICTAQVLLA	333	1.6000	18.18
40	INLWRVDAD	407	1.6000	18.18
41	FGRQHPFAP	513	1.6000	18.18
42	LVLITGYDA	539	1.6000	18.18
43	LVQQAHDRG	231	1.5000	17.05
44	LARPGKFGG	674	1.5000	17.05
45	LATRAKPLG	186	1.4000	15.91
46	LARAKANGI	399	1.4000	15.91
47	VVVVDCHDN	602	1.4000	15.91
48	LNALVGLAR	668	1.4000	15.91
49	VGLARPGKF	672	1.4000	15.91
50	YGSASILPI	737	1.4000	15.91
51	VFTQTAAVL	178	1.3600	15.45
52	LTGLEIANA	137	1.3000	14.77
53	MHRAARGPV	161	1.3000	14.77
54	LRAKVGEHA	618	1.3000	14.77
55	YIRMMGAEG	749	1.3000	14.77
56	LGTAFRPKV	905	1.3000	14.77
57	LLRNIIENP	98	1.2000	13.64
58	LRGAPHTAQ	877	1.2000	13.64
59	LVCSCPPVE	929	1.2000	13.64
60	VATMLAVIG	18	1.1000	12.50
61	LALQTREQH	315	1.1000	12.50
62	LTAIARRVH	356	1.1000	12.50
63	MGFGGPHAG	276	1.0000	11.36
64	MRVVVVDCH	600	1.0000	11.36
65	MMGAEGLRA	752	1.0000	11.36
66	LDSLPPAAS	55	0.9000	10.23
67	LAVLAAMYA	340	0.9000	10.23
68	VHAHAEAIA	363	0.9000	10.23
69	LRQLVADLQ	528	0.9000	10.23
70	MITYPSTHG	633	0.9000	10.23
71	LRNIIENPA	99	0.8000	9.09
72	LLALTLIAP	248	0.8000	9.09

73	IARRVHAHA	359	0.8000	9.09
74	LRALADKDI	475	0.8000	9.09
75	MGAEGLRAA	753	0.8000	9.09
76	ITVDDVAKR	808	0.8000	9.09
77	VSDHSTFAD	0	0.7000	7.95
78	LPGRLVGVS	296	0.7000	7.95
79	YRLALQTRE	313	0.7000	7.95
80	LDAFGVAAA	434	0.7000	7.95
81	ITYPSTHGV	634	0.7000	7.95
82	VAVRAHLAP	707	0.7000	7.95
83	FRPKVWPAV	909	0.7000	7.95
84	LEIANASML	140	0.6600	7.50
85	LGIEIVTAD	193	0.6000	6.82
86	VAFGTTQRF	264	0.6000	6.82
87	LIPSSAHGT	582	0.6000	6.82
88	LMITYPSTH	632	0.6000	6.82
89	VCSCPPVEA	930	0.6000	6.82
90	LVGVSVDSD	300	0.5000	5.68
91	LGDALVHDK	374	0.5000	5.68
92	YRTETSMMR	465	0.5000	5.68
93	LNAAAEMES	499	0.5000	5.68
94	VLYTGENGM	782	0.5000	5.68

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	LNLHKTFCI	687	4.3000	48.86
2	YGFHAPTMS	820	3.5000	39.77
3	LAVHAKHAR	286	3.1000	35.23
4	IVTADLRAG	197	2.9000	32.95
5	FLTHPAFTQ	456	2.9000	32.95
6	LRGITKLTG	799	2.9000	32.95
7	FGRQHPFAP	513	2.6000	29.55

8	YGSASILPI	737	2.4000	27.27
9	IRMMGAEGL	750	2.3600	26.82
10	MTLMHRAAR	158	2.3000	26.14
11	VLLAVLAAM	338	2.3000	26.14
12	MKLNAAAEM	497	2.3000	26.14
13	YIRMMGAEG	749	2.3000	26.14
14	MMRYLRALA	471	2.2000	25.00
15	MRYLRALAD	472	2.2000	25.00
16	LQSWLVLIT	535	2.2000	25.00
17	VRAHLAPFL	709	2.1600	24.55
18	LLNFQTLVT	127	2.0000	22.73
19	LAIHEYHAS	564	2.0000	22.73
20	LVGLARPGK	671	2.0000	22.73
21	ITWAYIRMM	745	2.0000	22.73
22	VLARAKANG	398	1.9000	21.59
23	MIPLGSCTM	489	1.8000	20.45
24	VHAKHARQL	288	1.7600	20.00
25	YRLALQTRE	313	1.7000	19.32
26	FRPKVWPAV	909	1.7000	19.32
27	YRTETSMMR	465	1.5000	17.05
28	VYEHDIAEI	642	1.5000	17.05
29	MVAHECILD	790	1.5000	17.05
30	FPVAGTLMV	829	1.5000	17.05
31	LAVKAVPAG	33	1.4000	15.91
32	LMHRAARGP	160	1.4000	15.91
33	VVDADVFTQ	173	1.4000	15.91
34	LAGMRVVVV	597	1.4000	15.91
35	YTPYQPEIS	112	1.3000	14.77
36	FGTTQRFGV	266	1.3000	14.77
37	FTQYRTETS	462	1.3000	14.77
38	LRAASLTAI	758	1.1000	12.50
39	WYTAYTPYQ	108	1.0000	11.36
40	FGVAAAAPA	437	1.0000	11.36
41	VRRIDGAYG	917	1.0000	11.36

42	FGVIAQLPG	212	0.9000	10.23
43	LQTREQHIR	317	0.9000	10.23
44	LDSQAVATM	13	0.8000	9.09
45	VLLRNIIEN	97	0.8000	9.09
46	VIAQLPGAS	214	0.8000	9.09
47	VSLQPNAGS	548	0.8000	9.09
48	VGPVAVRAH	704	0.8000	9.09
49	VWPAVRRID	913	0.8000	9.09
50	LNFQTLVTD	128	0.7000	7.95
51	YHGAGGLTA	350	0.7000	7.95
52	VGEHAERLS	622	0.7000	7.95
53	ICTAQVLLA	333	0.6000	6.82
54	INLWRVDAD	407	0.6000	6.82
55	WLVLITGYD	538	0.6000	6.82
56	LVLITGYDA	539	0.6000	6.82
57	FLPGHPFAP	716	0.6000	6.82
58	YGDRNLVCS	924	0.6000	6.82
59	LVQQAHDRG	231	0.5000	5.68
60	LARPGKFGG	674	0.5000	5.68
61	YTAYTPYQP	109	0.4000	4.55
62	YQPEISQGR	115	0.4000	4.55
63	FQTLVTDLT	130	0.4000	4.55
64	LATRAKPLG	186	0.4000	4.55
65	LARAKANGI	399	0.4000	4.55
66	VVVVDCHDN	602	0.4000	4.55
67	LNALVGLAR	668	0.4000	4.55
68	VGLARPGKF	672	0.4000	4.55
69	VFTQTAAVL	178	0.3600	4.09
70	LTGLEIANA	137	0.3000	3.41
71	MHRAARGPV	161	0.3000	3.41
72	YASYHGAGG	347	0.3000	3.41
73	WRVDADHVS	410	0.3000	3.41
74	LRAKVGEHA	618	0.3000	3.41
75	YIARRLDEY	771	0.3000	3.41

76	LGTAFRPKV	905	0.3000	3.41
77	LLRNIIENP	98	0.2000	2.27
78	LRGAPHTAQ	877	0.2000	2.27
79	LVCSCPPVE	929	0.2000	2.27
80	YDTHTPPVL	90	0.1600	1.82
81	VATMLAVIG	18	0.1000	1.14
82	YLAVHAKHA	285	0.1000	1.14
83	LALQTREQH	315	0.1000	1.14
84	LTAIARRVH	356	0.1000	1.14
85	LDSLPPAAS	55	-0.1000	0
86	LAVLAAMYA	340	-0.1000	0
87	VHAHAEAIA	363	-0.1000	0
88	LRQLVADLQ	528	-0.1000	0
89	MITYPSTHG	633	-0.1000	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	MRYLRALAD	472	4.8000	53.33
2	LNLHKTFCI	687	4.6000	51.11
3	MVAHECILD	790	4.1000	45.56
4	VVDADVFTQ	173	3.9000	43.33
5	IVTADLRAG	197	3.8000	42.22
6	LRGITKLTG	799	3.8000	42.22
7	VGPVAVRAH	704	3.6000	40.00
8	FLTHPAFTQ	456	3.4000	37.78
9	LQSWLVLIT	535	3.4000	37.78
10	IRMMGAEGL	750	3.4000	37.78
11	VWPAVRRID	913	3.4000	37.78
12	LNFQTLVTD	128	3.3000	36.67
13	LLNFQTLVT	127	3.2000	35.56
14	INLWRVDAD	407	3.2000	35.56
15	MMRYLRALA	471	3.2000	35.56

16	VRAHLAPFL	709	3.2000	35.56
17	VLLRNIIEN	97	3.0000	33.33
18	LALQTREQH	315	2.9000	32.22
19	VLLAVLAAM	338	2.9000	32.22
20	LTAIARRVH	356	2.9000	32.22
21	MKLNAAAEM	497	2.9000	32.22
22	VHAKHARQL	288	2.8000	31.11
23	VLARAKANG	398	2.8000	31.11
24	MRVVVVDCH	600	2.8000	31.11
25	LVCSCPPVE	929	2.8000	31.11
26	LRGAPHTAQ	877	2.7000	30.00
27	LAVHAKHAR	286	2.6000	28.89
28	LAIHEYHAS	564	2.6000	28.89
29	VVVVDCHDN	602	2.6000	28.89
30	ITWAYIRMM	745	2.6000	28.89
31	MIPLGSCTM	489	2.4000	26.67
32	LRQLVADLQ	528	2.4000	26.67
33	LMITYPSTH	632	2.4000	26.67
34	VSDHSTFAD	0	2.3000	25.56
35	LAVKAVPAG	33	2.3000	25.56
36	YRLALQTRE	313	2.3000	25.56
37	LGIEIVTAD	193	2.2000	24.44
38	LVGLARPGK	671	2.2000	24.44
39	LVGVSVDSD	300	2.1000	23.33
40	YGFHAPTMS	820	2.1000	23.33
41	VRRIDGAYG	917	1.9000	21.11
42	MTLMHRAAR	158	1.8000	20.00
43	LMHRAARGP	160	1.8000	20.00
44	VYEHDIAEI	642	1.8000	20.00
45	VIGVDSLDD	24	1.7000	18.89
46	LTLIAPPGE	251	1.7000	18.89
47	LAGMRVVVV	597	1.7000	18.89
48	VKRVVVDAD	169	1.6000	17.78
49	ICTAQVLLA	333	1.6000	17.78

50	LVLITGYDA	539	1.6000	17.78
51	LMVEPTESE	835	1.6000	17.78
52	WYTAYTPYQ	108	1.5000	16.67
53	LDSQAVATM	13	1.4000	15.56
54	VFTQTAAVL	178	1.4000	15.56
55	VIAQLPGAS	214	1.4000	15.56
56	LVQQAHDRG	231	1.4000	15.56
57	VSLQPNAGS	548	1.4000	15.56
58	LARPGKFGG	674	1.4000	15.56
59	LRAASLTAI	758	1.4000	15.56
60	LVTDLTGLE	133	1.3000	14.44
61	LTGLEIANA	137	1.3000	14.44
62	IANASMLDE	142	1.3000	14.44
63	LATRAKPLG	186	1.3000	14.44
64	LARVPGRAD	388	1.3000	14.44
65	LRAKVGEHA	618	1.3000	14.44
66	VGEHAERLS	622	1.3000	14.44
67	IRRDKATSN	324	1.2000	13.33
68	LAAMYASYH	343	1.2000	13.33
69	LADKDIALD	478	1.2000	13.33
70	WLVLITGYD	538	1.2000	13.33
71	YIRMMGAEG	749	1.2000	13.33
72	ITDWSALVQ	225	1.1000	12.22
73	LPGHPFAPE	717	1.1000	12.22
74	VATMLAVIG	18	1.0000	11.11
75	LRAGLPDGE	202	1.0000	11.11
76	FGRQHPFAP	513	1.0000	11.11
77	MMGAEGLRA	752	1.0000	11.11
78	MGFGGPHAG	276	0.9000	10.00
79	LAVLAAMYA	340	0.9000	10.00
80	VHAHAEAIA	363	0.9000	10.00
81	LRNIIENPA	99	0.8000	8.89
82	IARRVHAHA	359	0.8000	8.89
83	LIPSSAHGT	582	0.8000	8.89

84	MITYPSTHG	633	0.8000	8.89
85	MGAEGLRAA	753	0.8000	8.89
86	LEIANASML	140	0.7000	7.78
87	LARAKANGI	399	0.7000	7.78
88	LDAFGVAAA	434	0.7000	7.78
89	ICLIPSSAH	580	0.7000	7.78
90	VYVDGANLN	661	0.7000	7.78
91	YGSASILPI	737	0.7000	7.78
92	MIGIRAEID	855	0.7000	7.78
93	LAELRALAD	68	0.6000	6.67
94	LLRNIIENP	98	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	LRGITKLTG	799	5.5000	63.22
2	MRYLRALAD	472	4.0000	45.98
3	FGVIAQLPG	212	3.5000	40.23
4	YGSASILPI	737	3.5000	40.23
5	LVGLARPGK	671	3.1500	36.21
6	LLNFQTLVT	127	2.7000	31.03
7	FPVAGTLMV	829	2.6000	29.89
8	MTLMHRAAR	158	2.5000	28.74
9	MIPLGSCTM	489	2.5000	28.74
10	LQSWLVLIT	535	2.5000	28.74
11	YIRMMGAEG	749	2.5000	28.74
12	VRRIDGAYG	917	2.5000	28.74
13	WLVLITGYD	538	2.4000	27.59
14	VLLAVLAAM	338	2.3000	26.44
15	IRMMGAEGL	750	2.2600	25.98
16	YRTETSMMR	465	2.2000	25.29
17	MKLNAAAEM	497	2.2000	25.29
18	LNALVGLAR	668	2.2000	25.29

19	WAYIRMMGA	747	2.1000	24.14
20	WPAVRRIDG	914	2.1000	24.14
21	LAVLAAMYA	340	1.9000	21.84
22	LVLITGYDA	539	1.9000	21.84
23	LLALTLIAP	248	1.8000	20.69
24	YHGAGGLTA	350	1.8000	20.69
25	YAGLLAIHE	560	1.8000	20.69
26	ICTAQVLLA	333	1.7000	19.54
27	VIGVDSLDD	24	1.5000	17.24
28	VGLARPGKF	672	1.5000	17.24
29	WYTAYTPYQ	108	1.4500	16.67
30	MHRAARGPV	161	1.4000	16.09
31	IVTADLRAG	197	1.3000	14.94
32	YRLALQTRE	313	1.3000	14.94
33	VLLRNIIEN	97	1.2000	13.79
34	YLAVHAKHA	285	1.2000	13.79
35	VVVVDCHDN	602	1.2000	13.79
36	LNLHKTFCI	687	1.2000	13.79
37	MMRYLRALA	471	1.1000	12.64
38	LAGMRVVVV	597	1.1000	12.64
39	MMGAEGLRA	752	1.1000	12.64
40	LTLIAPPGE	251	1.0500	12.07
41	LTGLEIANA	137	1.0000	11.49
42	VLARAKANG	398	1.0000	11.49
43	FGVAAAAPA	437	1.0000	11.49
44	YGFHAPTMS	820	1.0000	11.49
45	VIAQLPGAS	214	0.9000	10.34
46	YPVLYTGEN	780	0.9000	10.34
47	FRPKVWPAV	909	0.8500	9.77
48	FGTTQRFGV	266	0.8000	9.20
49	LNAAAEMES	499	0.8000	9.20
50	LGTAFRPKV	905	0.7500	8.62
51	LLAVLAAMY	339	0.7000	8.05
52	LRAASLTAI	758	0.7000	8.05

53	MVAHECILD	790	0.7000	8.05
54	LDSLPPAAS	55	0.6000	6.90
55	VSMIGQGYY	82	0.6000	6.90
56	FGRQHPFAP	513	0.6000	6.90
57	LAVKAVPAG	33	0.5500	6.32
58	LVCSCPPVE	929	0.5500	6.32
59	VRAHLAPFL	709	0.5100	5.86
60	LAVHAKHAR	286	0.5000	5.75
61	VGPVAVRAH	704	0.5000	5.75
62	ITKLTGITV	802	0.5000	5.75
63	VVDADVFTQ	173	0.4000	4.60
64	ILPITWAYI	742	0.4000	4.60
65	ITWAYIRMM	745	0.4000	4.60
66	LRALADKDI	475	0.3000	3.45
67	MLAVIGVDS	21	0.2000	2.30
68	LRNIIENPA	99	0.2000	2.30
69	VTDLTGLEI	134	0.2000	2.30
70	MRVVVVDCH	600	0.1000	1.15
71	LTAITSANY	763	0.1000	1.15
72	VKAVPAGIL	35	0.0600	0.69
73	YYDTHTPPV	89	0.0500	0.57
74	LATRAKPLG	186	-0.0500	0
75	YTPYQPEIS	112	-0.1000	0
76	FQTLVTDLT	130	-0.1000	0
77	LPGRLVGVS	296	-0.1000	0
78	FTQYRTETS	462	-0.1000	0
79	VAVRAHLAP	707	-0.1000	0
80	LDSQAVATM	13	-0.2000	0
81	VATMLAVIG	18	-0.2000	0
82	LAELRALAD	68	-0.2000	0
83	LLRNIIENP	98	-0.2000	0
84	IANASMLDE	142	-0.2000	0
85	IAQLPGASG	215	-0.2000	0
86	LALTLIAPP	249	-0.2000	0

87	FLTHPAFTQ	456	-0.2000	0
88	VSLQPNAGS	548	-0.2000	0
89	LRGAPHTAQ	877	-0.2000	0
90	LMITYPSTH	632	-0.3000	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	LRGITKLTG	799	2.3000	33.82
2	LVGLARPGK	671	1.9000	27.94
3	WLVLITGYD	538	1.2000	17.65
4	LVLITGYDA	539	1.2000	17.65
5	MMRYLRALA	471	1.1000	16.18
6	MRYLRALAD	472	1.1000	16.18
7	YIRMMGAEG	749	1.1000	16.18
8	VRRIDGAYG	917	1.1000	16.18
9	WYTAYTPYQ	108	1.0000	14.71
10	LTGLEIANA	137	1.0000	14.71
11	MTLMHRAAR	158	1.0000	14.71
12	FGVAAAAPA	437	1.0000	14.71
13	MIPLGSCTM	489	1.0000	14.71
14	MRVVVVDCH	600	0.9800	14.41
15	VGPVAVRAH	704	0.8800	12.94
16	VLLAVLAAM	338	0.8000	11.76
17	YGSASILPI	737	0.8000	11.76
18	MKLNAAAEM	497	0.7000	10.29
19	VVDADVFTQ	173	0.6000	8.82
20	YLAVHAKHA	285	0.6000	8.82
21	WAYIRMMGA	747	0.5000	7.35
22	VIAQLPGAS	214	0.4000	5.88
23	LRQLVADLQ	528	0.4000	5.88
24	LTAIARRVH	356	0.3800	5.59
25	MHRAARGPV	161	0.3000	4.41

26	FGVIAQLPG	212	0.3000	4.41
27	LAVLAAMYA	340	0.3000	4.41
28	LMITYPSTH	632	0.2800	4.12
29	LDSLPPAAS	55	0.2000	2.94
30	LLNFQTLVT	127	0.2000	2.94
31	IRMMGAEGL	750	0.2000	2.94
32	LRNIIENPA	99	-0.1000	0
33	ICTAQVLLA	333	-0.1000	0
34	LNLHKTFCI	687	-0.2000	0
35	FPVAGTLMV	829	-0.2000	0
36	IVTADLRAG	197	-0.3000	0
37	VVVVDCHDN	602	-0.3000	0
38	VLARAKANG	398	-0.4000	0
39	LAGMRVVVV	597	-0.4000	0
40	ICLIPSSAH	580	-0.4200	0
41	FQTLVTDLT	130	-0.5000	0
42	VGLARPGKF	672	-0.5000	0
43	ILPITWAYI	742	-0.5000	0
44	YGFHAPTMS	820	-0.5000	0
45	LPGRLVGVS	296	-0.6000	0
46	LLAVLAAMY	339	-0.6000	0
47	VSLQPNAGS	548	-0.6000	0
48	LRGAPHTAQ	877	-0.6000	0
49	WSALVQQAH	228	-0.6200	0
50	MLAVIGVDS	21	-0.7000	0
51	FGTTQRFGV	266	-0.7000	0
52	VLARVPGRA	387	-0.7000	0
53	LDAFGVAAA	434	-0.7000	0
54	MMGAEGLRA	752	-0.7000	0
55	VSMIGQGYY	82	-0.8000	0
56	LLALTLIAP	248	-0.8000	0
57	YRTETSMMR	465	-0.9000	0
58	FGRQHPFAP	513	-0.9000	0
59	WPAVRRIDG	914	-0.9000	0

60	VKAVPAGIL	35	-1.0000	0
61	FFGVIAQLP	211	-1.1000	0
62	IARRVHAHA	359	-1.1000	0
63	LNALVGLAR	668	-1.1000	0
64	VLLRNIIEN	97	-1.2000	0
65	LALTLIAPP	249	-1.2000	0
66	LVGVSVDSD	300	-1.2000	0
67	YRLALQTRE	313	-1.2000	0
68	LRALADKDI	475	-1.2000	0
69	LNAAAEMES	499	-1.2000	0
70	YAGLLAIHE	560	-1.2000	0
71	LTAITSANY	763	-1.2000	0
72	LAAMYASYH	343	-1.2200	0
73	IAEICAAVH	647	-1.2200	0
74	LRALADANT	71	-1.3000	0
75	ITWAYIRMM	745	-1.3000	0
76	LRAASLTAI	758	-1.3000	0
77	FRPKVWPAV	909	-1.3000	0
78	VIGVDSLDD	24	-1.4000	0
79	LGTAFRPKV	905	-1.4000	0
80	VCSCPPVEA	930	-1.4000	0
81	IGLDSQAVA	11	-1.5000	0
82	LTLIAPPGE	251	-1.5000	0
83	VVLDAFGVA	432	-1.5000	0
84	VYEHDIAEI	642	-1.5000	0
85	LHKTFCIPH	689	-1.5200	0
86	YTPYQPEIS	112	-1.6000	0
87	VFTQTAAVL	178	-1.6000	0
88	IAQLPGASG	215	-1.6000	0
89	YFDTVLARV	383	-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	LRGITKLTG	799	5.1000	61.45
2	LVGLARPGK	671	4.0500	48.80
3	MRYLRALAD	472	3.9000	46.99
4	LLNFQTLVT	127	3.0000	36.14
5	LAVLAAMYA	340	2.9000	34.94
6	LVLITGYDA	539	2.9000	34.94
7	LQSWLVLIT	535	2.8000	33.73
8	ICTAQVLLA	333	2.7000	32.53
9	IRMMGAEGL	750	2.3000	27.71
10	VVDADVFTQ	173	2.1000	25.30
11	MMRYLRALA	471	2.1000	25.30
12	MMGAEGLRA	752	2.1000	25.30
13	VRRIDGAYG	917	2.1000	25.30
14	VGPVAVRAH	704	2.0800	25.06
15	LTGLEIANA	137	2.0000	24.10
16	MTLMHRAAR	158	2.0000	24.10
17	MIPLGSCTM	489	2.0000	24.10
18	LLALTLIAP	248	1.8000	21.69
19	VLLAVLAAM	338	1.8000	21.69
20	MKLNAAAEM	497	1.7000	20.48
21	LNALVGLAR	668	1.7000	20.48
22	MRVVVVDCH	600	1.6800	20.24
23	YGSASILPI	737	1.6000	19.28
24	LTAIARRVH	356	1.5800	19.04
25	VIAQLPGAS	214	1.5000	18.07
26	LRGAPHTAQ	877	1.5000	18.07
27	VIGVDSLDD	24	1.4000	16.87
28	VLLRNIIEN	97	1.4000	16.87
29	MHRAARGPV	161	1.4000	16.87
30	LNAAAEMES	499	1.4000	16.87
31	VVVVDCHDN	602	1.4000	16.87
32	LNLHKTFCI	687	1.3000	15.66
33	LMITYPSTH	632	1.2800	15.42

34	LDSLPPAAS	55	1.2000	14.46
35	LRNIIENPA	99	1.2000	14.46
36	WYTAYTPYQ	108	1.1500	13.86
37	FGVIAQLPG	212	1.1000	13.25
38	LRQLVADLQ	528	1.1000	13.25
39	LAGMRVVVV	597	1.1000	13.25
40	WAYIRMMGA	747	1.1000	13.25
41	LHKTFCIPH	689	1.0800	13.01
42	IVTADLRAG	197	0.9000	10.84
43	MLAVIGVDS	21	0.8000	9.64
44	YHGAGGLTA	350	0.8000	9.64
45	LRAASLTAI	758	0.8000	9.64
46	LGTAFRPKV	905	0.7500	9.04
47	LTLIAPPGE	251	0.6500	7.83
48	ITDWSALVQ	225	0.6000	7.23
49	VLARAKANG	398	0.6000	7.23
50	VGLARPGKF	672	0.6000	7.23
51	MVAHECILD	790	0.6000	7.23
52	ILDLRGITK	796	0.6000	7.23
53	FPVAGTLMV	829	0.6000	7.23
54	ICLIPSSAH	580	0.5800	6.99
55	VRAHLAPFL	709	0.5500	6.63
56	LPGRLVGVS	296	0.5000	6.02
57	ILPITWAYI	742	0.5000	6.02
58	ITKLTGITV	802	0.5000	6.02
59	LLAVLAAMY	339	0.4000	4.82
60	VLARVPGRA	387	0.4000	4.82
61	LRALADKDI	475	0.4000	4.82
62	VSLQPNAGS	548	0.4000	4.82
63	IGIRAEIDK	856	0.4000	4.82
64	LALQTREQH	315	0.3800	4.58
65	VSMIGQGYY	82	0.3000	3.61
66	VTDLTGLEI	134	0.3000	3.61
67	LDAFGVAAA	434	0.3000	3.61

68	WLVLITGYD	538	0.3000	3.61
69	YLAVHAKHA	285	0.2000	2.41
70	LAVKAVPAG	33	0.1500	1.81
71	LVCSCPPVE	929	0.1500	1.81
72	VKAVPAGIL	35	0.1000	1.20
73	LLAIHEYHA	563	0.1000	1.20
74	YIRMMGAEG	749	0.1000	1.20
75	VCSCPPVEA	930	0.1000	1.20
76	IARRVHAHA	359	-0.1000	0
77	LGDALVHDK	374	-0.1000	0
78	VAVRAHLAP	707	-0.1000	0
79	ITWAYIRMM	745	-0.1000	0
80	LLRNIIENP	98	-0.2000	0
81	LALTLIAPP	249	-0.2000	0
82	VSHLNLHKT	684	-0.2000	0
83	LTAITSANY	763	-0.2000	0
84	LAAMYASYH	343	-0.2200	0
85	IAEICAAVH	647	-0.2200	0
86	LAELRALAD	68	-0.3000	0
87	LRALADANT	71	-0.3000	0
88	YRTETSMMR	465	-0.3000	0
89	LRAKVGEHA	618	-0.3000	0
90	VAHECILDL	791	-0.3000	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	MRYLRALAD	472	5.6000	62.92
2	LRGITKLTG	799	5.4000	60.67
3	WLVLITGYD	538	4.0000	44.94
4	FGVIAQLPG	212	3.4000	38.20
5	YAGLLAIHE	560	3.4000	38.20
6	VIGVDSLDD	24	3.1000	34.83

7	WYTAYTPYQ	108	2.9500	33.15
8	LLNFQTLVT	127	2.9000	32.58
9	YRLALQTRE	313	2.9000	32.58
10	YGSASILPI	737	2.8000	31.46
11	LQSWLVLIT	535	2.7000	30.34
12	LTLIAPPGE	251	2.6500	29.78
13	VLLRNIIEN	97	2.4000	26.97
14	VVVVDCHDN	602	2.4000	26.97
15	YIRMMGAEG	749	2.4000	26.97
16	VRRIDGAYG	917	2.4000	26.97
17	LVGLARPGK	671	2.3500	26.40
18	VGPVAVRAH	704	2.3000	25.84
19	IRMMGAEGL	750	2.3000	25.84
20	MVAHECILD	790	2.3000	25.84
21	LVCSCPPVE	929	2.1500	24.16
22	MIPLGSCTM	489	2.1000	23.60
23	WAYIRMMGA	747	2.1000	23.60
24	YPVLYTGEN	780	2.1000	23.60
25	WPAVRRIDG	914	2.0000	22.47
26	VVDADVFTQ	173	1.9000	21.35
27	VLLAVLAAM	338	1.9000	21.35
28	LAVLAAMYA	340	1.9000	21.35
29	LVLITGYDA	539	1.9000	21.35
30	MRVVVVDCH	600	1.9000	21.35
31	FPVAGTLMV	829	1.9000	21.35
32	YHGAGGLTA	350	1.8000	20.22
33	LTAIARRVH	356	1.8000	20.22
34	MKLNAAAEM	497	1.8000	20.22
35	ICTAQVLLA	333	1.7000	19.10
36	LMITYPSTH	632	1.5000	16.85
37	LAELRALAD	68	1.4000	15.73
38	IANASMLDE	142	1.4000	15.73
39	FLTHPAFTQ	456	1.3000	14.61
40	LHKTFCIPH	689	1.3000	14.61

41	LRGAPHTAQ	877	1.3000	14.61
42	IVTADLRAG	197	1.2000	13.48
43	LLALTLIAP	248	1.2000	13.48
44	YLAVHAKHA	285	1.2000	13.48
45	LVGVSVDSD	300	1.2000	13.48
46	LVTDLTGLE	133	1.1000	12.36
47	MMRYLRALA	471	1.1000	12.36
48	MMGAEGLRA	752	1.1000	12.36
49	LTGLEIANA	137	1.0000	11.24
50	MTLMHRAAR	158	1.0000	11.24
51	FGVAAAAPA	437	1.0000	11.24
52	VLARAKANG	398	0.9000	10.11
53	LRQLVADLQ	528	0.9000	10.11
54	MIGIRAEID	855	0.9000	10.11
55	LNFQTLVTD	128	0.8000	8.99
56	ICLIPSSAH	580	0.8000	8.99
57	VWPAVRRID	913	0.8000	8.99
58	MHRAARGPV	161	0.7000	7.87
59	VKRVVVDAD	169	0.7000	7.87
60	WSALVQQAH	228	0.7000	7.87
61	YRTETSMMR	465	0.7000	7.87
62	LNALVGLAR	668	0.7000	7.87
63	LALQTREQH	315	0.6000	6.74
64	YGFHAPTMS	820	0.6000	6.74
65	VRAHLAPFL	709	0.5500	6.18
66	VIAQLPGAS	214	0.5000	5.62
67	LLAVLAAMY	339	0.5000	5.62
68	VGLARPGKF	672	0.5000	5.62
69	LNLHKTFCI	687	0.5000	5.62
70	LAVKAVPAG	33	0.4500	5.06
71	VSMIGQGYY	82	0.4000	4.49
72	ITDWSALVQ	225	0.4000	4.49
73	LNAAAEMES	499	0.4000	4.49
74	LAGMRVVVV	597	0.4000	4.49

75	LDSLPPAAS	55	0.2000	2.25
76	LRNIIENPA	99	0.2000	2.25
77	LGIEIVTAD	193	0.2000	2.25
78	INLWRVDAD	407	0.2000	2.25
79	YYPVLYTGE	779	0.2000	2.25
80	FRPKVWPAV	909	0.1500	1.69
81	VKAVPAGIL	35	0.1000	1.12
82	FQTLVTDLT	130	0.1000	1.12
83	FGTTQRFGV	266	0.1000	1.12
84	LGTAFRPKV	905	0.0500	0.56
85	LTAITSANY	763	-0.1000	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	LNLHKTFCI	687	4.4000	52.38
2	MMRYLRALA	471	3.2000	38.10
3	VVDADVFTQ	173	3.1000	36.90
4	LVGLARPGK	671	2.9000	34.52
5	LAVHAKHAR	286	2.6000	30.95
6	FLTHPAFTQ	456	2.6000	30.95
7	LAIHEYHAS	564	2.6000	30.95
8	IVTADLRAG	197	2.5000	29.76
9	LQSWLVLIT	535	2.5000	29.76
10	LRGITKLTG	799	2.5000	29.76
11	IRMMGAEGL	750	2.4000	28.57
12	VGPVAVRAH	704	2.3800	28.33
13	LLNFQTLVT	127	2.3000	27.38
14	VRAHLAPFL	709	2.2000	26.19
15	MRYLRALAD	472	2.1000	25.00
16	YGFHAPTMS	820	2.1000	25.00
17	LRGAPHTAQ	877	1.9000	22.62
18	MTLMHRAAR	158	1.8000	21.43

19	VHAKHARQL	288	1.8000	21.43
20	VLLAVLAAM	338	1.8000	21.43
21	MKLNAAAEM	497	1.8000	21.43
22	LALQTREQH	315	1.6800	20.00
23	LTAIARRVH	356	1.6800	20.00
24	ICTAQVLLA	333	1.6000	19.05
25	LRQLVADLQ	528	1.6000	19.05
26	LVLITGYDA	539	1.6000	19.05
27	VYEHDIAEI	642	1.6000	19.05
28	MRVVVVDCH	600	1.5800	18.81
29	VLARAKANG	398	1.5000	17.86
30	ITWAYIRMM	745	1.5000	17.86
31	LMHRAARGP	160	1.4000	16.67
32	VIAQLPGAS	214	1.4000	16.67
33	VSLQPNAGS	548	1.4000	16.67
34	LAGMRVVVV	597	1.4000	16.67
35	MVAHECILD	790	1.4000	16.67
36	LTGLEIANA	137	1.3000	15.48
37	MIPLGSCTM	489	1.3000	15.48
38	LRAKVGEHA	618	1.3000	15.48
39	VGEHAERLS	622	1.3000	15.48
40	LRAASLTAI	758	1.2000	14.29
41	LMITYPSTH	632	1.1800	14.05
42	LAVKAVPAG	33	1.0000	11.90
43	VLLRNIIEN	97	1.0000	11.90
44	MMGAEGLRA	752	1.0000	11.90
45	LAVLAAMYA	340	0.9000	10.71
46	VHAHAEAIA	363	0.9000	10.71
47	LRNIIENPA	99	0.8000	9.52
48	IARRVHAHA	359	0.8000	9.52
49	MGAEGLRAA	753	0.8000	9.52
50	WYTAYTPYQ	108	0.7000	8.33
51	LDAFGVAAA	434	0.7000	8.33
52	VWPAVRRID	913	0.7000	8.33

53	LNFQTLVTD	128	0.6000	7.14
54	FGRQHPFAP	513	0.6000	7.14
55	VVVVDCHDN	602	0.6000	7.14
56	VRRIDGAYG	917	0.6000	7.14
57	VCSCPPVEA	930	0.6000	7.14
58	LDSLPPAAS	55	0.5000	5.95
59	LARAKANGI	399	0.5000	5.95
60	INLWRVDAD	407	0.5000	5.95
61	YGSASILPI	737	0.5000	5.95
62	VFTQTAAVL	178	0.4000	4.76
63	LQTREQHIR	317	0.4000	4.76
64	LGDALVHDK	374	0.4000	4.76
65	LDSQAVATM	13	0.3000	3.57
66	MHRAARGPV	161	0.3000	3.57
67	ITDWSALVQ	225	0.3000	3.57
68	LPGRLVGVS	296	0.3000	3.57
69	LGTAFRPKV	905	0.3000	3.57
70	LLRNIIENP	98	0.2000	2.38
71	VLARVPGRA	387	0.2000	2.38
72	LVQQAHDRG	231	0.1000	1.19
73	LNAAAEMES	499	0.1000	1.19
74	LARPGKFGG	674	0.1000	1.19
75	LAAMYASYH	343	-0.0200	0
76	YTPYQPEIS	112	-0.1000	0
77	FTQYRTETS	462	-0.1000	0
78	LRALADKDI	475	-0.1000	0
79	LIPSSAHGT	582	-0.1000	0
80	LNALVGLAR	668	-0.1000	0
81	YIRMMGAEG	749	-0.1000	0
82	IGLDSQAVA	11	-0.2000	0
83	LLALTLIAP	248	-0.2000	0
84	LVCSCPPVE	929	-0.2000	0
85	VATMLAVIG	18	-0.3000	0
86	LEIANASML	140	-0.3000	0

87	YHGAGGLTA	350	-0.3000	0
88	ITYPSTHGV	634	-0.3000	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	FLTHPAFTQ	456	3.6000	42.86
2	LNLHKTFCI	687	3.4000	40.48
3	YGFHAPTMS	820	3.1000	36.90
4	MMRYLRALA	471	2.2000	26.19
5	VVDADVFTQ	173	2.1000	25.00
6	LVGLARPGK	671	1.9000	22.62
7	WYTAYTPYQ	108	1.7000	20.24
8	LAVHAKHAR	286	1.6000	19.05
9	FGRQHPFAP	513	1.6000	19.05
10	LAIHEYHAS	564	1.6000	19.05
11	IVTADLRAG	197	1.5000	17.86
12	LQSWLVLIT	535	1.5000	17.86
13	YGSASILPI	737	1.5000	17.86
14	LRGITKLTG	799	1.5000	17.86
15	IRMMGAEGL	750	1.4000	16.67
16	VGPVAVRAH	704	1.3800	16.43
17	LLNFQTLVT	127	1.3000	15.48
18	VRAHLAPFL	709	1.2000	14.29
19	MRYLRALAD	472	1.1000	13.10
20	FGVAAAAPA	437	1.0000	11.90
21	YTPYQPEIS	112	0.9000	10.71
22	FTQYRTETS	462	0.9000	10.71
23	YIRMMGAEG	749	0.9000	10.71
24	LRGAPHTAQ	877	0.9000	10.71
25	MTLMHRAAR	158	0.8000	9.52
26	VHAKHARQL	288	0.8000	9.52
27	VLLAVLAAM	338	0.8000	9.52

28	MKLNAAAEM	497	0.8000	9.52
29	YHGAGGLTA	350	0.7000	8.33
30	FRPKVWPAV	909	0.7000	8.33
31	LALQTREQH	315	0.6800	8.10
32	LTAIARRVH	356	0.6800	8.10
33	ICTAQVLLA	333	0.6000	7.14
34	LRQLVADLQ	528	0.6000	7.14
35	LVLITGYDA	539	0.6000	7.14
36	VYEHDIAEI	642	0.6000	7.14
37	MRVVVVDCH	600	0.5800	6.90
38	VLARAKANG	398	0.5000	5.95
39	ITWAYIRMM	745	0.5000	5.95
40	FPVAGTLMV	829	0.5000	5.95
41	LMHRAARGP	160	0.4000	4.76
42	VIAQLPGAS	214	0.4000	4.76
43	VSLQPNAGS	548	0.4000	4.76
44	LAGMRVVVV	597	0.4000	4.76
45	MVAHECILD	790	0.4000	4.76
46	LTGLEIANA	137	0.3000	3.57
47	FGTTQRFGV	266	0.3000	3.57
48	YRLALQTRE	313	0.3000	3.57
49	MIPLGSCTM	489	0.3000	3.57
50	LRAKVGEHA	618	0.3000	3.57
51	VGEHAERLS	622	0.3000	3.57
52	LRAASLTAI	758	0.2000	2.38
53	YGDRNLVCS	924	0.2000	2.38
54	LMITYPSTH	632	0.1800	2.14
55	YLAVHAKHA	285	0.1000	1.19
56	LAVLAAMYA	340	-0.1000	0
57	VHAHAEAIA	363	-0.1000	0
58	WRVDADHVS	410	-0.1000	0
59	WDHPYTREQ	892	-0.1000	0
60	LRNIIENPA	99	-0.2000	0
61	IARRVHAHA	359	-0.2000	0

62	MGAEGLRAA	753	-0.2000	0
63	FQTLVTDLT	130	-0.3000	0
64	LDAFGVAAA	434	-0.3000	0
65	VWPAVRRID	913	-0.3000	0
66	LNFQTLVTD	128	-0.4000	0
67	VVVVDCHDN	602	-0.4000	0
68	FLPGHPFAP	716	-0.4000	0
69	VRRIDGAYG	917	-0.4000	0
70	VCSCPPVEA	930	-0.4000	0
71	LDSLPPAAS	55	-0.5000	0
72	FGVIAQLPG	212	-0.5000	0
73	LARAKANGI	399	-0.5000	0
74	INLWRVDAD	407	-0.5000	0
75	WLVLITGYD	538	-0.5000	0
76	WSALVQQAH	228	-0.5200	0
77	YTAYTPYQP	109	-0.6000	0
78	VFTQTAAVL	178	-0.6000	0
79	LQTREQHIR	317	-0.6000	0
80	LGDALVHDK	374	-0.6000	0
81	LDSQAVATM	13	-0.7000	0
82	MHRAARGPV	161	-0.7000	0
83	ITDWSALVQ	225	-0.7000	0
84	LPGRLVGVS	296	-0.7000	0
85	WAYIRMMGA	747	-0.7000	0
86	LGTAFRPKV	905	-0.7000	0
87	YDTHTPPVL	90	-0.8000	0
88	LLRNIIENP	98	-0.8000	0
89	VLARVPGRA	387	-0.8000	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	LNLHKTFCI	687	5.3000	60.23

2	LAVHAKHAR	286	4.1000	46.59
3	IVTADLRAG	197	3.9000	44.32
4	LRGITKLTG	799	3.9000	44.32
5	IRMMGAEGL	750	3.3600	38.18
6	MTLMHRAAR	158	3.3000	37.50
7	VLLAVLAAM	338	3.3000	37.50
8	MKLNAAAEM	497	3.3000	37.50
9	MMRYLRALA	471	3.2000	36.36
10	MRYLRALAD	472	3.2000	36.36
11	LQSWLVLIT	535	3.2000	36.36
12	VRAHLAPFL	709	3.1600	35.91
13	LLNFQTLVT	127	3.0000	34.09
14	LAIHEYHAS	564	3.0000	34.09
15	LVGLARPGK	671	3.0000	34.09
16	ITWAYIRMM	745	3.0000	34.09
17	VLARAKANG	398	2.9000	32.95
18	MIPLGSCTM	489	2.8000	31.82
19	VHAKHARQL	288	2.7600	31.36
20	VYEHDIAEI	642	2.5000	28.41
21	MVAHECILD	790	2.5000	28.41
22	YGFHAPTMS	820	2.5000	28.41
23	LAVKAVPAG	33	2.4000	27.27
24	LMHRAARGP	160	2.4000	27.27
25	VVDADVFTQ	173	2.4000	27.27
26	LAGMRVVVV	597	2.4000	27.27
27	LRAASLTAI	758	2.1000	23.86
28	VRRIDGAYG	917	2.0000	22.73
29	LQTREQHIR	317	1.9000	21.59
30	FLTHPAFTQ	456	1.9000	21.59
31	LDSQAVATM	13	1.8000	20.45
32	VLLRNIIEN	97	1.8000	20.45
33	VIAQLPGAS	214	1.8000	20.45
34	VSLQPNAGS	548	1.8000	20.45
35	VGPVAVRAH	704	1.8000	20.45

36	VWPAVRRID	913	1.8000	20.45
37	LNFQTLVTD	128	1.7000	19.32
38	VGEHAERLS	622	1.7000	19.32
39	ICTAQVLLA	333	1.6000	18.18
40	INLWRVDAD	407	1.6000	18.18
41	FGRQHPFAP	513	1.6000	18.18
42	LVLITGYDA	539	1.6000	18.18
43	LVQQAHDRG	231	1.5000	17.05
44	LARPGKFGG	674	1.5000	17.05
45	LATRAKPLG	186	1.4000	15.91
46	LARAKANGI	399	1.4000	15.91
47	VVVVDCHDN	602	1.4000	15.91
48	LNALVGLAR	668	1.4000	15.91
49	VGLARPGKF	672	1.4000	15.91
50	YGSASILPI	737	1.4000	15.91
51	VFTQTAAVL	178	1.3600	15.45
52	LTGLEIANA	137	1.3000	14.77
53	MHRAARGPV	161	1.3000	14.77
54	LRAKVGEHA	618	1.3000	14.77
55	YIRMMGAEG	749	1.3000	14.77
56	LGTAFRPKV	905	1.3000	14.77
57	LLRNIIENP	98	1.2000	13.64
58	LRGAPHTAQ	877	1.2000	13.64
59	LVCSCPPVE	929	1.2000	13.64
60	VATMLAVIG	18	1.1000	12.50
61	LALQTREQH	315	1.1000	12.50
62	LTAIARRVH	356	1.1000	12.50
63	MGFGGPHAG	276	1.0000	11.36
64	MRVVVVDCH	600	1.0000	11.36
65	MMGAEGLRA	752	1.0000	11.36
66	LDSLPPAAS	55	0.9000	10.23
67	LAVLAAMYA	340	0.9000	10.23
68	VHAHAEAIA	363	0.9000	10.23
69	LRQLVADLQ	528	0.9000	10.23

70	MITYPSTHG	633	0.9000	10.23
71	LRNIIENPA	99	0.8000	9.09
72	LLALTLIAP	248	0.8000	9.09
73	IARRVHAHA	359	0.8000	9.09
74	LRALADKDI	475	0.8000	9.09
75	MGAEGLRAA	753	0.8000	9.09
76	ITVDDVAKR	808	0.8000	9.09
77	VSDHSTFAD	0	0.7000	7.95
78	LPGRLVGVS	296	0.7000	7.95
79	YRLALQTRE	313	0.7000	7.95
80	LDAFGVAAA	434	0.7000	7.95
81	ITYPSTHGV	634	0.7000	7.95
82	VAVRAHLAP	707	0.7000	7.95
83	FRPKVWPAV	909	0.7000	7.95
84	LEIANASML	140	0.6600	7.50
85	LGIEIVTAD	193	0.6000	6.82
86	VAFGTTQRF	264	0.6000	6.82
87	LIPSSAHGT	582	0.6000	6.82
88	LMITYPSTH	632	0.6000	6.82
89	VCSCPPVEA	930	0.6000	6.82
90	LVGVSVDSD	300	0.5000	5.68
91	LGDALVHDK	374	0.5000	5.68
92	YRTETSMMR	465	0.5000	5.68
93	LNAAAEMES	499	0.5000	5.68
94	VLYTGENGM	782	0.5000	5.68

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	LNLHKTFCI	687	5.3000	60.23
2	LAVHAKHAR	286	4.1000	46.59
3	IVTADLRAG	197	3.9000	44.32
4	LRGITKLTG	799	3.9000	44.32

5	IRMMGAEGL	750	3.3600	38.18
6	MTLMHRAAR	158	3.3000	37.50
7	VLLAVLAAM	338	3.3000	37.50
8	MKLNAAAEM	497	3.3000	37.50
9	MMRYLRALA	471	3.2000	36.36
10	MRYLRALAD	472	3.2000	36.36
11	LQSWLVLIT	535	3.2000	36.36
12	VRAHLAPFL	709	3.1600	35.91
13	LLNFQTLVT	127	3.0000	34.09
14	LAIHEYHAS	564	3.0000	34.09
15	LVGLARPGK	671	3.0000	34.09
16	ITWAYIRMM	745	3.0000	34.09
17	VLARAKANG	398	2.9000	32.95
18	MIPLGSCTM	489	2.8000	31.82
19	VHAKHARQL	288	2.7600	31.36
20	VYEHDIAEI	642	2.5000	28.41
21	MVAHECILD	790	2.5000	28.41
22	YGFHAPTMS	820	2.5000	28.41
23	LAVKAVPAG	33	2.4000	27.27
24	LMHRAARGP	160	2.4000	27.27
25	VVDADVFTQ	173	2.4000	27.27
26	LAGMRVVVV	597	2.4000	27.27
27	LRAASLTAI	758	2.1000	23.86
28	VRRIDGAYG	917	2.0000	22.73
29	LQTREQHIR	317	1.9000	21.59
30	FLTHPAFTQ	456	1.9000	21.59
31	LDSQAVATM	13	1.8000	20.45
32	VLLRNIIEN	97	1.8000	20.45
33	VIAQLPGAS	214	1.8000	20.45
34	VSLQPNAGS	548	1.8000	20.45
35	VGPVAVRAH	704	1.8000	20.45
36	VWPAVRRID	913	1.8000	20.45
37	LNFQTLVTD	128	1.7000	19.32
38	VGEHAERLS	622	1.7000	19.32

39	ICTAQVLLA	333	1.6000	18.18
40	INLWRVDAD	407	1.6000	18.18
41	FGRQHPFAP	513	1.6000	18.18
42	LVLITGYDA	539	1.6000	18.18
43	LVQQAHDRG	231	1.5000	17.05
44	LARPGKFGG	674	1.5000	17.05
45	LATRAKPLG	186	1.4000	15.91
46	LARAKANGI	399	1.4000	15.91
47	VVVVDCHDN	602	1.4000	15.91
48	LNALVGLAR	668	1.4000	15.91
49	VGLARPGKF	672	1.4000	15.91
50	YGSASILPI	737	1.4000	15.91
51	VFTQTAAVL	178	1.3600	15.45
52	LTGLEIANA	137	1.3000	14.77
53	MHRAARGPV	161	1.3000	14.77
54	LRAKVGEHA	618	1.3000	14.77
55	YIRMMGAEG	749	1.3000	14.77
56	LGTAFRPKV	905	1.3000	14.77
57	LLRNIIENP	98	1.2000	13.64
58	LRGAPHTAQ	877	1.2000	13.64
59	LVCSCPPVE	929	1.2000	13.64
60	VATMLAVIG	18	1.1000	12.50
61	LALQTREQH	315	1.1000	12.50
62	LTAIARRVH	356	1.1000	12.50
63	MGFGGPHAG	276	1.0000	11.36
64	MRVVVVDCH	600	1.0000	11.36
65	MMGAEGLRA	752	1.0000	11.36
66	LDSLPPAAS	55	0.9000	10.23
67	LAVLAAMYA	340	0.9000	10.23
68	VHAHAEAIA	363	0.9000	10.23
69	LRQLVADLQ	528	0.9000	10.23
70	MITYPSTHG	633	0.9000	10.23
71	LRNIIENPA	99	0.8000	9.09
72	LLALTLIAP	248	0.8000	9.09

73	IARRVHAHA	359	0.8000	9.09
74	LRALADKDI	475	0.8000	9.09
75	MGAEGLRAA	753	0.8000	9.09
76	ITVDDVAKR	808	0.8000	9.09
77	VSDHSTFAD	0	0.7000	7.95
78	LPGRLVGVS	296	0.7000	7.95
79	YRLALQTRE	313	0.7000	7.95
80	LDAFGVAAA	434	0.7000	7.95
81	ITYPSTHGV	634	0.7000	7.95
82	VAVRAHLAP	707	0.7000	7.95
83	FRPKVWPAV	909	0.7000	7.95
84	LEIANASML	140	0.6600	7.50
85	LGIEIVTAD	193	0.6000	6.82
86	VAFGTTQRF	264	0.6000	6.82
87	LIPSSAHGT	582	0.6000	6.82
88	LMITYPSTH	632	0.6000	6.82
89	VCSCPPVEA	930	0.6000	6.82
90	LVGVSVDSD	300	0.5000	5.68
91	LGDALVHDK	374	0.5000	5.68
92	YRTETSMMR	465	0.5000	5.68
93	LNAAAEMES	499	0.5000	5.68
94	VLYTGENGM	782	0.5000	5.68

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	LLNFQTLVT	127	5.5600	56.73
2	MMRYLRALA	471	5.3000	54.08
3	LNLHKTFCI	687	4.9600	50.61
4	LVLITGYDA	539	4.9000	50.00
5	IRMMGAEGL	750	4.4000	44.90
6	VRAHLAPFL	709	4.1000	41.84
7	LRGITKLTG	799	3.8000	38.78

8	MMGAEGLRA	752	3.7000	37.76
9	MITYPSTHG	633	3.6000	36.73
10	LVHDKYFDT	378	3.5000	35.71
11	MRYLRALAD	472	3.5000	35.71
12	ITGYDAVSL	542	3.5000	35.71
13	LAIHEYHAS	564	3.3000	33.67
14	LRAASLTAI	758	3.3000	33.67
15	LQSWLVLIT	535	3.2000	32.65
16	VRRIDGAYG	917	3.2000	32.65
17	LRNIIENPA	99	3.0000	30.61
18	MHRAARGPV	161	2.8000	28.57
19	MVAHECILD	790	2.8000	28.57
20	ITKLTGITV	802	2.8000	28.57
21	LAVLAAMYA	340	2.7000	27.55
22	LRALADKDI	475	2.7000	27.55
23	LNALVGLAR	668	2.7000	27.55
24	MIPLGSCTM	489	2.5800	26.33
25	VLLRNIIEN	97	2.5500	26.02
26	LEALLNFQT	124	2.5000	25.51
27	LEIANASML	140	2.4000	24.49
28	YHGAGGLTA	350	2.4000	24.49
29	VVLDAFGVA	432	2.4000	24.49
30	YVDGANLNA	662	2.4000	24.49
31	LVGLARPGK	671	2.4000	24.49
32	YGSASILPI	737	2.3500	23.98
33	VTDLTGLEI	134	2.3000	23.47
34	VLLAVLAAM	338	2.2800	23.27
35	VLITGYDAV	540	2.2000	22.45
36	VVVVDCHDN	602	2.2000	22.45
37	ILPITWAYI	742	2.2000	22.45
38	WAYIRMMGA	747	2.2000	22.45
39	VIGVDSLDD	24	2.1000	21.43
40	LRALADANT	71	2.1000	21.43
41	LVAVGADLL	241	2.1000	21.43

42	LLALTLIAP	248	2.1000	21.43
43	LARAKANGI	399	2.1000	21.43
44	LGTAFRPKV	905	2.1000	21.43
45	VAHECILDL	791	2.0500	20.92
46	MTLMHRAAR	158	2.0000	20.41
47	VAVGADLLA	242	2.0000	20.41
48	MKLNAAAEM	497	1.9800	20.20
49	VVVDADVFT	172	1.9000	19.39
50	FGTTQRFGV	266	1.9000	19.39
51	YRTETSMMR	465	1.9000	19.39
52	LYTGENGMV	783	1.9000	19.39
53	VKAVPAGIL	35	1.8000	18.37
54	IALDRSMIP	483	1.8000	18.37
55	MLAVIGVDS	21	1.7000	17.35
56	LVADLQSWL	531	1.7000	17.35
57	ICTAQVLLA	333	1.6000	16.33
58	IHEYHASRG	566	1.6000	16.33
59	VYEHDIAEI	642	1.5500	15.82
60	IRRDKATSN	324	1.5000	15.31
61	LIPSSAHGT	582	1.5000	15.31
62	LAGMRVVVV	597	1.5000	15.31
63	YIRMMGAEG	749	1.5000	15.31
64	MIGQGYYDT	84	1.4000	14.29
65	YASYHGAGG	347	1.4000	14.29
66	ICLIPSSAH	580	1.4000	14.29
67	LAPFLPGHP	713	1.4000	14.29
68	ITYPSTHGV	634	1.3600	13.88
69	IGADVAFGT	260	1.3000	13.27
70	LQPNAGSQG	550	1.3000	13.27
71	LLAIHEYHA	563	1.3000	13.27
72	LRAKVGEHA	618	1.3000	13.27
73	LMITYPSTH	632	1.3000	13.27
74	VLYTGENGM	782	1.2800	13.06
75	VDSLDDLAV	27	1.2000	12.24

76	WRVDADHVS	410	1.2000	12.24
77	LNAAAEMES	499	1.2000	12.24
78	FPVAGTLMV	829	1.1600	11.84
79	VTADLRAGL	198	1.1000	11.22
80	ITSANYIAR	766	1.1000	11.22
81	YGFHAPTMS	820	1.1000	11.22
82	IVTADLRAG	197	1.0000	10.20
83	VLARVPGRA	387	1.0000	10.20
84	VSHLNLHKT	684	1.0000	10.20
85	VAVRAHLAP	707	1.0000	10.20
86	IGIRAEIDK	856	1.0000	10.20
87	FRPKVWPAV	909	1.0000	10.20
88	YTAYTPYQP	109	0.9000	9.18
89	VLATRAKPL	185	0.9000	9.18
90	FGVIAQLPG	212	0.9000	9.18
91	MGFGGPHAG	276	0.9000	9.18
92	LAVHAKHAR	286	0.9000	9.18
93	VHAHAEAIA	363	0.9000	9.18
94	FLTHPAFTQ	456	0.9000	9.18

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	LLNFQTLVT	127	4.5600	46.53
2	MMRYLRALA	471	4.3000	43.88
3	LNLHKTFCI	687	3.9600	40.41
4	LVLITGYDA	539	3.9000	39.80
5	YHGAGGLTA	350	3.4000	34.69
6	YVDGANLNA	662	3.4000	34.69
7	IRMMGAEGL	750	3.4000	34.69
8	YGSASILPI	737	3.3500	34.18
9	WAYIRMMGA	747	3.2000	32.65
10	VRAHLAPFL	709	3.1000	31.63

11	FGTTQRFGV	266	2.9000	29.59
12	YRTETSMMR	465	2.9000	29.59
13	LRGITKLTG	799	2.8000	28.57
14	MMGAEGLRA	752	2.7000	27.55
15	MITYPSTHG	633	2.6000	26.53
16	LVHDKYFDT	378	2.5000	25.51
17	MRYLRALAD	472	2.5000	25.51
18	ITGYDAVSL	542	2.5000	25.51
19	YIRMMGAEG	749	2.5000	25.51
20	YASYHGAGG	347	2.4000	24.49
21	LAIHEYHAS	564	2.3000	23.47
22	LRAASLTAI	758	2.3000	23.47
23	WRVDADHVS	410	2.2000	22.45
24	LQSWLVLIT	535	2.2000	22.45
25	VRRIDGAYG	917	2.2000	22.45
26	FPVAGTLMV	829	2.1600	22.04
27	YGFHAPTMS	820	2.1000	21.43
28	LRNIIENPA	99	2.0000	20.41
29	FRPKVWPAV	909	2.0000	20.41
30	YTAYTPYQP	109	1.9000	19.39
31	FGVIAQLPG	212	1.9000	19.39
32	FLTHPAFTQ	456	1.9000	19.39
33	MHRAARGPV	161	1.8000	18.37
34	FGVPMGFGG	272	1.8000	18.37
35	YTGENGMVA	784	1.8000	18.37
36	MVAHECILD	790	1.8000	18.37
37	ITKLTGITV	802	1.8000	18.37
38	LAVLAAMYA	340	1.7000	17.35
39	LRALADKDI	475	1.7000	17.35
40	LNALVGLAR	668	1.7000	17.35
41	YTPYQPEIS	112	1.6000	16.33
42	MIPLGSCTM	489	1.5800	16.12
43	VLLRNIIEN	97	1.5500	15.82
44	LEALLNFQT	124	1.5000	15.31

45	FTQYRTETS	462	1.4600	14.90
46	LEIANASML	140	1.4000	14.29
47	VVLDAFGVA	432	1.4000	14.29
48	LVGLARPGK	671	1.4000	14.29
49	FLPGHPFAP	716	1.4000	14.29
50	WPAVRRIDG	914	1.4000	14.29
51	VTDLTGLEI	134	1.3000	13.27
52	VLLAVLAAM	338	1.2800	13.06
53	VLITGYDAV	540	1.2000	12.24
54	VVVVDCHDN	602	1.2000	12.24
55	ILPITWAYI	742	1.2000	12.24
56	VIGVDSLDD	24	1.1000	11.22
57	LRALADANT	71	1.1000	11.22
58	LVAVGADLL	241	1.1000	11.22
59	LLALTLIAP	248	1.1000	11.22
60	LARAKANGI	399	1.1000	11.22
61	LGTAFRPKV	905	1.1000	11.22
62	VAHECILDL	791	1.0500	10.71
63	MTLMHRAAR	158	1.0000	10.20
64	VAVGADLLA	242	1.0000	10.20
65	FGVAAAAPA	437	1.0000	10.20
66	MKLNAAAEM	497	0.9800	10.00
67	VVVDADVFT	172	0.9000	9.18
68	FGGPHAGYL	278	0.9000	9.18
69	YLAVHAKHA	285	0.9000	9.18
70	FCIPHGGGG	693	0.9000	9.18
71	LYTGENGMV	783	0.9000	9.18
72	VKAVPAGIL	35	0.8000	8.16
73	IALDRSMIP	483	0.8000	8.16
74	YPLGTAFRP	903	0.8000	8.16
75	FQTLVTDLT	130	0.7600	7.76
76	MLAVIGVDS	21	0.7000	7.14
77	YRLALQTRE	313	0.7000	7.14
78	LVADLQSWL	531	0.7000	7.14

79	ICTAQVLLA	333	0.6000	6.12
80	IHEYHASRG	566	0.6000	6.12
81	VYEHDIAEI	642	0.5500	5.61
82	IRRDKATSN	324	0.5000	5.10
83	FGRQHPFAP	513	0.5000	5.10
84	LIPSSAHGT	582	0.5000	5.10
85	LAGMRVVVV	597	0.5000	5.10
86	MIGQGYYDT	84	0.4000	4.08
87	YDTHTPPVL	90	0.4000	4.08
88	ICLIPSSAH	580	0.4000	4.08
89	LAPFLPGHP	713	0.4000	4.08
90	ITYPSTHGV	634	0.3600	3.67
91	IGADVAFGT	260	0.3000	3.06
92	WPEFGRQHP	510	0.3000	3.06
93	LQPNAGSQG	550	0.3000	3.06
94	YAGLLAIHE	560	0.3000	3.06

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	LLNFQTLVT	127	5.5600	56.73
2	MMRYLRALA	471	5.3000	54.08
3	LNLHKTFCI	687	4.9600	50.61
4	LVLITGYDA	539	4.9000	50.00
5	IRMMGAEGL	750	4.4000	44.90
6	VRAHLAPFL	709	4.1000	41.84
7	LRGITKLTG	799	3.8000	38.78
8	MMGAEGLRA	752	3.7000	37.76
9	MITYPSTHG	633	3.6000	36.73
10	LVHDKYFDT	378	3.5000	35.71
11	MRYLRALAD	472	3.5000	35.71
12	ITGYDAVSL	542	3.5000	35.71
13	LAIHEYHAS	564	3.3000	33.67

14	LRAASLTAI	758	3.3000	33.67
15	LQSWLVLIT	535	3.2000	32.65
16	VRRIDGAYG	917	3.2000	32.65
17	LRNIIENPA	99	3.0000	30.61
18	MHRAARGPV	161	2.8000	28.57
19	MVAHECILD	790	2.8000	28.57
20	ITKLTGITV	802	2.8000	28.57
21	LAVLAAMYA	340	2.7000	27.55
22	LRALADKDI	475	2.7000	27.55
23	LNALVGLAR	668	2.7000	27.55
24	MIPLGSCTM	489	2.5800	26.33
25	VLLRNIIEN	97	2.5500	26.02
26	LEALLNFQT	124	2.5000	25.51
27	LEIANASML	140	2.4000	24.49
28	YHGAGGLTA	350	2.4000	24.49
29	VVLDAFGVA	432	2.4000	24.49
30	YVDGANLNA	662	2.4000	24.49
31	LVGLARPGK	671	2.4000	24.49
32	YGSASILPI	737	2.3500	23.98
33	VTDLTGLEI	134	2.3000	23.47
34	VLLAVLAAM	338	2.2800	23.27
35	VLITGYDAV	540	2.2000	22.45
36	VVVVDCHDN	602	2.2000	22.45
37	ILPITWAYI	742	2.2000	22.45
38	WAYIRMMGA	747	2.2000	22.45
39	VIGVDSLDD	24	2.1000	21.43
40	LRALADANT	71	2.1000	21.43
41	LVAVGADLL	241	2.1000	21.43
42	LLALTLIAP	248	2.1000	21.43
43	LARAKANGI	399	2.1000	21.43
44	LGTAFRPKV	905	2.1000	21.43
45	VAHECILDL	791	2.0500	20.92
46	MTLMHRAAR	158	2.0000	20.41
47	VAVGADLLA	242	2.0000	20.41

48	MKLNAAAEM	497	1.9800	20.20
49	VVVDADVFT	172	1.9000	19.39
50	FGTTQRFGV	266	1.9000	19.39
51	YRTETSMMR	465	1.9000	19.39
52	LYTGENGMV	783	1.9000	19.39
53	VKAVPAGIL	35	1.8000	18.37
54	IALDRSMIP	483	1.8000	18.37
55	MLAVIGVDS	21	1.7000	17.35
56	LVADLQSWL	531	1.7000	17.35
57	ICTAQVLLA	333	1.6000	16.33
58	IHEYHASRG	566	1.6000	16.33
59	VYEHDIAEI	642	1.5500	15.82
60	IRRDKATSN	324	1.5000	15.31
61	LIPSSAHGT	582	1.5000	15.31
62	LAGMRVVVV	597	1.5000	15.31
63	YIRMMGAEG	749	1.5000	15.31
64	MIGQGYYDT	84	1.4000	14.29
65	YASYHGAGG	347	1.4000	14.29
66	ICLIPSSAH	580	1.4000	14.29
67	LAPFLPGHP	713	1.4000	14.29
68	ITYPSTHGV	634	1.3600	13.88
69	IGADVAFGT	260	1.3000	13.27
70	LQPNAGSQG	550	1.3000	13.27
71	LLAIHEYHA	563	1.3000	13.27
72	LRAKVGEHA	618	1.3000	13.27
73	LMITYPSTH	632	1.3000	13.27
74	VLYTGENGM	782	1.2800	13.06
75	VDSLDDLAV	27	1.2000	12.24
76	WRVDADHVS	410	1.2000	12.24
77	LNAAAEMES	499	1.2000	12.24
78	FPVAGTLMV	829	1.1600	11.84
79	VTADLRAGL	198	1.1000	11.22
80	ITSANYIAR	766	1.1000	11.22
81	YGFHAPTMS	820	1.1000	11.22

82	IVTADLRAG	197	1.0000	10.20
83	VLARVPGRA	387	1.0000	10.20
84	VSHLNLHKT	684	1.0000	10.20
85	VAVRAHLAP	707	1.0000	10.20
86	IGIRAEIDK	856	1.0000	10.20
87	FRPKVWPAV	909	1.0000	10.20
88	YTAYTPYQP	109	0.9000	9.18
89	VLATRAKPL	185	0.9000	9.18
90	FGVIAQLPG	212	0.9000	9.18
91	MGFGGPHAG	276	0.9000	9.18
92	LAVHAKHAR	286	0.9000	9.18
93	VHAHAEAIA	363	0.9000	9.18
94	FLTHPAFTQ	456	0.9000	9.18

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	IRMMGAEGL	750	4.7000	47.96
2	LVLITGYDA	539	4.3000	43.88
3	LPITWAYIR	743	4.0000	40.82
4	VVVVDCHDN	602	3.9000	39.80
5	YIRMMGAEG	749	3.6000	36.73
6	YRTETSMMR	465	3.3000	33.67
7	VRRIDGAYG	917	3.3000	33.67
8	LNALVGLAR	668	3.2000	32.65
9	VKAVPAGIL	35	3.1000	31.63
10	YLAVHAKHA	285	3.0000	30.61
11	YQPEISQGR	115	2.9000	29.59
12	MTLMHRAAR	158	2.9000	29.59
13	LMITYPSTH	632	2.9000	29.59
14	ILDLRGITK	796	2.9000	29.59
15	IEIVTADLR	195	2.7000	27.55
16	LVGLARPGK	671	2.7000	27.55

17	VLATRAKPL	185	2.5000	25.51
18	VGLARPGKF	672	2.5000	25.51
19	LLAVLAAMY	339	2.4000	24.49
20	LHKTFCIPH	689	2.3000	23.47
21	LRGITKLTG	799	2.2000	22.45
22	FFGVIAQLP	211	2.0000	20.41
23	LVAVGADLL	241	2.0000	20.41
24	VSMIGQGYY	82	1.9000	19.39
25	FGVIAQLPG	212	1.9000	19.39
26	LRALADKDI	475	1.9000	19.39
27	VGPVAVRAH	704	1.9000	19.39
28	ITSANYIAR	766	1.9000	19.39
29	IVTADLRAG	197	1.8000	18.37
30	FLTHPAFTQ	456	1.8000	18.37
31	LEIANASML	140	1.7000	17.35
32	MRYLRALAD	472	1.7000	17.35
33	LRAASLTAI	758	1.7000	17.35
34	ICLIPSSAH	580	1.6000	16.33
35	LRNIIENPA	99	1.5000	15.31
36	YRLALQTRE	313	1.5000	15.31
37	LAAMYASYH	343	1.5000	15.31
38	LARAKANGI	399	1.4000	14.29
39	FGRQHPFAP	513	1.4000	14.29
40	YAGLLAIHE	560	1.4000	14.29
41	FAPELPKGY	722	1.4000	14.29
42	YHGAGGLTA	350	1.3000	13.27
43	LTAIARRVH	356	1.3000	13.27
44	LNLHKTFCI	687	1.3000	13.27
45	MLAVIGVDS	21	1.2000	12.24
46	IGIRAEIDK	856	1.2000	12.24
47	LRGAPHTAQ	877	1.2000	12.24
48	FGVPMGFGG	272	1.1000	11.22
49	FGGPHAGYL	278	1.1000	11.22
50	YGSASILPI	737	1.1000	11.22

51	ILPITWAYI	742	1.1000	11.22
52	LTAITSANY	763	1.1000	11.22
53	YGFHAPTMS	820	1.1000	11.22
54	FGVAAAAPA	437	1.0000	10.20
55	MIPLGSCTM	489	1.0000	10.20
56	LRQLVADLQ	528	1.0000	10.20
57	MRVVVVDCH	600	1.0000	10.20
58	WAYIRMMGA	747	1.0000	10.20
59	YYPVLYTGE	779	1.0000	10.20
60	VIAQLPGAS	214	0.9000	9.18
61	IPLGSCTMK	490	0.9000	9.18
62	LIPSSAHGT	582	0.9000	9.18
63	WPAVRRIDG	914	0.9000	9.18
64	VATMLAVIG	18	0.8000	8.16
65	FGTTQRFGV	266	0.8000	8.16
66	LQTREQHIR	317	0.8000	8.16
67	LGDALVHDK	374	0.8000	8.16
68	VVDADVFTQ	173	0.7000	7.14
69	VHAKHARQL	288	0.7000	7.14
70	WRVDADHVS	410	0.7000	7.14
71	FCIPHGGGG	693	0.7000	7.14
72	WSALVQQAH	228	0.6000	6.12
73	FLPGHPFAP	716	0.6000	6.12
74	MMGAEGLRA	752	0.6000	6.12
75	MGFGGPHAG	276	0.5000	5.10
76	VLLAVLAAM	338	0.5000	5.10
77	LAVLAAMYA	340	0.5000	5.10
78	LLAIHEYHA	563	0.5000	5.10
79	VRAHLAPFL	709	0.5000	5.10
80	FCEAMIGIR	851	0.5000	5.10
81	VFTQTAAVL	178	0.4000	4.08
82	WLVLITGYD	538	0.4000	4.08
83	YPVLYTGEN	780	0.4000	4.08
84	LTLIAPPGE	251	0.3000	3.06

85	LAVHAKHAR	286	0.3000	3.06
86	IRRDKATSN	324	0.3000	3.06
87	VLAAMYASY	342	0.3000	3.06
88	FDTVLARVP	384	0.3000	3.06
89	LARVPGRAD	388	0.3000	3.06
90	ITKLTGITV	802	0.3000	3.06
91	WYTAYTPYQ	108	0.2000	2.04
92	VHDAGGQVY	654	0.2000	2.04
93	YHASRGEPH	569	0.1000	1.02
94	IAEICAAVH	647	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	IRMMGAEGL	750	4.7000	47.96
2	LVLITGYDA	539	4.3000	43.88
3	LPITWAYIR	743	4.0000	40.82
4	VVVVDCHDN	602	3.9000	39.80
5	YIRMMGAEG	749	3.6000	36.73
6	YRTETSMMR	465	3.3000	33.67
7	VRRIDGAYG	917	3.3000	33.67
8	LNALVGLAR	668	3.2000	32.65
9	VKAVPAGIL	35	3.1000	31.63
10	YLAVHAKHA	285	3.0000	30.61
11	YQPEISQGR	115	2.9000	29.59
12	MTLMHRAAR	158	2.9000	29.59
13	LMITYPSTH	632	2.9000	29.59
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22	FFGVIAQLP	211	2.0000	20.41
23	LVAVGADLL	241	2.0000	20.41
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27	VGPVAVRAH	704	1.9000	19.39
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29	IVTADLRAG	197	1.8000	18.37
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31	LEIANASML	140	1.7000	17.35
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66	LQTREQHIR	317	0.8000	8.16
67	LGDALVHDK	374	0.8000	8.16
68	VVDADVFTQ	173	0.7000	7.14
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