MHC Class-II Binding Peptide Prediction Results

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INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Mon Feb 1 13:23:14 2010
Length of input sequence	449 amino acids
Number of nanomers from input sequence	441
Number of nanomers with obligatory P1 anchor residue	135
Threshold setting	3
Number of alleles in query	51
Number of top scorers to be displayed	44

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	VRLAVGIEG	412	1.7000	28.33
2	LVIHPASTT	385	1.5000	25.00
3	FELAGGIEA	354	1.4000	23.33
4	FLVAQGLET	290	1.3000	21.67
5	YLGGHGAAI	220	0.9000	15.00
6	FVNALKLHS	366	0.6000	10.00
7	FGLEIPGNI	57	0.5000	8.33
8	VRSLVIHPA	382	0.5000	8.33
9	FAILNLAGA	102	0.4000	6.67
10	IVVHSATKY	212	0.0900	1.50
11	LGFAAARRF	430	-0.0100	0
12	YTRIGNPTT	66	-0.0300	0
13	FHYSLAKLG	128	-0.1000	0
14	YLIQPLAQG	201	-0.2000	0

15	VVHSATKYL	213	-0.3000	0
16	YNLFHYSLA	125	-0.3200	0
17	VQLLRDYGS	274	-0.4000	0
18	LRIERHVAN	301	-0.4000	0
19	YHGVVFAEL	255	-0.6500	0
20	WQAAVRPNT	151	-0.7300	0
21	ILNLAGAGD	104	-0.8000	0
22	VFAELGPPA	259	-0.8300	0
23	FAELGPPAF	260	-0.8300	0
24	VRPNTKAFF	155	-0.8600	0
25	LVAQGLETL	291	-0.9000	0
26	LGGHGAAIA	221	-1.0000	0
27	IHPASTTHA	387	-1.0100	0
28	FNAFLVAQG	287	-1.0200	0
29	YGSAASPFN	280	-1.0300	0
30	YAGLPSSPW	328	-1.1000	0
31	IDLLDTPAV	172	-1.2300	0
32	LSFELAGGI	352	-1.3000	0
33	VLSVNYAGL	323	-1.3500	0
34	VVEQRIAAL	76	-1.4000	0
35	LNLAGAGDH	105	-1.4000	0
36	LHSHVANIG	372	-1.4000	0
37	LVRLAVGIE	411	-1.4000	0
38	IGDVRSLVI	379	-1.4500	0
39	IAALEGGVA	81	-1.5000	0
40	FAAARRFSA	432	-1.5000	0
41	IYATTSYTF	39	-1.6000	0
42	LGIEVSFVD	135	-1.6000	0

ALLELE: DRB1_0102	Threshold for 3 % with score: 0.7	Highest Score achievable by any peptide: 6

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLAVGIEG	412	2.7000	45.00
2	LVIHPASTT	385	2.5000	41.67
3	VRSLVIHPA	382	1.5000	25.00
4	FELAGGIEA	354	1.4000	23.33
5	FLVAQGLET	290	1.3000	21.67

6	IVVHSATKY	212	1.0900	18.17
7	LFLSSGQAA	91	1.0000	16.67
8	LGFAAARRF	430	0.9900	16.50
9	VVHSATKYL	213	0.7000	11.67
10	VQLLRDYGS	274	0.6000	10.00
11	LRIERHVAN	301	0.6000	10.00
12	FVNALKLHS	366	0.6000	10.00
13	FGLEIPGNI	57	0.5000	8.33
14	FAILNLAGA	102	0.4000	6.67
15	ILNLAGAGD	104	0.2000	3.33
16	VFAELGPPA	259	0.1700	2.83
17	VRPNTKAFF	155	0.1400	2.33
18	LVAQGLETL	291	0.1000	1.67
19	IHPASTTHA	387	-0.0100	0
20	FHYSLAKLG	128	-0.1000	0
21	YLGGHGAAI	220	-0.1000	0
22	IDLLDTPAV	172	-0.2300	0
23	LSFELAGGI	352	-0.3000	0
24	VLSVNYAGL	323	-0.3500	0
25	VVEQRIAAL	76	-0.4000	0
26	LNLAGAGDH	105	-0.4000	0
27	LHSHVANIG	372	-0.4000	0
28	LVRLAVGIE	411	-0.4000	0
29	IGDVRSLVI	379	-0.4500	0
30	IAALEGGVA	81	-0.5000	0
31	IYATTSYTF	39	-0.6000	0
32	LGIEVSFVD	135	-0.6000	0
33	LIQPLAQGA	202	-0.6000	0
34	LELGFAAAR	428	-0.6000	0
35	VNYAGLPSS	326	-0.6300	0
36	IVSSPRLYG	114	-0.7000	0
37	LATGVSPGL	403	-0.7300	0
38	LEGGVAALF	84	-0.8000	0
39	FAELGPPAF	260	-0.8300	0
40	VPLIVDNTI	189	-0.9000	0
41	LEIPGNIYT	59	-1.0000	0
42	LSSGQAAET	93	-1.0000	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	VRPNTKAFF	155	4.9000	51.58
2	IVSSPRLYG	114	4.6000	48.42
3	LIVDNTIAT	191	4.6000	48.42
4	FVNALKLHS	366	4.2000	44.21
5	LVRLAVGIE	411	3.8000	40.00
6	VNYAGLPSS	326	3.6000	37.89
7	LLRDYGSAA	276	3.3700	35.47
8	VRLAVGIEG	412	3.3000	34.74
9	LVIHPASTT	385	3.1700	33.37
10	ILADLELGF	424	3.0000	31.58
11	YTFDDTAHA	45	2.9000	30.53
12	VVFAELGPP	258	2.9000	30.53
13	VVHSATKYL	213	2.8600	30.11
14	IVVHSATKY	212	2.8000	29.47
15	VHSATKYLG	214	2.6500	27.89
16	VIVDGGNFD	231	2.5100	26.42
17	VRSLVIHPA	382	2.3000	24.21
18	LRIERHVAN	301	2.2000	23.16
19	YLIQPLAQG	201	2.1000	22.11
20	LELGFAAAR	428	2.1000	22.11
21	LVAQGLETL	291	2.0600	21.68
22	LFGLEIPGN	56	1.8000	18.95
23	IHPASTTHA	387	1.8000	18.95
24	LEGGVAALF	84	1.7000	17.89
25	LFLSSGQAA	91	1.7000	17.89
26	VGIEGIDDI	416	1.7000	17.89
27	IHAGQHPDP	22	1.6000	16.84
28	LAKLGIEVS	132	1.6000	16.84
29	IEVSFVDDP	137	1.6000	16.84
30	LKLHSHVAN	370	1.6000	16.84
31	VVEQRIAAL	76	1.5600	16.42
32	IDLLDTPAV	172	1.5000	15.79
33	LNLAGAGDH	105	1.4000	14.74
34	WQAAVRPNT	151	1.4000	14.74
35	IVDNTIATP	192	1.4000	14.74
36	VANAQRVAE	307	1.4000	14.74
37	LHSHVANIG	372	1.3100	13.79

38	LGFAAARRF	430	1.3000	13.68
39	IAGVIVDGG	228	1.2000	12.63
40	LATGVSPGL	403	1.0600	11.16
41	LYGGTYNLF	120	1.0100	10.63
42	LPIYATTSY	37	1.0000	10.53
43	LRDYGSAAS	277	0.9000	9.47
44	MSADSNSTD	0	0.8700	9.16

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	FVNALKLHS	366	4.8000	52.75
2	YTFDDTAHA	45	3.9000	42.86
3	LIVDNTIAT	191	2.9000	31.87
4	LLRDYGSAA	276	2.3700	26.04
5	IVSSPRLYG	114	2.2000	24.18
6	VNYAGLPSS	326	2.2000	24.18
7	VRPNTKAFF	155	2.0000	21.98
8	FSADPQSVA	438	1.7700	19.45
9	FAILNLAGA	102	1.7000	18.68
10	WQAAVRPNT	151	1.7000	18.68
11	YLIQPLAQG	201	1.7000	18.68
12	FAAARRFSA	432	1.5000	16.48
13	LVIHPASTT	385	1.4700	16.15
14	LVRLAVGIE	411	1.4000	15.38
15	VRSLVIHPA	382	1.3000	14.29
16	LNLAGAGDH	105	0.9800	10.77
17	VVHSATKYL	213	0.9000	9.89
18	VVFAELGPP	258	0.9000	9.89
19	VRLAVGIEG	412	0.9000	9.89
20	FGLEIPGNI	57	0.8000	8.79
21	FELAGGIEA	354	0.8000	8.79
22	IHPASTTHA	387	0.8000	8.79
23	WSFETKQIH	15	0.7800	8.57
24	LFLSSGQAA	91	0.7000	7.69
25	YLGGHGAAI	220	0.7000	7.69
26	IVVHSATKY	212	0.5000	5.49

27	VIVDGGNFD	231	0.4100	4.51
28	FHYSLAKLG	128	0.4000	4.40
29	LRIERHVAN	301	0.4000	4.40
30	VHSATKYLG	214	0.2500	2.75
31	IERHVANAQ	303	0.2100	2.31
32	LAKLGIEVS	132	0.2000	2.20
33	FALKARVQL	268	0.2000	2.20
34	YTRIGNPTT	66	0.1000	1.10
35	LVAQGLETL	291	0.1000	1.10
36	ILADLELGF	424	0.1000	1.10
37	FLSSGQAAE	92	-0.1000	0
38	YGSAASPFN	280	-0.1000	0
39	FLVAQGLET	290	-0.2000	0
40	LKLHSHVAN	370	-0.2000	0
41	VSPGLVRLA	407	-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	FVNALKLHS	366	4.3000	48.86
2	IVSSPRLYG	114	3.7000	42.05
3	LIVDNTIAT	191	3.5800	40.68
4	LLRDYGSAA	276	3.1000	35.23
5	VRSLVIHPA	382	3.1000	35.23
6	VRPNTKAFF	155	3.0000	34.09
7	YTFDDTAHA	45	2.9000	32.95
8	VVHSATKYL	213	2.5000	28.41
9	LVIHPASTT	385	2.2000	25.00
10	VIVDGGNFD	231	2.1000	23.86
11	IERHVANAQ	303	1.9000	21.59
12	LFLSSGQAA	91	1.8000	20.45
13	VNYAGLPSS	326	1.8000	20.45
14	IHPASTTHA	387	1.8000	20.45
15	LAKLGIEVS	132	1.6000	18.18
16	ILADLELGF	424	1.6000	18.18
17	VRLAVGIEG	412	1.5800	17.95
18	IVVHSATKY	212	1.5000	17.05

19	LVAQGLETL	291	1.5000	17.05
20	LRIERHVAN	301	1.2800	14.55
21	VGIEGIDDI	416	1.1000	12.50
22	VNALKLHSH	367	1.0800	12.27
23	LVRLAVGIE	411	1.0000	11.36
24	IEVSFVDDP	137	0.9000	10.23
25	FAILNLAGA	102	0.7000	7.95
26	YLIQPLAQG	201	0.7000	7.95
27	LGGHGAAIA	221	0.7000	7.95
28	LKLHSHVAN	370	0.6800	7.73
29	VVEQRIAAL	76	0.6000	6.82
30	LHSHVANIG	372	0.6000	6.82
31	LELGFAAAR	428	0.6000	6.82
32	LNLAGAGDH	105	0.5800	6.59
33	VVFAELGPP	258	0.5000	5.68
34	LRDYGSAAS	277	0.5000	5.68
35	VSPGLVRLA	407	0.5000	5.68
36	FSADPQSVA	438	0.5000	5.68
37	IVDNTIATP	192	0.4000	4.55
38	VIHPASTTH	386	0.1800	2.05
39	LIQPLAQGA	202	0.1000	1.14
40	VHSATKYLG	214	0.1000	1.14
41	IAGVIVDGG	228	0.1000	1.14
42	WSFETKQIH	15	-0.1200	0

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	FVNALKLHS	366	4.3000	48.86
2	IVSSPRLYG	114	3.7000	42.05
3	LIVDNTIAT	191	3.5800	40.68
4	LLRDYGSAA	276	3.1000	35.23
5	VRSLVIHPA	382	3.1000	35.23
6	VRPNTKAFF	155	3.0000	34.09
7	YTFDDTAHA	45	2.9000	32.95
8	VVHSATKYL	213	2.5000	28.41
9	LVIHPASTT	385	2.2000	25.00

10	VIVDGGNFD	231	2.1000	23.86
11	IERHVANAQ	303	1.9000	21.59
12	LFLSSGQAA	91	1.8000	20.45
13	VNYAGLPSS	326	1.8000	20.45
14	IHPASTTHA	387	1.8000	20.45
15	LAKLGIEVS	132	1.6000	18.18
16	ILADLELGF	424	1.6000	18.18
17	VRLAVGIEG	412	1.5800	17.95
18	IVVHSATKY	212	1.5000	17.05
19	LVAQGLETL	291	1.5000	17.05
20	LRIERHVAN	301	1.2800	14.55
21	VGIEGIDDI	416	1.1000	12.50
22	VNALKLHSH	367	1.0800	12.27
23	LVRLAVGIE	411	1.0000	11.36
24	IEVSFVDDP	137	0.9000	10.23
25	FAILNLAGA	102	0.7000	7.95
26	YLIQPLAQG	201	0.7000	7.95
27	LGGHGAAIA	221	0.7000	7.95
28	LKLHSHVAN	370	0.6800	7.73
29	VVEQRIAAL	76	0.6000	6.82
30	LHSHVANIG	372	0.6000	6.82
31	LELGFAAAR	428	0.6000	6.82
32	LNLAGAGDH	105	0.5800	6.59
33	VVFAELGPP	258	0.5000	5.68
34	LRDYGSAAS	277	0.5000	5.68
35	VSPGLVRLA	407	0.5000	5.68
36	FSADPQSVA	438	0.5000	5.68
37	IVDNTIATP	192	0.4000	4.55
38	VIHPASTTH	386	0.1800	2.05
39	LIQPLAQGA	202	0.1000	1.14
40	VHSATKYLG	214	0.1000	1.14
41	IAGVIVDGG	228	0.1000	1.14
42	WSFETKQIH	15	-0.1200	0

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	FVNALKLHS	366	4.3000	48.86
2	IVSSPRLYG	114	3.7000	42.05
3	LIVDNTIAT	191	3.5800	40.68
4	LLRDYGSAA	276	3.1000	35.23
5	VRSLVIHPA	382	3.1000	35.23
6	VRPNTKAFF	155	3.0000	34.09
7	YTFDDTAHA	45	2.9000	32.95
8	VVHSATKYL	213	2.5000	28.41
9	LVIHPASTT	385	2.2000	25.00
10	VIVDGGNFD	231	2.1000	23.86
11	IERHVANAQ	303	1.9000	21.59
12	LFLSSGQAA	91	1.8000	20.45
13	VNYAGLPSS	326	1.8000	20.45
14	IHPASTTHA	387	1.8000	20.45
15	LAKLGIEVS	132	1.6000	18.18
16	ILADLELGF	424	1.6000	18.18
17	VRLAVGIEG	412	1.5800	17.95
18	IVVHSATKY	212	1.5000	17.05
19	LVAQGLETL	291	1.5000	17.05
20	LRIERHVAN	301	1.2800	14.55
21	VGIEGIDDI	416	1.1000	12.50
22	VNALKLHSH	367	1.0800	12.27
23	LVRLAVGIE	411	1.0000	11.36
24	IEVSFVDDP	137	0.9000	10.23
25	FAILNLAGA	102	0.7000	7.95
26	YLIQPLAQG	201	0.7000	7.95
27	LGGHGAAIA	221	0.7000	7.95
28	LKLHSHVAN	370	0.6800	7.73
29	VVEQRIAAL	76	0.6000	6.82
30	LHSHVANIG	372	0.6000	6.82
31	LELGFAAAR	428	0.6000	6.82
32	LNLAGAGDH	105	0.5800	6.59
33	VVFAELGPP	258	0.5000	5.68
34	LRDYGSAAS	277	0.5000	5.68
35	VSPGLVRLA	407	0.5000	5.68
36	FSADPQSVA	438	0.5000	5.68
37	IVDNTIATP	192	0.4000	4.55
38	VIHPASTTH	386	0.1800	2.05
39	LIQPLAQGA	202	0.1000	1.14
40	VHSATKYLG	214	0.1000	1.14
41	IAGVIVDGG	228	0.1000	1.14

42	WSFETKQIH	15	-0.1200	0

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	FVNALKLHS	366	5.2000	54.74
2	YTFDDTAHA	45	3.9000	41.05
3	VRPNTKAFF	155	3.9000	41.05
4	IVSSPRLYG	114	3.6000	37.89
5	LIVDNTIAT	191	3.6000	37.89
6	YLIQPLAQG	201	3.1000	32.63
7	LVRLAVGIE	411	2.8000	29.47
8	VNYAGLPSS	326	2.6000	27.37
9	WQAAVRPNT	151	2.4000	25.26
10	LLRDYGSAA	276	2.3700	24.95
11	VRLAVGIEG	412	2.3000	24.21
12	LVIHPASTT	385	2.1700	22.84
13	ILADLELGF	424	2.0000	21.05
14	VVFAELGPP	258	1.9000	20.00
15	VVHSATKYL	213	1.8600	19.58
16	FHYSLAKLG	128	1.8000	18.95
17	IVVHSATKY	212	1.8000	18.95
18	FSADPQSVA	438	1.7700	18.63
19	FGLEIPGNI	57	1.7000	17.89
20	FAILNLAGA	102	1.7000	17.89
21	VHSATKYLG	214	1.6500	17.37
22	YLGGHGAAI	220	1.6000	16.84
23	VIVDGGNFD	231	1.5100	15.89
24	FAAARRFSA	432	1.5000	15.79
25	FNAFLVAQG	287	1.4000	14.74
26	FLSSGQAAE	92	1.3000	13.68
27	VRSLVIHPA	382	1.3000	13.68
28	LRIERHVAN	301	1.2000	12.63
29	FALKARVQL	268	1.1600	12.21
30	LELGFAAAR	428	1.1000	11.58
31	LVAQGLETL	291	1.0600	11.16
32	FAELGPPAF	260	0.9000	9.47

33	LFGLEIPGN	56	0.8000	8.42
34	YTRIGNPTT	66	0.8000	8.42
35	FELAGGIEA	354	0.8000	8.42
36	IHPASTTHA	387	0.8000	8.42
37	LEGGVAALF	84	0.7000	7.37
38	LFLSSGQAA	91	0.7000	7.37
39	YSLAKLGIE	130	0.7000	7.37
40	WTQGRFPGF	240	0.7000	7.37
41	YGSAASPFN	280	0.7000	7.37
42	VGIEGIDDI	416	0.7000	7.37
43	IHAGQHPDP	22	0.6000	6.32
44	LAKLGIEVS	132	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	FVNALKLHS	366	4.3000	48.86
2	IVSSPRLYG	114	3.7000	42.05
3	LIVDNTIAT	191	3.5800	40.68
4	LLRDYGSAA	276	3.1000	35.23
5	VRSLVIHPA	382	3.1000	35.23
6	VRPNTKAFF	155	3.0000	34.09
7	YTFDDTAHA	45	2.9000	32.95
8	VVHSATKYL	213	2.5000	28.41
9	LVIHPASTT	385	2.2000	25.00
10	VIVDGGNFD	231	2.1000	23.86
11	IERHVANAQ	303	1.9000	21.59
12	LFLSSGQAA	91	1.8000	20.45
13	VNYAGLPSS	326	1.8000	20.45
14	IHPASTTHA	387	1.8000	20.45
15	LAKLGIEVS	132	1.6000	18.18
16	ILADLELGF	424	1.6000	18.18
17	VRLAVGIEG	412	1.5800	17.95
18	IVVHSATKY	212	1.5000	17.05
19	LVAQGLETL	291	1.5000	17.05
20	LRIERHVAN	301	1.2800	14.55
21	VGIEGIDDI	416	1.1000	12.50

22	VNALKLHSH	367	1.0800	12.27
23	LVRLAVGIE	411	1.0000	11.36
24	IEVSFVDDP	137	0.9000	10.23
25	FAILNLAGA	102	0.7000	7.95
26	YLIQPLAQG	201	0.7000	7.95
27	LGGHGAAIA	221	0.7000	7.95
28	LKLHSHVAN	370	0.6800	7.73
29	VVEQRIAAL	76	0.6000	6.82
30	LHSHVANIG	372	0.6000	6.82
31	LELGFAAAR	428	0.6000	6.82
32	LNLAGAGDH	105	0.5800	6.59
33	VVFAELGPP	258	0.5000	5.68
34	LRDYGSAAS	277	0.5000	5.68
35	VSPGLVRLA	407	0.5000	5.68
36	FSADPQSVA	438	0.5000	5.68
37	IVDNTIATP	192	0.4000	4.55
38	VIHPASTTH	386	0.1800	2.05
39	LIQPLAQGA	202	0.1000	1.14
40	VHSATKYLG	214	0.1000	1.14
41	IAGVIVDGG	228	0.1000	1.14
42	WSFETKQIH	15	-0.1200	0

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	YTFDDTAHA	45	4.1000	47.67
2	YGGTYNLFH	121	3.4800	40.47
3	LIVDNTIAT	191	2.7800	32.33
4	VVHSATKYL	213	2.7000	31.40
5	LVIHPASTT	385	2.3000	26.74
6	VRSLVIHPA	382	2.1000	24.42
7	IERHVANAQ	303	2.0000	23.26
8	IHPASTTHA	387	1.9000	22.09
9	VGIEGIDDI	416	1.8000	20.93
10	FAETISNPQ	163	1.6000	18.60
11	IVVHSATKY	212	1.6000	18.60
12	FVNALKLHS	366	1.6000	18.60

13	LRIERHVAN	301	1.4800	17.21
14	FGLEIPGNI	57	1.4000	16.28
15	FAILNLAGA	102	1.2000	13.95
16	YLIQPLAQG	201	1.2000	13.95
17	FHYSLAKLG	128	1.1000	12.79
18	YTRIGNPTT	66	0.9000	10.47
19	LGIEVSFVD	135	0.8000	9.30
20	LGGHGAAIA	221	0.8000	9.30
21	YAGLPSSPW	328	0.8000	9.30
22	FFAETISNP	162	0.7000	8.14
23	LHSHVANIG	372	0.7000	8.14
24	LAKLGIEVS	132	0.6000	6.98
25	LVRLAVGIE	411	0.5000	5.81
26	VQLLRDYGS	274	0.4000	4.65
27	LLRDYGSAA	276	0.4000	4.65
28	LFLSSGQAA	91	0.1000	1.16
29	VANIGDVRS	376	-0.0200	0
30	FNAFLVAQG	287	-0.2000	0
31	VRLAVGIEG	412	-0.2200	0
32	IEVSFVDDP	137	-0.3000	0
33	WSFETKQIH	15	-0.3200	0
34	FELAGGIEA	354	-0.3200	0
35	VIHPASTTH	386	-0.3200	0
36	VVEQRIAAL	76	-0.4000	0
37	YGSAASPFN	280	-0.4000	0
38	LNLAGAGDH	105	-0.4200	0
39	VNALKLHSH	367	-0.4200	0
40	MSADSNSTD	0	-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	LVIHPASTT	385	3.2000	33.33
2	IERHVANAQ	303	3.1000	32.29
3	IHPASTTHA	387	3.1000	32.29
4	IVVHSATKY	212	2.9000	30.21
5	VVHSATKYL	213	2.2000	22.92

6	LRDYGSAAS	277	2.2000	22.92
7	VRSLVIHPA	382	2.2000	22.92
8	VQLLRDYGS	274	2.1000	21.88
9	LGFAAARRF	430	2.0000	20.83
10	LGGHGAAIA	221	1.9000	19.79
11	VSPGLVRLA	407	1.9000	19.79
12	LHSHVANIG	372	1.8000	18.75
13	LPIYATTSY	37	1.6000	16.67
14	YGGTYNLFH	121	1.5800	16.46
15	IYATTSYTF	39	1.3000	13.54
16	VRLAVGIEG	412	1.2000	12.50
17	VIHPASTTH	386	1.1800	12.29
18	LEIPGNIYT	59	0.9000	9.38
19	LIQPLAQGA	202	0.9000	9.38
20	IVDGGNFDW	232	0.9000	9.38
21	FVNALKLHS	366	0.9000	9.38
22	LAARDDVLS	317	0.8000	8.33
23	LKLHSHVAN	370	0.7000	7.29
24	LKARVQLLR	270	0.6000	6.25
25	LIVDNTIAT	191	0.5000	5.21
26	LFLSSGQAA	91	0.4000	4.17
27	VANIGDVRS	376	0.3800	3.96
28	LSLRIERHV	299	0.3000	3.12
29	VNYAGLPSS	326	0.2000	2.08
30	IGDVRSLVI	379	0.2000	2.08
31	IYTRIGNPT	65	-0.2000	0
32	LNLAGAGDH	105	-0.2200	0
33	VPLIVDNTI	189	-0.2200	0
34	IEGIDDILA	418	-0.2200	0
35	VNALKLHSH	367	-0.3200	0
36	LGIEVSFVD	135	-0.5000	0
37	LAPKGTGAV	343	-0.5000	0
38	YTFDDTAHA	45	-0.6000	0
39	VVEQRIAAL	76	-0.6000	0
40	VEQRIAALE	77	-0.6000	0
41	FAETISNPQ	163	-0.6000	0
42	VLSFELAGG	351	-0.6000	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	IHPASTTHA	387	3.4000	38.64
2	VRSLVIHPA	382	2.9000	32.95
3	VQLLRDYGS	274	2.6000	29.55
4	LRDYGSAAS	277	2.2000	25.00
5	LPIYATTSY	37	1.9000	21.59
6	LVIHPASTT	385	1.9000	21.59
7	LVRLAVGIE	411	1.8000	20.45
8	VIHPASTTH	386	1.4800	16.82
9	LIVDNTIAT	191	1.2800	14.55
10	VVHSATKYL	213	1.2000	13.64
11	VANIGDVRS	376	1.1000	12.50
12	IVVHSATKY	212	1.0000	11.36
13	IERHVANAQ	303	1.0000	11.36
14	LAKLGIEVS	132	0.9000	10.23
15	IDLLDTPAV	172	0.9000	10.23
16	VPLIVDNTI	189	0.9000	10.23
17	YNLFHYSLA	125	0.8000	9.09
18	VRLAVGIEG	412	0.7800	8.86
19	FNAFLVAQG	287	0.7000	7.95
20	YAGLPSSPW	328	0.7000	7.95
21	IGDVRSLVI	379	0.7000	7.95
22	LNLAGAGDH	105	0.6800	7.73
23	YTFDDTAHA	45	0.6000	6.82
24	LEIPGNIYT	59	0.4800	5.45
25	YGGTYNLFH	121	0.4800	5.45
26	FAILNLAGA	102	0.4000	4.55
27	VNALKLHSH	367	0.3800	4.32
28	IEGIDDILA	418	0.3800	4.32
29	VNYAGLPSS	326	0.2000	2.27
30	FVNALKLHS	366	0.2000	2.27
31	LGIEVSFVD	135	0.1500	1.70
32	VLSFELAGG	351	0.1000	1.14
33	YTRIGNPTT	66	-0.1000	0
34	IYATTSYTF	39	-0.2000	0
35	VVEQRIAAL	76	-0.2000	0
36	IGNPTTDVV	69	-0.3000	0
37	LGGHGAAIA	221	-0.3000	0

38	LRIERHVAN	301	-0.3000	0
39	LHSHVANIG	372	-0.3000	0
40	LIQPLAQGA	202	-0.4000	0
41	LLRDYGSAA	276	-0.4000	0
42	LFGLEIPGN	56	-0.5000	0
43	VAALFLSSG	88	-0.6000	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	LVRLAVGIE	411	3.8000	40.43
2	FNAFLVAQG	287	3.0000	31.91
3	YGGTYNLFH	121	2.7000	28.72
4	YAGLPSSPW	328	2.6000	27.66
5	IHPASTTHA	387	2.4000	25.53
6	LPIYATTSY	37	2.0000	21.28
7	VRSLVIHPA	382	1.9000	20.21
8	LGIEVSFVD	135	1.8500	19.68
9	YTRIGNPTT	66	1.8000	19.15
10	YNLFHYSLA	125	1.8000	19.15
11	LVIHPASTT	385	1.8000	19.15
12	YLIQPLAQG	201	1.7000	18.09
13	VIHPASTTH	386	1.7000	18.09
14	YTFDDTAHA	45	1.6000	17.02
15	VQLLRDYGS	274	1.6000	17.02
16	FAILNLAGA	102	1.4000	14.89
17	YGSAASPFN	280	1.3000	13.83
18	VVHSATKYL	213	1.2000	12.77
19	LRDYGSAAS	277	1.2000	12.77
20	FVNALKLHS	366	1.2000	12.77
21	LIVDNTIAT	191	1.1800	12.55
22	IVVHSATKY	212	1.1000	11.70
23	VRLAVGIEG	412	1.0800	11.49
24	ILNLAGAGD	104	1.0000	10.64
25	LNLAGAGDH	105	0.9000	9.57
26	FAETISNPQ	163	0.9000	9.57
27	IERHVANAQ	303	0.8000	8.51

28	FPGFTTPDP	245	0.7000	7.45
29	LRIERHVAN	301	0.7000	7.45
30	VNALKLHSH	367	0.6000	6.38
31	LFGLEIPGN	56	0.5000	5.32
32	FTTPDPSYH	248	0.5000	5.32
33	MSADSNSTD	0	0.4000	4.26
34	YHGVVFAEL	255	0.4000	4.26
35	VLSFELAGG	351	0.4000	4.26
36	LEIPGNIYT	59	0.3800	4.04
37	FLSSGQAAE	92	0.3000	3.19
38	IDLLDTPAV	172	0.2000	2.13
39	VPLIVDNTI	189	0.1000	1.06
40	VANIGDVRS	376	0.1000	1.06
41	FHYSLAKLG	128	-0.1000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	IHPASTTHA	387	2.4000	27.27
2	VRSLVIHPA	382	1.9000	21.59
3	YNLFHYSLA	125	1.8000	20.45
4	FNAFLVAQG	287	1.7000	19.32
5	YAGLPSSPW	328	1.7000	19.32
6	YTFDDTAHA	45	1.6000	18.18
7	VQLLRDYGS	274	1.6000	18.18
8	YGGTYNLFH	121	1.4800	16.82
9	FAILNLAGA	102	1.4000	15.91
10	LRDYGSAAS	277	1.2000	13.64
11	FVNALKLHS	366	1.2000	13.64
12	LPIYATTSY	37	0.9000	10.23
13	YTRIGNPTT	66	0.9000	10.23
14	LVIHPASTT	385	0.9000	10.23
15	LVRLAVGIE	411	0.8000	9.09
16	VIHPASTTH	386	0.4800	5.45
17	YLIQPLAQG	201	0.4000	4.55
18	FPGFTTPDP	245	0.3000	3.41
19	LIVDNTIAT	191	0.2800	3.18

20	VVHSATKYL	213	0.2000	2.27
21	FAETISNPQ	163	0.1000	1.14
22	VANIGDVRS	376	0.1000	1.14
23	LAKLGIEVS	132	-0.1000	0
24	IDLLDTPAV	172	-0.1000	0
25	VPLIVDNTI	189	-0.1000	0
26	VRLAVGIEG	412	-0.2200	0
27	IGDVRSLVI	379	-0.3000	0
28	LNLAGAGDH	105	-0.3200	0
29	FELAGGIEA	354	-0.3200	0
30	LEIPGNIYT	59	-0.5200	0
31	YHGVVFAEL	255	-0.6000	0
32	VNALKLHSH	367	-0.6200	0
33	IEGIDDILA	418	-0.6200	0
34	YGSAASPFN	280	-0.7000	0
35	FTTPDPSYH	248	-0.7200	0
36	VNYAGLPSS	326	-0.8000	0
37	LGIEVSFVD	135	-0.8500	0
38	FLVAQGLET	290	-0.9000	0
39	VLSFELAGG	351	-0.9000	0
40	FGLEIPGNI	57	-1.1000	0
41	IYATTSYTF	39	-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	LVRLAVGIE	411	4.8000	51.06
2	IHPASTTHA	387	3.4000	36.17
3	LPIYATTSY	37	3.0000	31.91
4	VRSLVIHPA	382	2.9000	30.85
5	LGIEVSFVD	135	2.8500	30.32
6	LVIHPASTT	385	2.8000	29.79
7	VIHPASTTH	386	2.7000	28.72
8	VQLLRDYGS	274	2.6000	27.66
9	VVHSATKYL	213	2.2000	23.40
10	LRDYGSAAS	277	2.2000	23.40
11	LIVDNTIAT	191	2.1800	23.19

12	IVVHSATKY	212	2.1000	22.34
13	VRLAVGIEG	412	2.0800	22.13
14	ILNLAGAGD	104	2.0000	21.28
15	FNAFLVAQG	287	2.0000	21.28
16	LNLAGAGDH	105	1.9000	20.21
17	IERHVANAQ	303	1.8000	19.15
18	YGGTYNLFH	121	1.7000	18.09
19	LRIERHVAN	301	1.7000	18.09
20	YAGLPSSPW	328	1.6000	17.02
21	VNALKLHSH	367	1.6000	17.02
22	LFGLEIPGN	56	1.5000	15.96
23	MSADSNSTD	0	1.4000	14.89
24	VLSFELAGG	351	1.4000	14.89
25	LEIPGNIYT	59	1.3800	14.68
26	IDLLDTPAV	172	1.2000	12.77
27	VPLIVDNTI	189	1.1000	11.70
28	VANIGDVRS	376	1.1000	11.70
29	LHSHVANIG	372	1.0000	10.64
30	LAKLGIEVS	132	0.9000	9.57
31	IGDVRSLVI	379	0.9000	9.57
32	YTRIGNPTT	66	0.8000	8.51
33	VVEQRIAAL	76	0.8000	8.51
34	YNLFHYSLA	125	0.8000	8.51
35	IQPLAQGAD	203	0.8000	8.51
36	VAEFLAARD	313	0.8000	8.51
37	IYATTSYTF	39	0.7000	7.45
38	VAALFLSSG	88	0.7000	7.45
39	YLIQPLAQG	201	0.7000	7.45
40	IAGVIVDGG	228	0.7000	7.45
41	VIVDGGNFD	231	0.7000	7.45
42	YTFDDTAHA	45	0.6000	6.38
43	FAILNLAGA	102	0.4000	4.26
44	LETLSLRIE	296	0.4000	4.26

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	YTFDDTAHA	45	4.1000	45.56
2	VVHSATKYL	213	3.6600	40.67
3	LIVDNTIAT	191	3.4800	38.67
4	LVIHPASTT	385	3.0000	33.33
5	YGGTYNLFH	121	2.9000	32.22
6	IVVHSATKY	212	2.9000	32.22
7	VGIEGIDDI	416	2.7000	30.00
8	YLIQPLAQG	201	2.6000	28.89
9	FHYSLAKLG	128	2.5000	27.78
10	FGLEIPGNI	57	2.3000	25.56
11	LRIERHVAN	301	2.2800	25.33
12	LHSHVANIG	372	2.1000	23.33
13	VRSLVIHPA	382	2.1000	23.33
14	FVNALKLHS	366	2.0000	22.22
15	LGIEVSFVD	135	1.9000	21.11
16	IHPASTTHA	387	1.9000	21.11
17	LVRLAVGIE	411	1.9000	21.11
18	FFAETISNP	162	1.7000	18.89
19	YTRIGNPTT	66	1.6000	17.78
20	IYATTSYTF	39	1.3000	14.44
21	IERHVANAQ	303	1.3000	14.44
22	FAILNLAGA	102	1.2000	13.33
23	FNAFLVAQG	287	1.2000	13.33
24	VRLAVGIEG	412	1.1800	13.11
25	LAKLGIEVS	132	1.0000	11.11
26	IDLLDTPAV	172	1.0000	11.11
27	LVAQGLETL	291	0.9600	10.67
28	VRPNTKAFF	155	0.9000	10.00
29	FAETISNPQ	163	0.9000	10.00
30	IVSSPRLYG	114	0.8000	8.89
31	LGGHGAAIA	221	0.8000	8.89
32	VQLLRDYGS	274	0.8000	8.89
33	YAGLPSSPW	328	0.8000	8.89
34	IEVSFVDDP	137	0.7000	7.78
35	MSADSNSTD	0	0.6000	6.67
36	ILADLELGF	424	0.6000	6.67
37	VVEQRIAAL	76	0.5600	6.22
38	LPIYATTSY	37	0.5000	5.56
39	VIVDGGNFD	231	0.5000	5.56
40	VPLIVDNTI	189	0.4000	4.44
41	LLRDYGSAA	276	0.4000	4.44

42	LRDYGSAAS	277	0.4000	4.44
43	YGSAASPFN	280	0.4000	4.44
44	VANIGDVRS	376	0.3800	4.22

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	IHPASTTHA	387	3.4000	38.64
2	VRSLVIHPA	382	2.9000	32.95
3	VQLLRDYGS	274	2.6000	29.55
4	LRDYGSAAS	277	2.2000	25.00
5	LPIYATTSY	37	1.9000	21.59
6	LVIHPASTT	385	1.9000	21.59
7	LVRLAVGIE	411	1.8000	20.45
8	VIHPASTTH	386	1.4800	16.82
9	LIVDNTIAT	191	1.2800	14.55
10	VVHSATKYL	213	1.2000	13.64
11	VANIGDVRS	376	1.1000	12.50
12	IVVHSATKY	212	1.0000	11.36
13	IERHVANAQ	303	1.0000	11.36
14	LAKLGIEVS	132	0.9000	10.23
15	IDLLDTPAV	172	0.9000	10.23
16	VPLIVDNTI	189	0.9000	10.23
17	YNLFHYSLA	125	0.8000	9.09
18	VRLAVGIEG	412	0.7800	8.86
19	FNAFLVAQG	287	0.7000	7.95
20	YAGLPSSPW	328	0.7000	7.95
21	IGDVRSLVI	379	0.7000	7.95
22	LNLAGAGDH	105	0.6800	7.73
23	YTFDDTAHA	45	0.6000	6.82
24	LEIPGNIYT	59	0.4800	5.45
25	YGGTYNLFH	121	0.4800	5.45
26	FAILNLAGA	102	0.4000	4.55
27	VNALKLHSH	367	0.3800	4.32
28	IEGIDDILA	418	0.3800	4.32
29	VNYAGLPSS	326	0.2000	2.27
30	FVNALKLHS	366	0.2000	2.27

31	LGIEVSFVD	135	0.1500	1.70
32	VLSFELAGG	351	0.1000	1.14
33	YTRIGNPTT	66	-0.1000	0
34	IYATTSYTF	39	-0.2000	0
35	VVEQRIAAL	76	-0.2000	0
36	IGNPTTDVV	69	-0.3000	0
37	LGGHGAAIA	221	-0.3000	0
38	LRIERHVAN	301	-0.3000	0
39	LHSHVANIG	372	-0.3000	0
40	LIQPLAQGA	202	-0.4000	0
41	LLRDYGSAA	276	-0.4000	0
42	LFGLEIPGN	56	-0.5000	0
43	VAALFLSSG	88	-0.6000	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	YTFDDTAHA	45	4.1000	47.67
2	YGGTYNLFH	121	3.4800	40.47
3	LIVDNTIAT	191	2.7800	32.33
4	VVHSATKYL	213	2.7000	31.40
5	LVIHPASTT	385	2.3000	26.74
6	VRSLVIHPA	382	2.1000	24.42
7	IERHVANAQ	303	2.0000	23.26
8	IHPASTTHA	387	1.9000	22.09
9	VGIEGIDDI	416	1.8000	20.93
10	FAETISNPQ	163	1.6000	18.60
11	IVVHSATKY	212	1.6000	18.60
12	FVNALKLHS	366	1.6000	18.60
13	LRIERHVAN	301	1.4800	17.21
14	FGLEIPGNI	57	1.4000	16.28
15	FAILNLAGA	102	1.2000	13.95
16	YLIQPLAQG	201	1.2000	13.95
17	FHYSLAKLG	128	1.1000	12.79
18	YTRIGNPTT	66	0.9000	10.47
19	LGIEVSFVD	135	0.8000	9.30
20	LGGHGAAIA	221	0.8000	9.30

21	YAGLPSSPW	328	0.8000	9.30
22	FFAETISNP	162	0.7000	8.14
23	LHSHVANIG	372	0.7000	8.14
24	LAKLGIEVS	132	0.6000	6.98
25	LVRLAVGIE	411	0.5000	5.81
26	VQLLRDYGS	274	0.4000	4.65
27	LLRDYGSAA	276	0.4000	4.65
28	LFLSSGQAA	91	0.1000	1.16
29	VANIGDVRS	376	-0.0200	0
30	FNAFLVAQG	287	-0.2000	0
31	VRLAVGIEG	412	-0.2200	0
32	IEVSFVDDP	137	-0.3000	0
33	WSFETKQIH	15	-0.3200	0
34	FELAGGIEA	354	-0.3200	0
35	VIHPASTTH	386	-0.3200	0
36	VVEQRIAAL	76	-0.4000	0
37	YGSAASPFN	280	-0.4000	0
38	LNLAGAGDH	105	-0.4200	0
39	VNALKLHSH	367	-0.4200	0
40	MSADSNSTD	0	-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	VVHSATKYL	213	6.6200	57.07
2	IYATTSYTF	39	5.7000	49.14
3	IGDVRSLVI	379	5.3000	45.69
4	YHGVVFAEL	255	4.5000	38.79
5	IVVHSATKY	212	3.7000	31.90
6	FALKARVQL	268	3.6000	31.03
7	YGGTYNLFH	121	3.5000	30.17
8	FLVAQGLET	290	3.5000	30.17
9	VLSVNYAGL	323	3.5000	30.17
10	LVIHPASTT	385	3.5000	30.17
11	FVNALKLHS	366	3.4000	29.31
12	VRLAVGIEG	412	3.4000	29.31
13	IVSSPRLYG	114	3.3000	28.45

14	LGFAAARRF	430	3.1000	26.72
15	FGLEIPGNI	57	3.0000	25.86
16	FHYSLAKLG	128	3.0000	25.86
17	LVAQGLETL	291	3.0000	25.86
18	VPLIVDNTI	189	2.9000	25.00
19	YLGGHGAAI	220	2.9000	25.00
20	FELAGGIEA	354	2.9000	25.00
21	LFLSSGQAA	91	2.8000	24.14
22	VAHRNGVPL	183	2.5000	21.55
23	LIVDNTIAT	191	1.7200	14.83
24	LATGVSPGL	403	1.7000	14.66
25	LEIPGNIYT	59	1.6000	13.79
26	LFHYSLAKL	127	1.6000	13.79
27	VDNTIATPY	193	1.6000	13.79
28	LRIERHVAN	301	1.6000	13.79
29	LYGGTYNLF	120	1.5000	12.93
30	LSFELAGGI	352	1.5000	12.93
31	LKLHSHVAN	370	1.5000	12.93
32	YTRIGNPTT	66	1.4000	12.07
33	YNLFHYSLA	125	1.4000	12.07
34	VRPNTKAFF	155	1.4000	12.07
35	LLDTPAVSE	174	1.4000	12.07
36	VVEQRIAAL	76	1.3000	11.21
37	FLSSGQAAE	92	1.3000	11.21
38	FAETISNPQ	163	1.3000	11.21
39	YAGLPSSPW	328	1.2000	10.34
40	VGIEGIDDI	416	1.2000	10.34
41	LGIEVSFVD	135	1.1000	9.48
42	LPIYATTSY	37	1.0200	8.79
43	IVDGGNFDW	232	1.0000	8.62
44	VRSLVIHPA	382	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	VVHSATKYL	213	6.6200	57.07
2	IYATTSYTF	39	5.7000	49.14

3	IGDVRSLVI	379	5.3000	45.69
4	YHGVVFAEL	255	4.5000	38.79
5	IVVHSATKY	212	3.7000	31.90
6	FALKARVQL	268	3.6000	31.03
7	YGGTYNLFH	121	3.5000	30.17
8	FLVAQGLET	290	3.5000	30.17
9	VLSVNYAGL	323	3.5000	30.17
10	LVIHPASTT	385	3.5000	30.17
11	FVNALKLHS	366	3.4000	29.31
12	VRLAVGIEG	412	3.4000	29.31
13	IVSSPRLYG	114	3.3000	28.45
14	LGFAAARRF	430	3.1000	26.72
15	FGLEIPGNI	57	3.0000	25.86
16	FHYSLAKLG	128	3.0000	25.86
17	LVAQGLETL	291	3.0000	25.86
18	VPLIVDNTI	189	2.9000	25.00
19	YLGGHGAAI	220	2.9000	25.00
20	FELAGGIEA	354	2.9000	25.00
21	LFLSSGQAA	91	2.8000	24.14
22	VAHRNGVPL	183	2.5000	21.55
23	LIVDNTIAT	191	1.7200	14.83
24	LATGVSPGL	403	1.7000	14.66
25	LEIPGNIYT	59	1.6000	13.79
26	LFHYSLAKL	127	1.6000	13.79
27	VDNTIATPY	193	1.6000	13.79
28	LRIERHVAN	301	1.6000	13.79
29	LYGGTYNLF	120	1.5000	12.93
30	LSFELAGGI	352	1.5000	12.93
31	LKLHSHVAN	370	1.5000	12.93
32	YTRIGNPTT	66	1.4000	12.07
33	YNLFHYSLA	125	1.4000	12.07
34	VRPNTKAFF	155	1.4000	12.07
35	LLDTPAVSE	174	1.4000	12.07
36	VVEQRIAAL	76	1.3000	11.21
37	FLSSGQAAE	92	1.3000	11.21
38	FAETISNPQ	163	1.3000	11.21
39	YAGLPSSPW	328	1.2000	10.34
40	VGIEGIDDI	416	1.2000	10.34
41	LGIEVSFVD	135	1.1000	9.48
42	LPIYATTSY	37	1.0200	8.79
43	IVDGGNFDW	232	1.0000	8.62

44	VRSLVIHPA	382	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	LVRLAVGIE	411	4.5000	52.33
2	FVNALKLHS	366	4.3000	50.00
3	FALKARVQL	268	3.2000	37.21
4	FNAFLVAQG	287	2.8000	32.56
5	VEQRIAALE	77	2.7000	31.40
6	VRPNTKAFF	155	2.7000	31.40
7	LRDYGSAAS	277	2.7000	31.40
8	WHERAKRLA	336	2.6000	30.23
9	FETKQIHAG	17	2.5000	29.07
10	FAILNLAGA	102	2.4000	27.91
11	LFHYSLAKL	127	2.4000	27.91
12	YLIQPLAQG	201	2.0000	23.26
13	VRSLVIHPA	382	1.9000	22.09
14	YSLAKLGIE	130	1.7000	19.77
15	LNLAGAGDH	105	1.6000	18.60
16	ILNLAGAGD	104	1.5000	17.44
17	LAPKGTGAV	343	1.5000	17.44
18	IQPLAQGAD	203	1.4000	16.28
19	IVSSPRLYG	114	1.3000	15.12
20	FLSSGQAAE	92	1.2000	13.95
21	VLSFELAGG	351	1.2000	13.95
22	LRIERHVAN	301	1.1000	12.79
23	VNALKLHSH	367	1.1000	12.79
24	VRLAVGIEG	412	1.0000	11.63
25	WSFETKQIH	15	0.9000	10.47
26	LFGLEIPGN	56	0.8000	9.30
27	LKARVQLLR	270	0.8000	9.30
28	LPIYATTSY	37	0.7000	8.14
29	WQAAVRPNT	151	0.7000	8.14
30	VVFAELGPP	258	0.7000	8.14
31	LETLSLRIE	296	0.7000	8.14
32	VANAQRVAE	307	0.7000	8.14

33	YTFDDTAHA	45	0.6000	6.98
34	VHSATKYLG	214	0.5000	5.81
35	FGLEIPGNI	57	0.4000	4.65
36	VVHSATKYL	213	0.3000	3.49
37	VNYAGLPSS	326	0.3000	3.49
38	FLVAQGLET	290	0.2000	2.33
39	YGGTYNLFH	121	0.1000	1.16
40	FHYSLAKLG	128	0.1000	1.16
41	FAAARRFSA	432	0.1000	1.16

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

Rank	Sequence	At Position	Score	% of Highest Score
1	FVNALKLHS	366	4.3000	53.75
2	LRDYGSAAS	277	2.7000	33.75
3	WHERAKRLA	336	2.6000	32.50
4	FAILNLAGA	102	2.4000	30.00
5	FALKARVQL	268	2.2000	27.50
6	VRSLVIHPA	382	1.9000	23.75
7	VRPNTKAFF	155	1.8000	22.50
8	FNAFLVAQG	287	1.5000	18.75
9	LVRLAVGIE	411	1.5000	18.75
10	LFHYSLAKL	127	1.4000	17.50
11	FETKQIHAG	17	1.2000	15.00
12	LAPKGTGAV	343	1.2000	15.00
13	LKARVQLLR	270	0.8000	10.00
14	YLIQPLAQG	201	0.7000	8.75
15	YTFDDTAHA	45	0.6000	7.50
16	LNLAGAGDH	105	0.3800	4.75
17	VVFAELGPP	258	0.3000	3.75
18	VNYAGLPSS	326	0.3000	3.75
19	FGLEIPGNI	57	0.2000	2.50
20	FAAARRFSA	432	0.1000	1.25
21	VLSFELAGG	351	-0.1000	0
22	VNALKLHSH	367	-0.1200	0
23	WQAAVRPNT	151	-0.2000	0
24	VEQRIAALE	77	-0.3000	0

25	VRLAVGIEG	412	-0.3000	0
26	WSFETKQIH	15	-0.3200	0
27	LPIYATTSY	37	-0.4000	0
28	YNLFHYSLA	125	-0.4000	0
29	FELAGGIEA	354	-0.4000	0
30	VVHSATKYL	213	-0.7000	0
31	FLVAQGLET	290	-0.7000	0
32	LSLRIERHV	299	-0.7000	0
33	IVDNTIATP	192	-0.8000	0
34	VHSATKYLG	214	-0.8000	0
35	YLGGHGAAI	220	-0.8000	0
36	VQLLRDYGS	274	-0.9000	0
37	LRIERHVAN	301	-0.9000	0
38	LVIHPASTT	385	-0.9000	0
39	IYTRIGNPT	65	-1.0000	0
40	YHGVVFAEL	255	-1.1000	0
41	YGGTYNLFH	121	-1.1200	0
42	LFGLEIPGN	56	-1.2000	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	LRDYGSAAS	277	3.7000	46.25
2	FVNALKLHS	366	3.3000	41.25
3	VRSLVIHPA	382	2.9000	36.25
4	VRPNTKAFF	155	2.8000	35.00
5	LVRLAVGIE	411	2.5000	31.25
6	LFHYSLAKL	127	2.4000	30.00
7	LAPKGTGAV	343	2.2000	27.50
8	LKARVQLLR	270	1.8000	22.50
9	WHERAKRLA	336	1.6000	20.00
10	FAILNLAGA	102	1.4000	17.50
11	LNLAGAGDH	105	1.3800	17.25
12	VVFAELGPP	258	1.3000	16.25
13	VNYAGLPSS	326	1.3000	16.25
14	FALKARVQL	268	1.2000	15.00
15	IVSSPRLYG	114	1.0000	12.50

16	VLSFELAGG	351	0.9000	11.25
17	VNALKLHSH	367	0.8800	11.00
18	VEQRIAALE	77	0.7000	8.75
19	VRLAVGIEG	412	0.7000	8.75
20	LPIYATTSY	37	0.6000	7.50
21	FNAFLVAQG	287	0.5000	6.25
22	VVHSATKYL	213	0.3000	3.75
23	LSLRIERHV	299	0.3000	3.75
24	FETKQIHAG	17	0.2000	2.50
25	IVDNTIATP	192	0.2000	2.50
26	VHSATKYLG	214	0.2000	2.50
27	VQLLRDYGS	274	0.1000	1.25
28	LRIERHVAN	301	0.1000	1.25
29	LVIHPASTT	385	0.1000	1.25
30	LFGLEIPGN	56	-0.2000	0
31	ILNLAGAGD	104	-0.2000	0
32	LAKLGIEVS	132	-0.3000	0
33	VAHRNGVPL	183	-0.3000	0
34	YLIQPLAQG	201	-0.3000	0
35	IQPLAQGAD	203	-0.3000	0
36	LGGHGAAIA	221	-0.3000	0
37	LGFAAARRF	430	-0.3000	0
38	YTFDDTAHA	45	-0.4000	0
39	VVEQRIAAL	76	-0.4000	0
40	VSPGLVRLA	407	-0.4000	0
41	IAALEGGVA	81	-0.5000	0
42	LAARDDVLS	317	-0.5000	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	LVRLAVGIE	411	5.5000	63.95
2	VEQRIAALE	77	3.7000	43.02
3	VRPNTKAFF	155	3.7000	43.02
4	LRDYGSAAS	277	3.7000	43.02
5	LFHYSLAKL	127	3.4000	39.53
6	FVNALKLHS	366	3.3000	38.37

7	VRSLVIHPA	382	2.9000	33.72
8	LNLAGAGDH	105	2.6000	30.23
9	ILNLAGAGD	104	2.5000	29.07
10	LAPKGTGAV	343	2.5000	29.07
11	IQPLAQGAD	203	2.4000	27.91
12	IVSSPRLYG	114	2.3000	26.74
13	FALKARVQL	268	2.2000	25.58
14	VLSFELAGG	351	2.2000	25.58
15	LRIERHVAN	301	2.1000	24.42
16	VNALKLHSH	367	2.1000	24.42
17	VRLAVGIEG	412	2.0000	23.26
18	LFGLEIPGN	56	1.8000	20.93
19	LKARVQLLR	270	1.8000	20.93
20	FNAFLVAQG	287	1.8000	20.93
21	LPIYATTSY	37	1.7000	19.77
22	VVFAELGPP	258	1.7000	19.77
23	LETLSLRIE	296	1.7000	19.77
24	VANAQRVAE	307	1.7000	19.77
25	WHERAKRLA	336	1.6000	18.60
26	FETKQIHAG	17	1.5000	17.44
27	VHSATKYLG	214	1.5000	17.44
28	FAILNLAGA	102	1.4000	16.28
29	VVHSATKYL	213	1.3000	15.12
30	VNYAGLPSS	326	1.3000	15.12
31	LGIEVSFVD	135	1.0000	11.63
32	YLIQPLAQG	201	1.0000	11.63
33	LVIHPASTT	385	1.0000	11.63
34	IYTRIGNPT	65	0.9000	10.47
35	YSLAKLGIE	130	0.7000	8.14
36	VAHRNGVPL	183	0.7000	8.14
37	VVEQRIAAL	76	0.6000	6.98
38	IVDNTIATP	192	0.6000	6.98
39	LSLRIERHV	299	0.6000	6.98
40	LGFAAARRF	430	0.6000	6.98
41	LKLHSHVAN	370	0.5000	5.81
42	LIVDNTIAT	191	0.3000	3.49
43	VAEFLAARD	313	0.3000	3.49
44	FLSSGQAAE	92	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	FVNALKLHS	366	4.9000	56.32
2	FALKARVQL	268	3.2000	36.78
3	LRDYGSAAS	277	2.7000	31.03
4	LPIYATTSY	37	2.4000	27.59
5	FAILNLAGA	102	2.4000	27.59
6	VRSLVIHPA	382	2.4000	27.59
7	WHERAKRLA	336	2.3000	26.44
8	VRPNTKAFF	155	1.8000	20.69
9	FETKQIHAG	17	1.7000	19.54
10	FNAFLVAQG	287	1.5000	17.24
11	YNLFHYSLA	125	1.4000	16.09
12	LFHYSLAKL	127	1.4000	16.09
13	LKARVQLLR	270	1.4000	16.09
14	IHPASTTHA	387	1.3000	14.94
15	IYTRIGNPT	65	1.0000	11.49
16	FAAARRFSA	432	0.9500	10.92
17	LVIHPASTT	385	0.9000	10.34
18	LVRLAVGIE	411	0.8000	9.20
19	YLIQPLAQG	201	0.7000	8.05
20	WSFETKQIH	15	0.6800	7.82
21	YTFDDTAHA	45	0.6000	6.90
22	IVSSPRLYG	114	0.6000	6.90
23	VRLAVGIEG	412	0.5800	6.67
24	VNYAGLPSS	326	0.5000	5.75
25	LAPKGTGAV	343	0.5000	5.75
26	FELAGGIEA	354	0.4800	5.52
27	LAKLGIEVS	132	0.4000	4.60
28	VNALKLHSH	367	0.3800	4.37
29	YAGLPSSPW	328	0.3000	3.45
30	VHSATKYLG	214	0.1000	1.15
31	LRIERHVAN	301	0.1000	1.15
32	FTTPDPSYH	248	0.0800	0.92
33	FLVAQGLET	290	-0.1000	0
34	VLSFELAGG	351	-0.1000	0
35	VEQRIAALE	77	-0.3000	0
36	FFAETISNP	162	-0.3000	0
37	VAHRNGVPL	183	-0.3000	0

38	LNLAGAGDH	105	-0.3200	0
39	VIHPASTTH	386	-0.3200	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	FVNALKLHS	366	6.1000	60.40
2	LVRLAVGIE	411	4.6000	45.54
3	FALKARVQL	268	3.7000	36.63
4	FETKQIHAG	17	3.2000	31.68
5	IVSSPRLYG	114	3.1000	30.69
6	FNAFLVAQG	287	2.8000	27.72
7	WHERAKRLA	336	2.8000	27.72
8	VEQRIAALE	77	2.7000	26.73
9	VRPNTKAFF	155	2.7000	26.73
10	LRDYGSAAS	277	2.7000	26.73
11	LKARVQLLR	270	2.6000	25.74
12	VRSLVIHPA	382	2.6000	25.74
13	VRLAVGIEG	412	2.6000	25.74
14	FAILNLAGA	102	2.4000	23.76
15	LFHYSLAKL	127	2.4000	23.76
16	YLIQPLAQG	201	2.0000	19.80
17	FLVAQGLET	290	2.0000	19.80
18	LFGLEIPGN	56	1.9500	19.31
19	YGGTYNLFH	121	1.9000	18.81
20	WQAAVRPNT	151	1.8500	18.32
21	LPIYATTSY	37	1.8000	17.82
22	YSLAKLGIE	130	1.8000	17.82
23	VNALKLHSH	367	1.8000	17.82
24	LNLAGAGDH	105	1.7000	16.83
25	LRIERHVAN	301	1.6000	15.84
26	LAPKGTGAV	343	1.6000	15.84
27	ILNLAGAGD	104	1.5000	14.85
28	IQPLAQGAD	203	1.5000	14.85
29	VNYAGLPSS	326	1.4500	14.36
30	FLSSGQAAE	92	1.2000	11.88
31	VHSATKYLG	214	1.2000	11.88

32	VANAQRVAE	307	1.2000	11.88
33	VLSFELAGG	351	1.2000	11.88
34	FELAGGIEA	354	1.2000	11.88
35	YGSAASPFN	280	1.1500	11.39
36	WSFETKQIH	15	1.0000	9.90
37	LIVDNTIAT	191	0.9000	8.91
38	VVHSATKYL	213	0.9000	8.91
39	LETLSLRIE	296	0.9000	8.91
40	VVFAELGPP	258	0.8000	7.92
41	FHYSLAKLG	128	0.7000	6.93
42	YTFDDTAHA	45	0.6000	5.94
43	FAAARRFSA	432	0.6000	5.94
44	FGLEIPGNI	57	0.5000	4.95

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	FVNALKLHS	366	6.1000	73.49
2	VRSLVIHPA	382	3.0000	36.14
3	FAILNLAGA	102	2.8000	33.73
4	IVSSPRLYG	114	2.1000	25.30
5	LVRLAVGIE	411	2.0000	24.10
6	VRPNTKAFF	155	1.8000	21.69
7	VNYAGLPSS	326	1.4500	17.47
8	FNAFLVAQG	287	1.4000	16.87
9	YLIQPLAQG	201	1.3000	15.66
10	VRLAVGIEG	412	1.3000	15.66
11	FELAGGIEA	354	1.2000	14.46
12	FLVAQGLET	290	1.1000	13.25
13	YGGTYNLFH	121	1.0800	13.01
14	VNALKLHSH	367	0.9800	11.81
15	WQAAVRPNT	151	0.9500	11.45
16	FAAARRFSA	432	0.6000	7.23
17	LNLAGAGDH	105	0.4800	5.78
18	VVFAELGPP	258	0.4000	4.82
19	LFGLEIPGN	56	0.3500	4.22
20	LAKLGIEVS	132	0.2000	2.41

21	VVHSATKYL	213	0.2000	2.41
22	VQLLRDYGS	274	0.2000	2.41
23	YTFDDTAHA	45	-0.1000	0
24	VHSATKYLG	214	-0.1000	0
25	FALKARVQL	268	-0.1000	0
26	IDLLDTPAV	172	-0.1500	0
27	LRDYGSAAS	277	-0.2000	0
28	WHERAKRLA	336	-0.2000	0
29	VLSFELAGG	351	-0.2000	0
30	YTRIGNPTT	66	-0.2500	0
31	FHYSLAKLG	128	-0.3000	0
32	IGDVRSLVI	379	-0.3000	0
33	FGLEIPGNI	57	-0.4000	0
34	LKARVQLLR	270	-0.4000	0
35	IHPASTTHA	387	-0.4000	0
36	FPGFTTPDP	245	-0.4500	0
37	YNLFHYSLA	125	-0.5000	0
38	LVIHPASTT	385	-0.5000	0
39	FAELGPPAF	260	-0.6500	0
40	LIVDNTIAT	191	-0.7000	0
41	VVEQRIAAL	76	-0.8000	0
42	ILNLAGAGD	104	-0.8000	0
43	IVDNTIATP	192	-0.8000	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	FVNALKLHS	366	4.0000	47.62
2	VRSLVIHPA	382	3.8000	45.24
3	LVIHPASTT	385	3.0000	35.71
4	VRPNTKAFF	155	2.9000	34.52
5	IERHVANAQ	303	2.9000	34.52
6	IVVHSATKY	212	2.2000	26.19
7	LGGHGAAIA	221	2.2000	26.19
8	IVSSPRLYG	114	2.1000	25.00
9	VNYAGLPSS	326	2.0000	23.81
10	LKLHSHVAN	370	2.0000	23.81

11	LRDYGSAAS	277	1.9000	22.62
12	VNALKLHSH	367	1.7800	21.19
13	LHSHVANIG	372	1.6000	19.05
14	VVHSATKYL	213	1.5000	17.86
15	LGFAAARRF	430	1.5000	17.86
16	YLIQPLAQG	201	1.3000	15.48
17	WHERAKRLA	336	1.3000	15.48
18	VVEQRIAAL	76	1.2000	14.29
19	VLSFELAGG	351	1.2000	14.29
20	LVRLAVGIE	411	1.2000	14.29
21	FAILNLAGA	102	1.1000	13.10
22	VHSATKYLG	214	1.1000	13.10
23	LRIERHVAN	301	1.0000	11.90
24	IHPASTTHA	387	1.0000	11.90
25	VRLAVGIEG	412	1.0000	11.90
26	LVAQGLETL	291	0.9000	10.71
27	VSPGLVRLA	407	0.9000	10.71
28	LAKLGIEVS	132	0.8000	9.52
29	FNAFLVAQG	287	0.8000	9.52
30	FALKARVQL	268	0.7000	8.33
31	VQLLRDYGS	274	0.7000	8.33
32	LFHYSLAKL	127	0.6000	7.14
33	FAAARRFSA	432	0.6000	7.14
34	LKARVQLLR	270	0.4000	4.76
35	LNLAGAGDH	105	0.3800	4.52
36	LPIYATTSY	37	0.3000	3.57
37	IVDNTIATP	192	0.3000	3.57
38	VVFAELGPP	258	0.3000	3.57
39	LFGLEIPGN	56	0.2000	2.38
40	LETLSLRIE	296	0.2000	2.38
41	LFLSSGQAA	91	0.1000	1.19
42	FETKQIHAG	17	-0.1000	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	FVNALKLHS	366	5.1000	61.45

2	VRSLVIHPA	382	4.0000	48.19
3	IVSSPRLYG	114	3.1000	37.35
4	LVRLAVGIE	411	3.0000	36.14
5	VRPNTKAFF	155	2.8000	33.73
6	VNYAGLPSS	326	2.4500	29.52
7	VRLAVGIEG	412	2.3000	27.71
8	VNALKLHSH	367	1.9800	23.86
9	FAILNLAGA	102	1.8000	21.69
10	LNLAGAGDH	105	1.4800	17.83
11	VVFAELGPP	258	1.4000	16.87
12	LFGLEIPGN	56	1.3500	16.27
13	LAKLGIEVS	132	1.2000	14.46
14	VVHSATKYL	213	1.2000	14.46
15	VQLLRDYGS	274	1.2000	14.46
16	VHSATKYLG	214	0.9000	10.84
17	IDLLDTPAV	172	0.8500	10.24
18	LRDYGSAAS	277	0.8000	9.64
19	VLSFELAGG	351	0.8000	9.64
20	IGDVRSLVI	379	0.7000	8.43
21	LKARVQLLR	270	0.6000	7.23
22	IHPASTTHA	387	0.6000	7.23
23	LVIHPASTT	385	0.5000	6.02
24	FNAFLVAQG	287	0.4000	4.82
25	LIVDNTIAT	191	0.3000	3.61
26	YLIQPLAQG	201	0.3000	3.61
27	VVEQRIAAL	76	0.2000	2.41
28	ILNLAGAGD	104	0.2000	2.41
29	IVDNTIATP	192	0.2000	2.41
30	IQPLAQGAD	203	0.2000	2.41
31	FELAGGIEA	354	0.2000	2.41
32	LGGHGAAIA	221	0.1000	1.20
33	FLVAQGLET	290	0.1000	1.20
34	YGGTYNLFH	121	0.0800	0.96
35	WQAAVRPNT	151	-0.0500	0
36	LRIERHVAN	301	-0.1000	0
37	LGFAAARRF	430	-0.1000	0
38	IVVHSATKY	212	-0.3000	0
39	IERHVANAQ	303	-0.3000	0
40	LVAQGLETL	291	-0.4000	0
41	IEGIDDILA	418	-0.4000	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	FVNALKLHS	366	5.1000	61.45
2	VRSLVIHPA	382	4.0000	48.19
3	IVSSPRLYG	114	3.1000	37.35
4	LVRLAVGIE	411	3.0000	36.14
5	VRPNTKAFF	155	2.8000	33.73
6	VNYAGLPSS	326	2.4500	29.52
7	VRLAVGIEG	412	2.3000	27.71
8	VNALKLHSH	367	1.9800	23.86
9	FAILNLAGA	102	1.8000	21.69
10	LNLAGAGDH	105	1.4800	17.83
11	VVFAELGPP	258	1.4000	16.87
12	LFGLEIPGN	56	1.3500	16.27
13	LAKLGIEVS	132	1.2000	14.46
14	VVHSATKYL	213	1.2000	14.46
15	VQLLRDYGS	274	1.2000	14.46
16	VHSATKYLG	214	0.9000	10.84
17	IDLLDTPAV	172	0.8500	10.24
18	LRDYGSAAS	277	0.8000	9.64
19	VLSFELAGG	351	0.8000	9.64
20	IGDVRSLVI	379	0.7000	8.43
21	LKARVQLLR	270	0.6000	7.23
22	IHPASTTHA	387	0.6000	7.23
23	LVIHPASTT	385	0.5000	6.02
24	FNAFLVAQG	287	0.4000	4.82
25	LIVDNTIAT	191	0.3000	3.61
26	YLIQPLAQG	201	0.3000	3.61
27	VVEQRIAAL	76	0.2000	2.41
28	ILNLAGAGD	104	0.2000	2.41
29	IVDNTIATP	192	0.2000	2.41
30	IQPLAQGAD	203	0.2000	2.41
31	FELAGGIEA	354	0.2000	2.41
32	LGGHGAAIA	221	0.1000	1.20
33	FLVAQGLET	290	0.1000	1.20
34	YGGTYNLFH	121	0.0800	0.96
35	WQAAVRPNT	151	-0.0500	0

36	LRIERHVAN	301	-0.1000	0
37	LGFAAARRF	430	-0.1000	0
38	IVVHSATKY	212	-0.3000	0
39	IERHVANAQ	303	-0.3000	0
40	LVAQGLETL	291	-0.4000	0
41	IEGIDDILA	418	-0.4000	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	LIVDNTIAT	191	3.9000	42.86
2	FVNALKLHS	366	3.8000	41.76
3	LLRDYGSAA	276	3.3700	37.03
4	IVSSPRLYG	114	3.2000	35.16
5	VNYAGLPSS	326	3.2000	35.16
6	VRPNTKAFF	155	3.0000	32.97
7	YTFDDTAHA	45	2.9000	31.87
8	LVIHPASTT	385	2.4700	27.14
9	LVRLAVGIE	411	2.4000	26.37
10	VRSLVIHPA	382	2.3000	25.27
11	LNLAGAGDH	105	1.9800	21.76
12	VVHSATKYL	213	1.9000	20.88
13	VVFAELGPP	258	1.9000	20.88
14	VRLAVGIEG	412	1.9000	20.88
15	IHPASTTHA	387	1.8000	19.78
16	LFLSSGQAA	91	1.7000	18.68
17	IVVHSATKY	212	1.5000	16.48
18	VIVDGGNFD	231	1.4100	15.49
19	LRIERHVAN	301	1.4000	15.38
20	VHSATKYLG	214	1.2500	13.74
21	IERHVANAQ	303	1.2100	13.30
22	LAKLGIEVS	132	1.2000	13.19
23	LVAQGLETL	291	1.1000	12.09
24	ILADLELGF	424	1.1000	12.09
25	LFGLEIPGN	56	1.0000	10.99
26	LKLHSHVAN	370	0.8000	8.79
27	VSPGLVRLA	407	0.8000	8.79

28	VGIEGIDDI	416	0.8000	8.79
29	FSADPQSVA	438	0.7700	8.46
30	FAILNLAGA	102	0.7000	7.69
31	WQAAVRPNT	151	0.7000	7.69
32	YLIQPLAQG	201	0.7000	7.69
33	LGGHGAAIA	221	0.7000	7.69
34	IHAGQHPDP	22	0.6000	6.59
35	VVEQRIAAL	76	0.6000	6.59
36	IEVSFVDDP	137	0.6000	6.59
37	LELGFAAAR	428	0.6000	6.59
38	IDLLDTPAV	172	0.5000	5.49
39	LRDYGSAAS	277	0.5000	5.49
40	FAAARRFSA	432	0.5000	5.49
41	VQLLRDYGS	274	0.4500	4.95
42	IVDNTIATP	192	0.4000	4.40
43	VNALKLHSH	367	0.2800	3.08
44	IVDGGNFDW	232	0.2000	2.20

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	FVNALKLHS	366	5.0000	59.52
2	VRSLVIHPA	382	2.8000	33.33
3	YLIQPLAQG	201	2.3000	27.38
4	WHERAKRLA	336	2.3000	27.38
5	FAILNLAGA	102	2.1000	25.00
6	LVIHPASTT	385	2.0000	23.81
7	VRPNTKAFF	155	1.9000	22.62
8	IERHVANAQ	303	1.9000	22.62
9	FNAFLVAQG	287	1.8000	21.43
10	FALKARVQL	268	1.7000	20.24
11	FAAARRFSA	432	1.6000	19.05
12	IVVHSATKY	212	1.2000	14.29
13	LGGHGAAIA	221	1.2000	14.29
14	IVSSPRLYG	114	1.1000	13.10
15	VNYAGLPSS	326	1.0000	11.90
16	LKLHSHVAN	370	1.0000	11.90

17	FETKQIHAG	17	0.9000	10.71
18	LRDYGSAAS	277	0.9000	10.71
19	VNALKLHSH	367	0.7800	9.29
20	LHSHVANIG	372	0.6000	7.14
21	WQAAVRPNT	151	0.5000	5.95
22	VVHSATKYL	213	0.5000	5.95
23	LGFAAARRF	430	0.5000	5.95
24	WSFETKQIH	15	0.3800	4.52
25	YNLFHYSLA	125	0.3000	3.57
26	YTFDDTAHA	45	0.2000	2.38
27	VVEQRIAAL	76	0.2000	2.38
28	VLSFELAGG	351	0.2000	2.38
29	LVRLAVGIE	411	0.2000	2.38
30	VHSATKYLG	214	0.1000	1.19
31	LVAQGLETL	291	-0.1000	0
32	FELAGGIEA	354	-0.1000	0
33	VSPGLVRLA	407	-0.1000	0
34	LAKLGIEVS	132	-0.2000	0
35	VQLLRDYGS	274	-0.3000	0
36	LFHYSLAKL	127	-0.4000	0
37	FPGFTTPDP	245	-0.5000	0
38	YGGTYNLFH	121	-0.5200	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	FVNALKLHS	366	5.4000	61.36
2	VRPNTKAFF	155	3.8000	43.18
3	YLIQPLAQG	201	3.7000	42.05
4	FNAFLVAQG	287	3.2000	36.36
5	VRSLVIHPA	382	2.8000	31.82
6	LVIHPASTT	385	2.7000	30.68
7	FALKARVQL	268	2.6600	30.23
8	IVSSPRLYG	114	2.5000	28.41
9	IVVHSATKY	212	2.5000	28.41
10	LGFAAARRF	430	2.4000	27.27
11	FETKQIHAG	17	2.3000	26.14

12	WHERAKRLA	336	2.3000	26.14
13	FAILNLAGA	102	2.1000	23.86
14	LHSHVANIG	372	2.0000	22.73
15	LKLHSHVAN	370	1.8000	20.45
16	VLSFELAGG	351	1.6000	18.18
17	LVRLAVGIE	411	1.6000	18.18
18	FAAARRFSA	432	1.6000	18.18
19	VHSATKYLG	214	1.5000	17.05
20	VVHSATKYL	213	1.4600	16.59
21	FHYSLAKLG	128	1.4000	15.91
22	VNYAGLPSS	326	1.4000	15.91
23	VRLAVGIEG	412	1.4000	15.91
24	LRDYGSAAS	277	1.3000	14.77
25	WQAAVRPNT	151	1.2000	13.64
26	LGGHGAAIA	221	1.2000	13.64
27	IERHVANAQ	303	1.2000	13.64
28	VVEQRIAAL	76	1.1600	13.18
29	LKARVQLLR	270	0.9000	10.23
30	LVAQGLETL	291	0.8600	9.77
31	LRIERHVAN	301	0.8000	9.09
32	FLVAQGLET	290	0.7000	7.95
33	LPIYATTSY	37	0.6000	6.82
34	LETLSLRIE	296	0.6000	6.82
35	LFHYSLAKL	127	0.5600	6.36
36	FPGFTTPDP	245	0.5000	5.68
37	YNLFHYSLA	125	0.3000	3.41
38	IVDNTIATP	192	0.3000	3.41
39	VVFAELGPP	258	0.3000	3.41
40	YTFDDTAHA	45	0.2000	2.27
41	LAKLGIEVS	132	0.2000	2.27
42	VNALKLHSH	367	0.2000	2.27
43	FAELGPPAF	260	0.1000	1.14
44	VQLLRDYGS	274	0.1000	1.14

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

Rank	Sequence	At Position	Score	% of Highest Score

1	FVNALKLHS	366	4.0000	47.62
2	VRSLVIHPA	382	3.8000	45.24
3	LVIHPASTT	385	3.0000	35.71
4	VRPNTKAFF	155	2.9000	34.52
5	IERHVANAQ	303	2.9000	34.52
6	IVVHSATKY	212	2.2000	26.19
7	LGGHGAAIA	221	2.2000	26.19
8	IVSSPRLYG	114	2.1000	25.00
9	VNYAGLPSS	326	2.0000	23.81
10	LKLHSHVAN	370	2.0000	23.81
11	LRDYGSAAS	277	1.9000	22.62
12	VNALKLHSH	367	1.7800	21.19
13	LHSHVANIG	372	1.6000	19.05
14	VVHSATKYL	213	1.5000	17.86
15	LGFAAARRF	430	1.5000	17.86
16	YLIQPLAQG	201	1.3000	15.48
17	WHERAKRLA	336	1.3000	15.48
18	VVEQRIAAL	76	1.2000	14.29
19	VLSFELAGG	351	1.2000	14.29
20	LVRLAVGIE	411	1.2000	14.29
21	FAILNLAGA	102	1.1000	13.10
22	VHSATKYLG	214	1.1000	13.10
23	LRIERHVAN	301	1.0000	11.90
24	IHPASTTHA	387	1.0000	11.90
25	VRLAVGIEG	412	1.0000	11.90
26	LVAQGLETL	291	0.9000	10.71
27	VSPGLVRLA	407	0.9000	10.71
28	LAKLGIEVS	132	0.8000	9.52
29	FNAFLVAQG	287	0.8000	9.52
30	FALKARVQL	268	0.7000	8.33
31	VQLLRDYGS	274	0.7000	8.33
32	LFHYSLAKL	127	0.6000	7.14
33	FAAARRFSA	432	0.6000	7.14
34	LKARVQLLR	270	0.4000	4.76
35	LNLAGAGDH	105	0.3800	4.52
36	LPIYATTSY	37	0.3000	3.57
37	IVDNTIATP	192	0.3000	3.57
38	VVFAELGPP	258	0.3000	3.57
39	LFGLEIPGN	56	0.2000	2.38
40	LETLSLRIE	296	0.2000	2.38
41	LFLSSGQAA	91	0.1000	1.19

42	FETKQIHAG	17	-0.1000	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	FVNALKLHS	366	6.5000	74.71
2	VRPNTKAFF	155	3.7000	42.53
3	IVSSPRLYG	114	3.5000	40.23
4	LVRLAVGIE	411	3.4000	39.08
5	VRSLVIHPA	382	3.0000	34.48
6	FAILNLAGA	102	2.8000	32.18
7	FNAFLVAQG	287	2.8000	32.18
8	YLIQPLAQG	201	2.7000	31.03
9	VRLAVGIEG	412	2.7000	31.03
10	VNYAGLPSS	326	1.8500	21.26
11	FLVAQGLET	290	1.8000	20.69
12	WQAAVRPNT	151	1.6500	18.97
13	VVFAELGPP	258	1.4000	16.09
14	VHSATKYLG	214	1.3000	14.94
15	FAELGPPAF	260	1.2500	14.37
16	VLSFELAGG	351	1.2000	13.79
17	FELAGGIEA	354	1.2000	13.79
18	VVHSATKYL	213	1.1600	13.33
19	LFGLEIPGN	56	1.1500	13.22
20	FHYSLAKLG	128	1.1000	12.64
21	LKARVQLLR	270	1.1000	12.64
22	FALKARVQL	268	0.8600	9.89
23	IDLLDTPAV	172	0.8500	9.77
24	LGFAAARRF	430	0.8000	9.20
25	LAKLGIEVS	132	0.6000	6.90
26	VQLLRDYGS	274	0.6000	6.90
27	IGDVRSLVI	379	0.6000	6.90
28	FAAARRFSA	432	0.6000	6.90
29	FPGFTTPDP	245	0.5500	6.32
30	FETKQIHAG	17	0.5000	5.75
31	FGLEIPGNI	57	0.5000	5.75
32	YGGTYNLFH	121	0.5000	5.75

33	YTRIGNPTT	66	0.4500	5.17
34	VNALKLHSH	367	0.4000	4.60
35	ILNLAGAGD	104	0.3000	3.45
36	IQPLAQGAD	203	0.3000	3.45
37	YSLAKLGIE	130	0.2000	2.30
38	IVDNTIATP	192	0.2000	2.30
39	LRDYGSAAS	277	0.2000	2.30
40	LVIHPASTT	385	0.2000	2.30
41	VVEQRIAAL	76	0.1600	1.84

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	VRPNTKAFF	155	4.8000	54.55
2	FVNALKLHS	366	4.4000	50.00
3	VRSLVIHPA	382	3.8000	43.18
4	LVIHPASTT	385	3.7000	42.05
5	IVSSPRLYG	114	3.5000	39.77
6	IVVHSATKY	212	3.5000	39.77
7	LGFAAARRF	430	3.4000	38.64
8	LHSHVANIG	372	3.0000	34.09
9	LKLHSHVAN	370	2.8000	31.82
10	YLIQPLAQG	201	2.7000	30.68
11	VLSFELAGG	351	2.6000	29.55
12	LVRLAVGIE	411	2.6000	29.55
13	VHSATKYLG	214	2.5000	28.41
14	VVHSATKYL	213	2.4600	27.95
15	VNYAGLPSS	326	2.4000	27.27
16	VRLAVGIEG	412	2.4000	27.27
17	LRDYGSAAS	277	2.3000	26.14
18	LGGHGAAIA	221	2.2000	25.00
19	FNAFLVAQG	287	2.2000	25.00
20	IERHVANAQ	303	2.2000	25.00
21	VVEQRIAAL	76	2.1600	24.55
22	LKARVQLLR	270	1.9000	21.59
23	LVAQGLETL	291	1.8600	21.14
24	LRIERHVAN	301	1.8000	20.45

25	FALKARVQL	268	1.6600	18.86
26	LPIYATTSY	37	1.6000	18.18
27	LETLSLRIE	296	1.6000	18.18
28	LFHYSLAKL	127	1.5600	17.73
29	FETKQIHAG	17	1.3000	14.77
30	IVDNTIATP	192	1.3000	14.77
31	VVFAELGPP	258	1.3000	14.77
32	WHERAKRLA	336	1.3000	14.77
33	LAKLGIEVS	132	1.2000	13.64
34	VNALKLHSH	367	1.2000	13.64
35	FAILNLAGA	102	1.1000	12.50
36	VQLLRDYGS	274	1.1000	12.50
37	VANAQRVAE	307	1.1000	12.50
38	LFGLEIPGN	56	1.0000	11.36
39	LSLRIERHV	299	1.0000	11.36
40	IHPASTTHA	387	1.0000	11.36
41	VSPGLVRLA	407	0.9000	10.23
42	LGIEVSFVD	135	0.8000	9.09
43	IDLLDTPAV	172	0.7000	7.95
44	LAPKGTGAV	343	0.7000	7.95

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

Rank	Sequence	At Position	Score	% of Highest Score
1	FVNALKLHS	366	5.4000	61.36
2	VRPNTKAFF	155	3.8000	43.18
3	YLIQPLAQG	201	3.7000	42.05
4	FNAFLVAQG	287	3.2000	36.36
5	VRSLVIHPA	382	2.8000	31.82
6	LVIHPASTT	385	2.7000	30.68
7	FALKARVQL	268	2.6600	30.23
8	IVSSPRLYG	114	2.5000	28.41
9	IVVHSATKY	212	2.5000	28.41
10	LGFAAARRF	430	2.4000	27.27
11	FETKQIHAG	17	2.3000	26.14
12	WHERAKRLA	336	2.3000	26.14
13	FAILNLAGA	102	2.1000	23.86

14	LHSHVANIG	372	2.0000	22.73
15	LKLHSHVAN	370	1.8000	20.45
16	VLSFELAGG	351	1.6000	18.18
17	LVRLAVGIE	411	1.6000	18.18
18	FAAARRFSA	432	1.6000	18.18
19	VHSATKYLG	214	1.5000	17.05
20	VVHSATKYL	213	1.4600	16.59
21	FHYSLAKLG	128	1.4000	15.91
22	VNYAGLPSS	326	1.4000	15.91
23	VRLAVGIEG	412	1.4000	15.91
24	LRDYGSAAS	277	1.3000	14.77
25	WQAAVRPNT	151	1.2000	13.64
26	LGGHGAAIA	221	1.2000	13.64
27	IERHVANAQ	303	1.2000	13.64
28	VVEQRIAAL	76	1.1600	13.18
29	LKARVQLLR	270	0.9000	10.23
30	LVAQGLETL	291	0.8600	9.77
31	LRIERHVAN	301	0.8000	9.09
32	FLVAQGLET	290	0.7000	7.95
33	LPIYATTSY	37	0.6000	6.82
34	LETLSLRIE	296	0.6000	6.82
35	LFHYSLAKL	127	0.5600	6.36
36	FPGFTTPDP	245	0.5000	5.68
37	YNLFHYSLA	125	0.3000	3.41
38	IVDNTIATP	192	0.3000	3.41
39	VVFAELGPP	258	0.3000	3.41
40	YTFDDTAHA	45	0.2000	2.27
41	LAKLGIEVS	132	0.2000	2.27
42	VNALKLHSH	367	0.2000	2.27
43	FAELGPPAF	260	0.1000	1.14
44	VQLLRDYGS	274	0.1000	1.14

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVRLAVGIE	411	4.2000	46.67
2	FVNALKLHS	366	4.0000	44.44

3	LKLHSHVAN	370	4.0000	44.44
4	LVIHPASTT	385	3.9000	43.33
5	VRPNTKAFF	155	3.8000	42.22
6	VRSLVIHPA	382	3.8000	42.22
7	IERHVANAQ	303	3.7000	41.11
8	IVSSPRLYG	114	3.4000	37.78
9	IVVHSATKY	212	3.3000	36.67
10	LETLSLRIE	296	3.2000	35.56
11	LRIERHVAN	301	3.0000	33.33
12	VNALKLHSH	367	3.0000	33.33
13	LHSHVANIG	372	2.9000	32.22
14	VANAQRVAE	307	2.7000	30.00
15	YLIQPLAQG	201	2.6000	28.89
16	VVHSATKYL	213	2.5000	27.78
17	VLSFELAGG	351	2.5000	27.78
18	LGIEVSFVD	135	2.4000	26.67
19	VHSATKYLG	214	2.4000	26.67
20	LGFAAARRF	430	2.4000	26.67
21	VRLAVGIEG	412	2.3000	25.56
22	LFGLEIPGN	56	2.2000	24.44
23	VVEQRIAAL	76	2.2000	24.44
24	ILNLAGAGD	104	2.2000	24.44
25	LGGHGAAIA	221	2.2000	24.44
26	FNAFLVAQG	287	2.1000	23.33
27	VNYAGLPSS	326	2.0000	22.22
28	LRDYGSAAS	277	1.9000	21.11
29	LVAQGLETL	291	1.9000	21.11
30	FALKARVQL	268	1.7000	18.89
31	VEQRIAALE	77	1.6000	17.78
32	LNLAGAGDH	105	1.6000	17.78
33	LFHYSLAKL	127	1.6000	17.78
34	LPIYATTSY	37	1.4000	15.56
35	WHERAKRLA	336	1.3000	14.44
36	FETKQIHAG	17	1.2000	13.33
37	FAILNLAGA	102	1.1000	12.22
38	IQPLAQGAD	203	1.1000	12.22
39	IHPASTTHA	387	1.0000	11.11
40	VSPGLVRLA	407	0.9000	10.00
41	LAKLGIEVS	132	0.8000	8.89
42	IVDNTIATP	192	0.7000	7.78
43	VVFAELGPP	258	0.7000	7.78

44	VQLLRDYGS	274	0.7000	7.78

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	FVNALKLHS	366	6.5000	74.71
2	VRPNTKAFF	155	3.7000	42.53
3	IVSSPRLYG	114	3.5000	40.23
4	LVRLAVGIE	411	3.4000	39.08
5	VRSLVIHPA	382	3.0000	34.48
6	FAILNLAGA	102	2.8000	32.18
7	FNAFLVAQG	287	2.8000	32.18
8	YLIQPLAQG	201	2.7000	31.03
9	VRLAVGIEG	412	2.7000	31.03
10	VNYAGLPSS	326	1.8500	21.26
11	FLVAQGLET	290	1.8000	20.69
12	WQAAVRPNT	151	1.6500	18.97
13	VVFAELGPP	258	1.4000	16.09
14	VHSATKYLG	214	1.3000	14.94
15	FAELGPPAF	260	1.2500	14.37
16	VLSFELAGG	351	1.2000	13.79
17	FELAGGIEA	354	1.2000	13.79
18	VVHSATKYL	213	1.1600	13.33
19	LFGLEIPGN	56	1.1500	13.22
20	FHYSLAKLG	128	1.1000	12.64
21	LKARVQLLR	270	1.1000	12.64
22	FALKARVQL	268	0.8600	9.89
23	IDLLDTPAV	172	0.8500	9.77
24	LGFAAARRF	430	0.8000	9.20
25	LAKLGIEVS	132	0.6000	6.90
26	VQLLRDYGS	274	0.6000	6.90
27	IGDVRSLVI	379	0.6000	6.90
28	FAAARRFSA	432	0.6000	6.90
29	FPGFTTPDP	245	0.5500	6.32
30	FETKQIHAG	17	0.5000	5.75
31	FGLEIPGNI	57	0.5000	5.75
32	YGGTYNLFH	121	0.5000	5.75

33	YTRIGNPTT	66	0.4500	5.17
34	VNALKLHSH	367	0.4000	4.60
35	ILNLAGAGD	104	0.3000	3.45
36	IQPLAQGAD	203	0.3000	3.45
37	YSLAKLGIE	130	0.2000	2.30
38	IVDNTIATP	192	0.2000	2.30
39	LRDYGSAAS	277	0.2000	2.30
40	LVIHPASTT	385	0.2000	2.30
41	VVEQRIAAL	76	0.1600	1.84

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	FVNALKLHS	366	4.3000	63.24
2	FAILNLAGA	102	2.8000	41.18
3	VRSLVIHPA	382	2.3000	33.82
4	LVRLAVGIE	411	1.9000	27.94
5	VRPNTKAFF	155	1.8000	26.47
6	FNAFLVAQG	287	1.4000	20.59
7	YLIQPLAQG	201	1.3000	19.12
8	LNLAGAGDH	105	0.3800	5.59
9	IVSSPRLYG	114	0.3000	4.41
10	VVFAELGPP	258	0.3000	4.41
11	VNYAGLPSS	326	0.3000	4.41
12	VNALKLHSH	367	0.2800	4.12
13	FAAARRFSA	432	0.1000	1.47
14	YTFDDTAHA	45	-0.1000	0
15	WQAAVRPNT	151	-0.2000	0
16	LRDYGSAAS	277	-0.2000	0
17	VLSFELAGG	351	-0.2000	0
18	VRLAVGIEG	412	-0.3000	0
19	VVHSATKYL	213	-0.4000	0
20	WHERAKRLA	336	-0.4000	0
21	FELAGGIEA	354	-0.4000	0
22	FGLEIPGNI	57	-0.5000	0
23	YNLFHYSLA	125	-0.5000	0
24	VQLLRDYGS	274	-0.5000	0

25	LVIHPASTT	385	-0.5000	0
26	FALKARVQL	268	-0.6000	0
27	FLVAQGLET	290	-0.7000	0
28	YGGTYNLFH	121	-0.7200	0
29	LFGLEIPGN	56	-0.8000	0
30	VVEQRIAAL	76	-0.8000	0
31	ILNLAGAGD	104	-0.8000	0
32	IVDNTIATP	192	-0.8000	0
33	VHSATKYLG	214	-0.8000	0
34	FHYSLAKLG	128	-0.9000	0
35	LAKLGIEVS	132	-0.9000	0
36	IQPLAQGAD	203	-0.9000	0
37	LGGHGAAIA	221	-0.9000	0
38	YHGVVFAEL	255	-1.0000	0
39	WSFETKQIH	15	-1.0200	0
40	IAALEGGVA	81	-1.1000	0
41	YAGLPSSPW	328	-1.1000	0
42	YSLAKLGIE	130	-1.3000	0
43	IDLLDTPAV	172	-1.3000	0

ALLELE: DRB1_1311	Threshold for 3 % with score: 2.0	Highest Score achievable by any peptide: 8.3

Rank	Sequence	At Position	Score	% of Highest Score
1	FVNALKLHS	366	5.1000	61.45
2	VRSLVIHPA	382	4.0000	48.19
3	IVSSPRLYG	114	3.1000	37.35
4	LVRLAVGIE	411	3.0000	36.14
5	VRPNTKAFF	155	2.8000	33.73
6	VNYAGLPSS	326	2.4500	29.52
7	VRLAVGIEG	412	2.3000	27.71
8	VNALKLHSH	367	1.9800	23.86
9	FAILNLAGA	102	1.8000	21.69
10	LNLAGAGDH	105	1.4800	17.83
11	VVFAELGPP	258	1.4000	16.87
12	LFGLEIPGN	56	1.3500	16.27
13	LAKLGIEVS	132	1.2000	14.46
14	VVHSATKYL	213	1.2000	14.46

15	VQLLRDYGS	274	1.2000	14.46
16	VHSATKYLG	214	0.9000	10.84
17	IDLLDTPAV	172	0.8500	10.24
18	LRDYGSAAS	277	0.8000	9.64
19	VLSFELAGG	351	0.8000	9.64
20	IGDVRSLVI	379	0.7000	8.43
21	LKARVQLLR	270	0.6000	7.23
22	IHPASTTHA	387	0.6000	7.23
23	LVIHPASTT	385	0.5000	6.02
24	FNAFLVAQG	287	0.4000	4.82
25	LIVDNTIAT	191	0.3000	3.61
26	YLIQPLAQG	201	0.3000	3.61
27	VVEQRIAAL	76	0.2000	2.41
28	ILNLAGAGD	104	0.2000	2.41
29	IVDNTIATP	192	0.2000	2.41
30	IQPLAQGAD	203	0.2000	2.41
31	FELAGGIEA	354	0.2000	2.41
32	LGGHGAAIA	221	0.1000	1.20
33	FLVAQGLET	290	0.1000	1.20
34	YGGTYNLFH	121	0.0800	0.96
35	WQAAVRPNT	151	-0.0500	0
36	LRIERHVAN	301	-0.1000	0
37	LGFAAARRF	430	-0.1000	0
38	IVVHSATKY	212	-0.3000	0
39	IERHVANAQ	303	-0.3000	0
40	LVAQGLETL	291	-0.4000	0
41	IEGIDDILA	418	-0.4000	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	FVNALKLHS	366	6.1000	68.54
2	LVRLAVGIE	411	5.0000	56.18
3	IVSSPRLYG	114	3.4000	38.20
4	VRSLVIHPA	382	3.0000	33.71
5	FAILNLAGA	102	2.8000	31.46
6	VRPNTKAFF	155	2.7000	30.34

7	FNAFLVAQG	287	2.7000	30.34
8	YLIQPLAQG	201	2.6000	29.21
9	VRLAVGIEG	412	2.6000	29.21
10	LFGLEIPGN	56	2.3500	26.40
11	YGGTYNLFH	121	2.3000	25.84
12	VNALKLHSH	367	2.2000	24.72
13	FLVAQGLET	290	2.0000	22.47
14	ILNLAGAGD	104	1.9000	21.35
15	IQPLAQGAD	203	1.9000	21.35
16	WQAAVRPNT	151	1.8500	20.79
17	YSLAKLGIE	130	1.8000	20.22
18	LNLAGAGDH	105	1.7000	19.10
19	FLSSGQAAE	92	1.5000	16.85
20	VNYAGLPSS	326	1.4500	16.29
21	LETLSLRIE	296	1.3000	14.61
22	VVHSATKYL	213	1.2000	13.48
23	VHSATKYLG	214	1.2000	13.48
24	VANAQRVAE	307	1.2000	13.48
25	FELAGGIEA	354	1.2000	13.48
26	YGSAASPFN	280	1.1500	12.92
27	VLSFELAGG	351	1.1000	12.36
28	FHYSLAKLG	128	1.0000	11.24
29	FALKARVQL	268	0.9000	10.11
30	LRIERHVAN	301	0.9000	10.11
31	VVFAELGPP	258	0.8000	8.99
32	YTRIGNPTT	66	0.6500	7.30
33	FAAARRFSA	432	0.6000	6.74
34	FETKQIHAG	17	0.4000	4.49
35	LKLHSHVAN	370	0.4000	4.49
36	LVIHPASTT	385	0.4000	4.49
37	WSFETKQIH	15	0.3000	3.37
38	FAELGPPAF	260	0.2500	2.81
39	VVEQRIAAL	76	0.2000	2.25
40	LAKLGIEVS	132	0.2000	2.25
41	LIVDNTIAT	191	0.2000	2.25
42	VQLLRDYGS	274	0.2000	2.25
43	IDLLDTPAV	172	0.1500	1.69

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	FVNALKLHS	366	4.0000	47.62
2	VRSLVIHPA	382	3.8000	45.24
3	LVIHPASTT	385	3.0000	35.71
4	VRPNTKAFF	155	2.9000	34.52
5	IERHVANAQ	303	2.9000	34.52
6	IVVHSATKY	212	2.2000	26.19
7	LGGHGAAIA	221	2.2000	26.19
8	IVSSPRLYG	114	2.1000	25.00
9	VNYAGLPSS	326	2.0000	23.81
10	LKLHSHVAN	370	2.0000	23.81
11	LRDYGSAAS	277	1.9000	22.62
12	VNALKLHSH	367	1.7800	21.19
13	LHSHVANIG	372	1.6000	19.05
14	VVHSATKYL	213	1.5000	17.86
15	LGFAAARRF	430	1.5000	17.86
16	YLIQPLAQG	201	1.3000	15.48
17	WHERAKRLA	336	1.3000	15.48
18	VVEQRIAAL	76	1.2000	14.29
19	VLSFELAGG	351	1.2000	14.29
20	LVRLAVGIE	411	1.2000	14.29
21	FAILNLAGA	102	1.1000	13.10
22	VHSATKYLG	214	1.1000	13.10
23	LRIERHVAN	301	1.0000	11.90
24	IHPASTTHA	387	1.0000	11.90
25	VRLAVGIEG	412	1.0000	11.90
26	LVAQGLETL	291	0.9000	10.71
27	VSPGLVRLA	407	0.9000	10.71
28	LAKLGIEVS	132	0.8000	9.52
29	FNAFLVAQG	287	0.8000	9.52
30	FALKARVQL	268	0.7000	8.33
31	VQLLRDYGS	274	0.7000	8.33
32	LFHYSLAKL	127	0.6000	7.14
33	FAAARRFSA	432	0.6000	7.14
34	LKARVQLLR	270	0.4000	4.76
35	LNLAGAGDH	105	0.3800	4.52
36	LPIYATTSY	37	0.3000	3.57
37	IVDNTIATP	192	0.3000	3.57

38	VVFAELGPP	258	0.3000	3.57
39	LFGLEIPGN	56	0.2000	2.38
40	LETLSLRIE	296	0.2000	2.38
41	LFLSSGQAA	91	0.1000	1.19
42	FETKQIHAG	17	-0.1000	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	FVNALKLHS	366	5.0000	59.52
2	VRSLVIHPA	382	2.8000	33.33
3	YLIQPLAQG	201	2.3000	27.38
4	WHERAKRLA	336	2.3000	27.38
5	FAILNLAGA	102	2.1000	25.00
6	LVIHPASTT	385	2.0000	23.81
7	VRPNTKAFF	155	1.9000	22.62
8	IERHVANAQ	303	1.9000	22.62
9	FNAFLVAQG	287	1.8000	21.43
10	FALKARVQL	268	1.7000	20.24
11	FAAARRFSA	432	1.6000	19.05
12	IVVHSATKY	212	1.2000	14.29
13	LGGHGAAIA	221	1.2000	14.29
14	IVSSPRLYG	114	1.1000	13.10
15	VNYAGLPSS	326	1.0000	11.90
16	LKLHSHVAN	370	1.0000	11.90
17	FETKQIHAG	17	0.9000	10.71
18	LRDYGSAAS	277	0.9000	10.71
19	VNALKLHSH	367	0.7800	9.29
20	LHSHVANIG	372	0.6000	7.14
21	WQAAVRPNT	151	0.5000	5.95
22	VVHSATKYL	213	0.5000	5.95
23	LGFAAARRF	430	0.5000	5.95
24	WSFETKQIH	15	0.3800	4.52
25	YNLFHYSLA	125	0.3000	3.57
26	YTFDDTAHA	45	0.2000	2.38
27	VVEQRIAAL	76	0.2000	2.38
28	VLSFELAGG	351	0.2000	2.38

29	LVRLAVGIE	411	0.2000	2.38
30	VHSATKYLG	214	0.1000	1.19
31	LVAQGLETL	291	-0.1000	0
32	FELAGGIEA	354	-0.1000	0
33	VSPGLVRLA	407	-0.1000	0
34	LAKLGIEVS	132	-0.2000	0
35	VQLLRDYGS	274	-0.3000	0
36	LFHYSLAKL	127	-0.4000	0
37	FPGFTTPDP	245	-0.5000	0
38	YGGTYNLFH	121	-0.5200	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	VRPNTKAFF	155	4.8000	54.55
2	FVNALKLHS	366	4.4000	50.00
3	VRSLVIHPA	382	3.8000	43.18
4	LVIHPASTT	385	3.7000	42.05
5	IVSSPRLYG	114	3.5000	39.77
6	IVVHSATKY	212	3.5000	39.77
7	LGFAAARRF	430	3.4000	38.64
8	LHSHVANIG	372	3.0000	34.09
9	LKLHSHVAN	370	2.8000	31.82
10	YLIQPLAQG	201	2.7000	30.68
11	VLSFELAGG	351	2.6000	29.55
12	LVRLAVGIE	411	2.6000	29.55
13	VHSATKYLG	214	2.5000	28.41
14	VVHSATKYL	213	2.4600	27.95
15	VNYAGLPSS	326	2.4000	27.27
16	VRLAVGIEG	412	2.4000	27.27
17	LRDYGSAAS	277	2.3000	26.14
18	LGGHGAAIA	221	2.2000	25.00
19	FNAFLVAQG	287	2.2000	25.00
20	IERHVANAQ	303	2.2000	25.00
21	VVEQRIAAL	76	2.1600	24.55
22	LKARVQLLR	270	1.9000	21.59
23	LVAQGLETL	291	1.8600	21.14

24	LRIERHVAN	301	1.8000	20.45
25	FALKARVQL	268	1.6600	18.86
26	LPIYATTSY	37	1.6000	18.18
27	LETLSLRIE	296	1.6000	18.18
28	LFHYSLAKL	127	1.5600	17.73
29	FETKQIHAG	17	1.3000	14.77
30	IVDNTIATP	192	1.3000	14.77
31	VVFAELGPP	258	1.3000	14.77
32	WHERAKRLA	336	1.3000	14.77
33	LAKLGIEVS	132	1.2000	13.64
34	VNALKLHSH	367	1.2000	13.64
35	FAILNLAGA	102	1.1000	12.50
36	VQLLRDYGS	274	1.1000	12.50
37	VANAQRVAE	307	1.1000	12.50
38	LFGLEIPGN	56	1.0000	11.36
39	LSLRIERHV	299	1.0000	11.36
40	IHPASTTHA	387	1.0000	11.36
41	VSPGLVRLA	407	0.9000	10.23
42	LGIEVSFVD	135	0.8000	9.09
43	IDLLDTPAV	172	0.7000	7.95
44	LAPKGTGAV	343	0.7000	7.95

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VRPNTKAFF	155	4.8000	54.55
2	FVNALKLHS	366	4.4000	50.00
3	VRSLVIHPA	382	3.8000	43.18
4	LVIHPASTT	385	3.7000	42.05
5	IVSSPRLYG	114	3.5000	39.77
6	IVVHSATKY	212	3.5000	39.77
7	LGFAAARRF	430	3.4000	38.64
8	LHSHVANIG	372	3.0000	34.09
9	LKLHSHVAN	370	2.8000	31.82
10	YLIQPLAQG	201	2.7000	30.68
11	VLSFELAGG	351	2.6000	29.55
12	LVRLAVGIE	411	2.6000	29.55

13	VHSATKYLG	214	2.5000	28.41
14	VVHSATKYL	213	2.4600	27.95
15	VNYAGLPSS	326	2.4000	27.27
16	VRLAVGIEG	412	2.4000	27.27
17	LRDYGSAAS	277	2.3000	26.14
18	LGGHGAAIA	221	2.2000	25.00
19	FNAFLVAQG	287	2.2000	25.00
20	IERHVANAQ	303	2.2000	25.00
21	VVEQRIAAL	76	2.1600	24.55
22	LKARVQLLR	270	1.9000	21.59
23	LVAQGLETL	291	1.8600	21.14
24	LRIERHVAN	301	1.8000	20.45
25	FALKARVQL	268	1.6600	18.86
26	LPIYATTSY	37	1.6000	18.18
27	LETLSLRIE	296	1.6000	18.18
28	LFHYSLAKL	127	1.5600	17.73
29	FETKQIHAG	17	1.3000	14.77
30	IVDNTIATP	192	1.3000	14.77
31	VVFAELGPP	258	1.3000	14.77
32	WHERAKRLA	336	1.3000	14.77
33	LAKLGIEVS	132	1.2000	13.64
34	VNALKLHSH	367	1.2000	13.64
35	FAILNLAGA	102	1.1000	12.50
36	VQLLRDYGS	274	1.1000	12.50
37	VANAQRVAE	307	1.1000	12.50
38	LFGLEIPGN	56	1.0000	11.36
39	LSLRIERHV	299	1.0000	11.36
40	IHPASTTHA	387	1.0000	11.36
41	VSPGLVRLA	407	0.9000	10.23
42	LGIEVSFVD	135	0.8000	9.09
43	IDLLDTPAV	172	0.7000	7.95
44	LAPKGTGAV	343	0.7000	7.95

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

Rank	Sequence	At Position	Score	% of Highest Score
1	LVIHPASTT	385	4.8000	48.98

2	VRLAVGIEG	412	4.4000	44.90
3	LFHYSLAKL	127	4.2000	42.86
4	IVSSPRLYG	114	4.1000	41.84
5	YNLFHYSLA	125	3.9000	39.80
6	LRDYGSAAS	277	3.7000	37.76
7	VRSLVIHPA	382	3.5500	36.22
8	LEIPGNIYT	59	3.3000	33.67
9	IVVHSATKY	212	3.0000	30.61
10	VLSFELAGG	351	3.0000	30.61
11	FVNALKLHS	366	2.9000	29.59
12	LPIYATTSY	37	2.7600	28.16
13	VQLLRDYGS	274	2.7000	27.55
14	FLVAQGLET	290	2.7000	27.55
15	IGDVRSLVI	379	2.6000	26.53
16	LIVDNTIAT	191	2.4600	25.10
17	VLSVNYAGL	323	2.3000	23.47
18	VVHSATKYL	213	2.1600	22.04
19	IYTRIGNPT	65	2.1000	21.43
20	VPLIVDNTI	189	2.1000	21.43
21	LLRDYGSAA	276	2.1000	21.43
22	FELAGGIEA	354	2.1000	21.43
23	VVFAELGPP	258	2.0000	20.41
24	LHSHVANIG	372	2.0000	20.41
25	IEGIDDILA	418	2.0000	20.41
26	LYGGTYNLF	120	1.8000	18.37
27	LGGHGAAIA	221	1.8000	18.37
28	VNYAGLPSS	326	1.8000	18.37
29	LKLHSHVAN	370	1.8000	18.37
30	LFLSSGQAA	91	1.7000	17.35
31	VAHRNGVPL	183	1.7000	17.35
32	LRIERHVAN	301	1.7000	17.35
33	VRPNTKAFF	155	1.6000	16.33
34	IYATTSYTF	39	1.5000	15.31
35	LGIEVSFVD	135	1.5000	15.31
36	IVDGGNFDW	232	1.5000	15.31
37	VGIEGIDDI	416	1.4500	14.80
38	LAQGADIVV	206	1.4000	14.29
39	YLGGHGAAI	220	1.4000	14.29
40	LKARVQLLR	270	1.4000	14.29
41	LATGVSPGL	403	1.4000	14.29
42	FAAARRFSA	432	1.4000	14.29

43	WQAAVRPNT	151	1.3000	13.27
44	LVAQGLETL	291	1.3000	13.27

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

Rank	Sequence	At Position	Score	% of Highest Score
1	YNLFHYSLA	125	4.9000	50.00
2	FVNALKLHS	366	3.9000	39.80
3	LVIHPASTT	385	3.8000	38.78
4	FLVAQGLET	290	3.7000	37.76
5	VRLAVGIEG	412	3.4000	34.69
6	LFHYSLAKL	127	3.2000	32.65
7	IVSSPRLYG	114	3.1000	31.63
8	FELAGGIEA	354	3.1000	31.63
9	LRDYGSAAS	277	2.7000	27.55
10	VRSLVIHPA	382	2.5500	26.02
11	YLGGHGAAI	220	2.4000	24.49
12	FAAARRFSA	432	2.4000	24.49
13	LEIPGNIYT	59	2.3000	23.47
14	WQAAVRPNT	151	2.3000	23.47
15	FAILNLAGA	102	2.2000	22.45
16	YTRIGNPTT	66	2.1000	21.43
17	FALKARVQL	268	2.1000	21.43
18	FNAFLVAQG	287	2.1000	21.43
19	IVVHSATKY	212	2.0000	20.41
20	VLSFELAGG	351	2.0000	20.41
21	YGGTYNLFH	121	1.9000	19.39
22	LPIYATTSY	37	1.7600	17.96
23	VQLLRDYGS	274	1.7000	17.35
24	IGDVRSLVI	379	1.6000	16.33
25	LIVDNTIAT	191	1.4600	14.90
26	FGLEIPGNI	57	1.4000	14.29
27	YHGVVFAEL	255	1.4000	14.29
28	VLSVNYAGL	323	1.3000	13.27
29	FPGFTTPDP	245	1.2600	12.86
30	VVHSATKYL	213	1.1600	11.84
31	IYTRIGNPT	65	1.1000	11.22

32	VPLIVDNTI	189	1.1000	11.22
33	YLIQPLAQG	201	1.1000	11.22
34	LLRDYGSAA	276	1.1000	11.22
35	VVFAELGPP	258	1.0000	10.20
36	LHSHVANIG	372	1.0000	10.20
37	IEGIDDILA	418	1.0000	10.20
38	LYGGTYNLF	120	0.8000	8.16
39	LGGHGAAIA	221	0.8000	8.16
40	VNYAGLPSS	326	0.8000	8.16
41	LKLHSHVAN	370	0.8000	8.16
42	LFLSSGQAA	91	0.7000	7.14
43	VAHRNGVPL	183	0.7000	7.14
44	LRIERHVAN	301	0.7000	7.14

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	LVIHPASTT	385	4.8000	48.98
2	VRLAVGIEG	412	4.4000	44.90
3	LFHYSLAKL	127	4.2000	42.86
4	IVSSPRLYG	114	4.1000	41.84
5	YNLFHYSLA	125	3.9000	39.80
6	LRDYGSAAS	277	3.7000	37.76
7	VRSLVIHPA	382	3.5500	36.22
8	LEIPGNIYT	59	3.3000	33.67
9	IVVHSATKY	212	3.0000	30.61
10	VLSFELAGG	351	3.0000	30.61
11	FVNALKLHS	366	2.9000	29.59
12	LPIYATTSY	37	2.7600	28.16
13	VQLLRDYGS	274	2.7000	27.55
14	FLVAQGLET	290	2.7000	27.55
15	IGDVRSLVI	379	2.6000	26.53
16	LIVDNTIAT	191	2.4600	25.10
17	VLSVNYAGL	323	2.3000	23.47
18	VVHSATKYL	213	2.1600	22.04
19	IYTRIGNPT	65	2.1000	21.43
20	VPLIVDNTI	189	2.1000	21.43

21	LLRDYGSAA	276	2.1000	21.43
22	FELAGGIEA	354	2.1000	21.43
23	VVFAELGPP	258	2.0000	20.41
24	LHSHVANIG	372	2.0000	20.41
25	IEGIDDILA	418	2.0000	20.41
26	LYGGTYNLF	120	1.8000	18.37
27	LGGHGAAIA	221	1.8000	18.37
28	VNYAGLPSS	326	1.8000	18.37
29	LKLHSHVAN	370	1.8000	18.37
30	LFLSSGQAA	91	1.7000	17.35
31	VAHRNGVPL	183	1.7000	17.35
32	LRIERHVAN	301	1.7000	17.35
33	VRPNTKAFF	155	1.6000	16.33
34	IYATTSYTF	39	1.5000	15.31
35	LGIEVSFVD	135	1.5000	15.31
36	IVDGGNFDW	232	1.5000	15.31
37	VGIEGIDDI	416	1.4500	14.80
38	LAQGADIVV	206	1.4000	14.29
39	YLGGHGAAI	220	1.4000	14.29
40	LKARVQLLR	270	1.4000	14.29
41	LATGVSPGL	403	1.4000	14.29
42	FAAARRFSA	432	1.4000	14.29
43	WQAAVRPNT	151	1.3000	13.27
44	LVAQGLETL	291	1.3000	13.27

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLAVGIEG	412	3.5000	35.71
2	LGFAAARRF	430	2.8000	28.57
3	LNLAGAGDH	105	2.4000	24.49
4	FHYSLAKLG	128	2.4000	24.49
5	FVNALKLHS	366	2.4000	24.49
6	FGLEIPGNI	57	2.2000	22.45
7	VVHSATKYL	213	2.2000	22.45
8	IYATTSYTF	39	2.1000	21.43
9	FELAGGIEA	354	2.0000	20.41

10	IVVHSATKY	212	1.8000	18.37
11	VRSLVIHPA	382	1.8000	18.37
12	YHGVVFAEL	255	1.7000	17.35
13	VQLLRDYGS	274	1.7000	17.35
14	FLVAQGLET	290	1.6000	16.33
15	VLSVNYAGL	323	1.6000	16.33
16	VNALKLHSH	367	1.6000	16.33
17	YGGTYNLFH	121	1.3000	13.27
18	YLIQPLAQG	201	1.2000	12.24
19	FAILNLAGA	102	1.1000	11.22
20	LVRLAVGIE	411	1.1000	11.22
21	LELGFAAAR	428	1.0000	10.20
22	LVIHPASTT	385	0.8000	8.16
23	LFLSSGQAA	91	0.7000	7.14
24	VVFAELGPP	258	0.7000	7.14
25	IGDVRSLVI	379	0.6000	6.12
26	IVSSPRLYG	114	0.5000	5.10
27	VPLIVDNTI	189	0.5000	5.10
28	YLGGHGAAI	220	0.5000	5.10
29	LPIYATTSY	37	0.2000	2.04
30	FAELGPPAF	260	0.2000	2.04
31	LPSSPWHER	331	0.2000	2.04
32	FAAARRFSA	432	0.2000	2.04
33	VDNTIATPY	193	0.1000	1.02
34	VHSATKYLG	214	0.1000	1.02
35	LKARVQLLR	270	0.1000	1.02
36	YTRIGNPTT	66	-0.1000	0
37	IAALEGGVA	81	-0.1000	0
38	LRIERHVAN	301	-0.1000	0
39	FAETISNPQ	163	-0.2000	0
40	LVAQGLETL	291	-0.2000	0
41	IEGIDDILA	418	-0.2000	0

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

Rank	Sequence	At Position	Score	% of Highest Score
1	VRLAVGIEG	412	3.5000	35.71

2	LGFAAARRF	430	2.8000	28.57
3	LNLAGAGDH	105	2.4000	24.49
4	FHYSLAKLG	128	2.4000	24.49
5	FVNALKLHS	366	2.4000	24.49
6	FGLEIPGNI	57	2.2000	22.45
7	VVHSATKYL	213	2.2000	22.45
8	IYATTSYTF	39	2.1000	21.43
9	FELAGGIEA	354	2.0000	20.41
10	IVVHSATKY	212	1.8000	18.37
11	VRSLVIHPA	382	1.8000	18.37
12	YHGVVFAEL	255	1.7000	17.35
13	VQLLRDYGS	274	1.7000	17.35
14	FLVAQGLET	290	1.6000	16.33
15	VLSVNYAGL	323	1.6000	16.33
16	VNALKLHSH	367	1.6000	16.33
17	YGGTYNLFH	121	1.3000	13.27
18	YLIQPLAQG	201	1.2000	12.24
19	FAILNLAGA	102	1.1000	11.22
20	LVRLAVGIE	411	1.1000	11.22
21	LELGFAAAR	428	1.0000	10.20
22	LVIHPASTT	385	0.8000	8.16
23	LFLSSGQAA	91	0.7000	7.14
24	VVFAELGPP	258	0.7000	7.14
25	IGDVRSLVI	379	0.6000	6.12
26	IVSSPRLYG	114	0.5000	5.10
27	VPLIVDNTI	189	0.5000	5.10
28	YLGGHGAAI	220	0.5000	5.10
29	LPIYATTSY	37	0.2000	2.04
30	FAELGPPAF	260	0.2000	2.04
31	LPSSPWHER	331	0.2000	2.04
32	FAAARRFSA	432	0.2000	2.04
33	VDNTIATPY	193	0.1000	1.02
34	VHSATKYLG	214	0.1000	1.02
35	LKARVQLLR	270	0.1000	1.02
36	YTRIGNPTT	66	-0.1000	0
37	IAALEGGVA	81	-0.1000	0
38	LRIERHVAN	301	-0.1000	0
39	FAETISNPQ	163	-0.2000	0
40	LVAQGLETL	291	-0.2000	0
41	IEGIDDILA	418	-0.2000	0