MHC Class-II Binding Peptide Prediction Results

HELP	HOME	MHC & Prediction Algorithm

INPUT & PARAMETER INFORMATION

Antigen Name	test
Scanned on	Sun Jan 31 12:50:56 2010
Length of input sequence	560 amino acids
Number of nanomers from input sequence	552
Number of nanomers with obligatory P1 anchor residue	173
Threshold setting	3
Number of alleles in query	3
Number of top scorers to be displayed	56

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	IVNANAAHL	163	2.1000	35.00
2	LLNLPAARV	9	1.7000	28.33
3	FGRLKALGR	382	1.4000	23.33
4	LLRSHAVTL	186	1.2000	20.00
5	VVMIGMLSS	413	1.2000	20.00
6	IGMLSSVVG	416	1.1000	18.33
7	LVLAAGPDG	39	1.0700	17.83
8	LQRQLGILS	529	1.0000	16.67
9	LGLFNPLSV	425	0.9800	16.33
10	FVRQAHQIC	136	0.9000	15.00
11	LRVEVGAPS	75	0.7000	11.67
12	LGRMESKPL	388	0.7000	11.67
13	MIGMLSSVV	415	0.6000	10.00
14	WREIVNANA	160	0.4000	6.67

15	IVKFLSEQV	208	0.2800	4.67
16	WAYQRSEAL	344	0.2000	3.33
17	LNSLLNLPA	6	0.1000	1.67
18	VVSYSAQPS	28	0.1000	1.67
19	VKFLSEQVL	209	0.1000	1.67
20	VENAIATAV	330	-0.0100	0
21	LRRGHKMII	396	-0.0100	0
22	VITVVSYSA	25	-0.0500	0
23	ICPVGAVVA	143	-0.0500	0
24	IIGMRGSYG	403	-0.2000	0
25	LAGLEPTLT	543	-0.2100	0
26	YSAQPSARL	31	-0.3000	0
27	MPIIAVSSL	178	-0.3000	0
28	YQRSEALAD	346	-0.4000	0
29	MRGSYGGVV	406	-0.4000	0
30	YGGVVMIGM	410	-0.4700	0
31	LKMIQRLLR	482	-0.5000	0
32	LAFIDTPGV	90	-0.5300	0
33	VVGLGLFNP	422	-0.6000	0
34	VGGLGQPHL	98	-0.6300	0
35	LSSVVGLGL	419	-0.6500	0
36	VGAVVATKT	146	-0.6600	0
37	VRSEAKANV	455	-0.7000	0
38	IRSATEQLA	232	-0.8000	0
39	LRGGLAFID	86	-0.9000	0
40	VEVGAPSPL	77	-1.0000	0
41	LGLLPEADA	110	-1.0000	0
42	FLSEQVLSR	211	-1.0000	0
43	VMIGMLSSV	414	-1.0000	0
44	FNPLSVGAG	428	-1.0000	0
45	LSVGAGLIL	431	-1.0000	0
46	LKALGRMES	385	-1.0100	0
47	VRRAPHAGG	63	-1.1000	0
48	VRQAHQICP	137	-1.1000	0
49	LGILSQVND	533	-1.1000	0
50	LAVSLGSEL	239	-1.2000	0
51	LQRARVPMP	171	-1.2300	0
52	IIAVSSLLR	180	-1.2500	0
53	LLRGGLAFI	85	-1.3000	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	IVNANAAHL	163	3.1000	51.67
2	LLNLPAARV	9	2.7000	45.00
3	LLRSHAVTL	186	2.2000	36.67
4	VVMIGMLSS	413	2.2000	36.67
5	IGMLSSVVG	416	2.1000	35.00
6	LVLAAGPDG	39	2.0700	34.50
7	LQRQLGILS	529	2.0000	33.33
8	LGLFNPLSV	425	1.9800	33.00
9	LRVEVGAPS	75	1.7000	28.33
10	LGRMESKPL	388	1.7000	28.33
11	MIGMLSSVV	415	1.6000	26.67
12	FGRLKALGR	382	1.4000	23.33
13	IVKFLSEQV	208	1.2800	21.33
14	LNSLLNLPA	6	1.1000	18.33
15	VVSYSAQPS	28	1.1000	18.33
16	VKFLSEQVL	209	1.1000	18.33
17	VVITVVSYS	24	1.0000	16.67
18	VENAIATAV	330	0.9900	16.50
19	LRRGHKMII	396	0.9900	16.50
20	VITVVSYSA	25	0.9500	15.83
21	ICPVGAVVA	143	0.9500	15.83
22	FVRQAHQIC	136	0.9000	15.00
23	IIGMRGSYG	403	0.8000	13.33
24	LAGLEPTLT	543	0.7900	13.17
25	MPIIAVSSL	178	0.7000	11.67
26	MRGSYGGVV	406	0.6000	10.00
27	LKMIQRLLR	482	0.5000	8.33
28	LAFIDTPGV	90	0.4700	7.83
29	VVGLGLFNP	422	0.4000	6.67
30	VGGLGQPHL	98	0.3700	6.17
31	LSSVVGLGL	419	0.3500	5.83
32	VGAVVATKT	146	0.3400	5.67
33	VRSEAKANV	455	0.3000	5.00
34	IRSATEQLA	232	0.2000	3.33
35	LRGGLAFID	86	0.1000	1.67
36	LKALGRMES	385	-0.0100	0

37	VRRAPHAGG	63	-0.1000	0
38	VRQAHQICP	137	-0.1000	0
39	LGILSQVND	533	-0.1000	0
40	LAVSLGSEL	239	-0.2000	0
41	LQRARVPMP	171	-0.2300	0
42	IIAVSSLLR	180	-0.2500	0
43	LLRGGLAFI	85	-0.3000	0
44	LFNPLSVGA	427	-0.5000	0
45	IRELQRQLG	526	-0.5000	0
46	LRSHAVTLN	187	-0.5100	0
47	WREIVNANA	160	-0.6000	0
48	ISFVVSKQS	470	-0.6500	0
49	VNANAAHLQ	164	-0.6600	0
50	LPEADAVLV	113	-0.7000	0
51	VGLGLFNPL	423	-0.7000	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	LRRGHKMII	396	6.4000	67.37
2	VVSDTSQEF	121	5.3000	55.79
3	VVITVVSYS	24	4.9700	52.32
4	LKMIQRLLR	482	4.7000	49.47
5	MIIGMRGSY	402	4.5000	47.37
6	VVMIGMLSS	413	4.4000	46.32
7	LKALGRMES	385	4.3000	45.26
8	VVNDPNLRD	249	3.9000	41.05
9	LVVSDTSQE	120	3.8700	40.74
10	VMIGMLSSV	414	3.6700	38.63
11	VRAGVLGEI	224	3.6000	37.89
12	MLSSVVGLG	418	3.6000	37.89
13	LVLAAGPDG	39	3.5000	36.84
14	LQRARVPMP	171	3.5000	36.84
15	VRRAPHAGG	63	3.2000	33.68
16	LAFIDTPGV	90	3.1000	32.63
17	LLRGGLAFI	85	3.0000	31.58
18	VDHDLRTRF	295	3.0000	31.58

19	VRSEAKANV	455	3.0000	31.58
20	LRSHAVTLN	187	2.9000	30.53
21	LRGGLAFID	86	2.8000	29.47
22	MRGSYGGVV	406	2.8000	29.47
23	FVDDISFVV	466	2.8000	29.47
24	MPIIAVSSL	178	2.7300	28.74
25	VLRVEVGAP	74	2.7000	28.42
26	IAVSSLLRS	181	2.7000	28.42
27	VVGLGLFNP	422	2.7000	28.42
28	LQRQLGILS	529	2.7000	28.42
29	IQRLLRDHY	485	2.6000	27.37
30	IVNANAAHL	163	2.5600	26.95
31	LLRSHAVTL	186	2.5600	26.95
32	IPVDDISTD	54	2.4700	26.00
33	IGNDVENAI	326	2.4100	25.37
34	IGMLSSVVG	416	2.4000	25.26
35	VGAGLILGR	433	2.4000	25.26
36	VVSYSAQPS	28	2.3000	24.21
37	LLRDHYREI	488	2.3000	24.21
38	IRELQRQLG	526	2.3000	24.21
39	LRVEVGAPS	75	2.1000	22.11
40	LLNSLLNLP	5	2.0100	21.16
41	VRQAHQICP	137	2.0000	21.05
42	VLGDGFNDL	283	1.9700	20.74
43	ITRSLTESL	500	1.9600	20.63
44	FPAIVKFLS	205	1.9000	20.00
45	LLNLPAARV	9	1.8000	18.95
46	ISTDVRRAP	59	1.8000	18.95
47	FNPLSVGAG	428	1.8000	18.95
48	VGDDEATVV	17	1.7000	17.89
49	VPMPIIAVS	176	1.7000	17.89
50	IIAVSSLLR	180	1.7000	17.89
51	VTLNDKELN	192	1.7000	17.89
52	LRDHYREIA	489	1.7000	17.89
53	VEVGAPSPL	77	1.6300	17.16
54	VSYSAQPSA	29	1.6000	16.84
55	FVRQAHQIC	136	1.6000	16.84
56	VVATKTDLY	149	1.6000	16.84