

Table 3. Binding prediction accuracy of ProPred algorithm for different MHC class II alleles when peptide length was incorporated

	ProPred: DRB1*0101	ProPred: DRB1*0401	ProPred: DRB1*1501
Combination rule	0.369	0.499	0.310
Highest scoring register	0.307 ¹	0.494 ¹	0.297 ¹
Mod. 2: Equilibrium formula	0.379	0.538	0.291

Matrices were obtained from the ProPred website and used to calculate a score for each register within a peptide. To each score the approximate affinity of an all-alanine 9mer to MHC was added ($pIC_{50} = 6.169$, Doytchinova and Flower 2003). The mean Pearson correlation coefficient between predicted and experimentally determined pIC_{50} values is shown. ¹Highest ProPred-predicted scores from all eligible registers were used as baseline predictions following recent precedents (Brusic *et al.* 1998, Nielsen *et al.* 2004, Murugan and Dai 2005).