Table 4. Binding prediction accuracy of ISC-PLS algorithm for MHC class II alleles having small data sets

	ISC-PLS	ISC-PLS of 0401[1]	**Mod. 1**: Regression fit	**Mod. 1**: Regression fit of 0401[2]	**Alt. 1**: Length as variable	**Mod. 2**: Equil. formula
DRB1*0404	0.462 ± 0.017	0.468	0.410 ± 0.033	0.458 ± 0.029	0.390 ± 0.020	0.439 ± 0.032
DRB1*0405	0.664 ± 0.014	0.542	0.682 ± 0.013	0.625 ± 0.008	0.680 ± 0.015	**0.742 ± 0.010**

Five-fold cross-validation (5x-CV) was used and repeated five times. Mean A_{ROC} scores between predicted and experimentally determined pIC_{50} values are shown with standard errors of the mean. Highest scores are shown in bold with multiple scores in bold if pair-wise differences were not statistically significant. A threshold of 500 nM (Sette 1994) was used to distinguish binding from non-binding peptides. [1]The ISC-PLS algorithm was derived for the DRB1*0401 data set first and then used to make predictions on the peptides in the *0404 or *0405 data sets. Note: no standard error is listed in this case due to the lack of different training and test sets which provide the basis for obtaining multiple AROC scores and subsequently standard error. [2]The regression fit for DRB1*0401 was used as the basis of the modification rather than the regression fit for *0404 or *0405.