



**Figure 4. Length distribution of amino terminal PFR for MHC-II binding and non-binding peptides. All peptide data for the three alleles in the AntiJen and IEDB data sets are included in the figure. Binding peptides have an affinity stronger than 50 nM. The PFR is defined, as the residues flanking the peptide-binding core as determined by the SMM-align method.**