

Figure 5. Kullback-Leibler logo visualizations of peptide binding motifs. The upper panel depicts the motif for the DRB1*0101 allele, and the lower panel the motif for the DRB1*1302 alleles. From left the different columns show the motif estimated by the SMM-align, Gibbs sample, and TEPITOPE methods, respectively. The height of a column in the logo is proportional to the relative information content in the sequence motif, and the letter height is proportional to the amino acid frequency [22].