Dengue is a major public health problem that affects over 100 tropical and subtropical countries. Dengue viruses (DENV) are comprised of four serotypes (DENV-1 to -4) that show substantial genetic diversity, both within and between serotypes. The co-circulation of various DENV serotypes is considered a risk factor associated with the emergence of dengue severe disease, dengue hemorrhagic fever/dengue shock syndrome (DHF or DSS). Early diagnosis is extremely important to reduce the morbidity and mortality of DHF and DSS, and recently, at least two DENV NS1 antigen capture immunoassays have become available for the early diagnosis of dengue. Nevertheless, these assays are unable to distinguish between DENV serotypes because the antibodies used to detect DENV NS1 are directed against cross-reactive antigenic determinants shared by all four DENV serotypes. The production of epitope-specific monoclonal antibodies (MAbs) holds potential for developing type-specific NS1 antigen assays. Thus, the identification of B-cell epitopes has become a prerequisite for the production of type-specific NS1 antigen assays. This work aimed at the identification of DENV serotype specific B-cell antigenic epitopes in the NS1 protein. Since consensus predictions are more reliable than individual predictions, DENV NS1 protein sequences retrieved from NCBI GenBank database were submitted to ABCpred server, Bcepred, BCPREDS and Antibody Epitope Prediction engines. ABCpred server predicts B cell epitopes, using artificial neural network. Bcepred and Antibody Epitope Prediction predict linear B-cell epitopes using physicochemical properties (hydrophilicity, flexibility/mobility, accessibility, polarity, exposed surface and turns) or a combination of properties. BCPREDS server uses AAP method, BCPred and FBCPred. BCEPREDS was unable to detect any epitope only present DENV-1, but by using AAP analyses we could find one epitope specific for DENV-1. The Bcepred and the Antibody Epitope Prediction programs were able to detect most of the specific epitopes to each DENV serotype. Considering the analyses for NS1 epitope prediction altogether, we were able to observe that 8 epitopes were exclusively present in DENV-1, 16 in DENV-2, 10 in DENV-3 and 15 in DENV-4. The epitopes of DENV-1 and DENV-3 were closely related to each other than the epitopes from DENV-2 and DENV-4. Most of the predicted epitopes with the best scores were shared amongst all serotypes, showing that this protein is highly conserved among DENV serotypes. However, the non-conserved NS1peptides identified in this study may prove critical for developing a diagnostic test that can be used early in dengue infection and differentiate amongst DENV serotypes.