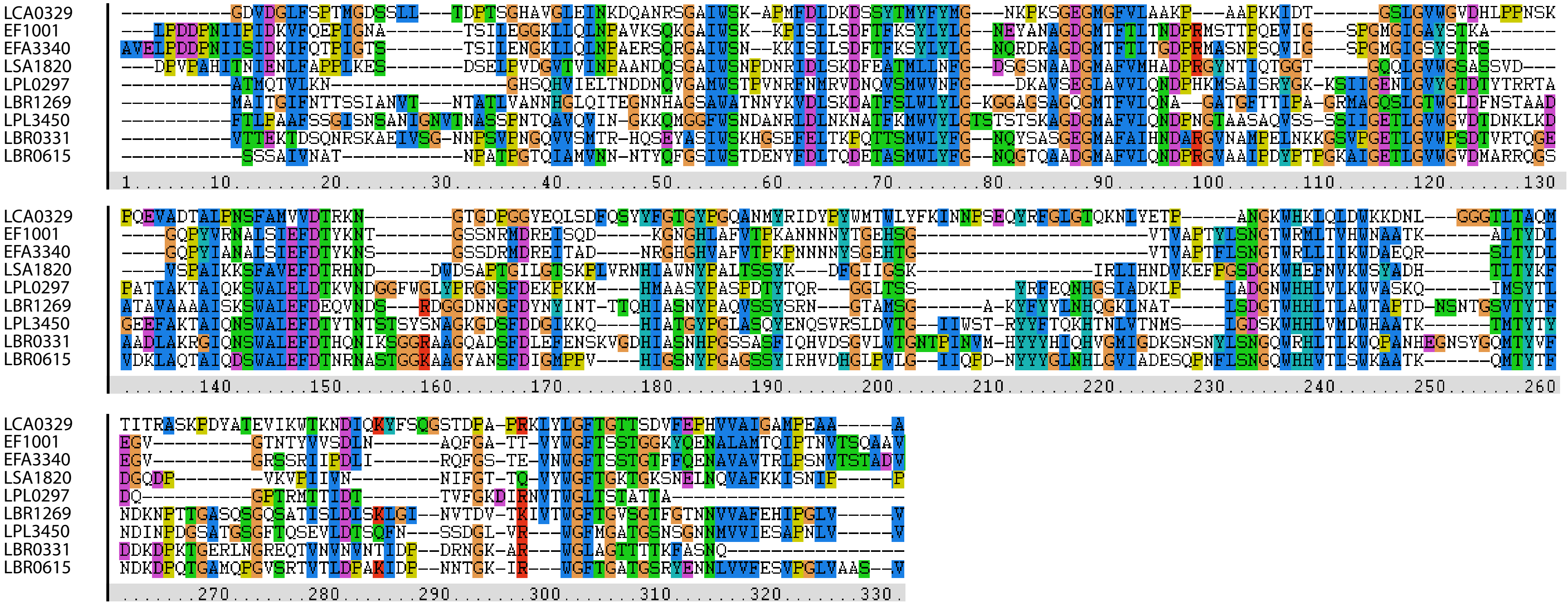

**Figure 7:**
Multiple sequence aligment of ConA-like lectins/glucanases domains of Csc proteins. See additional file Table 7 for details of domain architectures. Colour coding of highly conserved residues: dark blue, hydrophobic (W, F, L, V, I, M, A); red, basic (R, K); purple, acidic (D, E); green, neutral and small (T, S, N, Q); light blue, cyclic and neutral (Y, H); light brown, glycine (G); olive, proline (P).