

Figure S1: Distribution of Jaccard indices for interacting proteins based on MIPS FunCat.

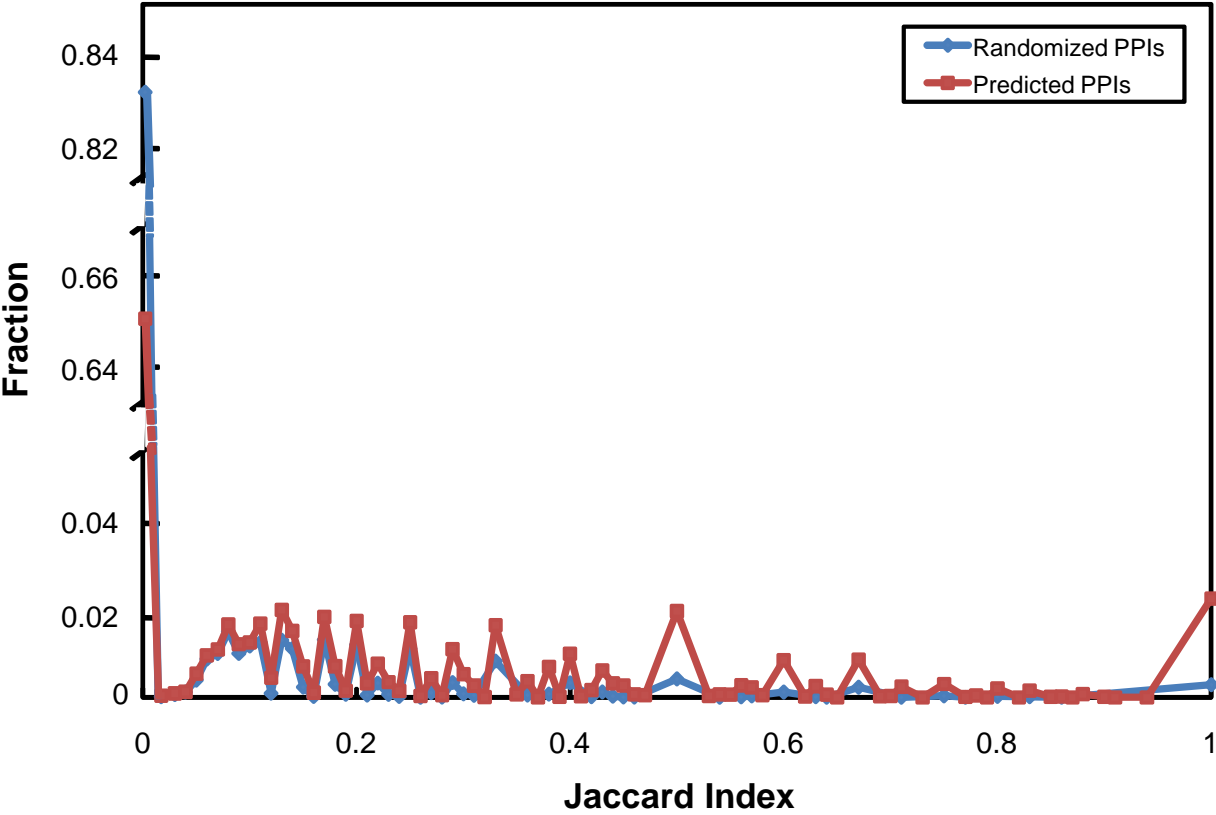
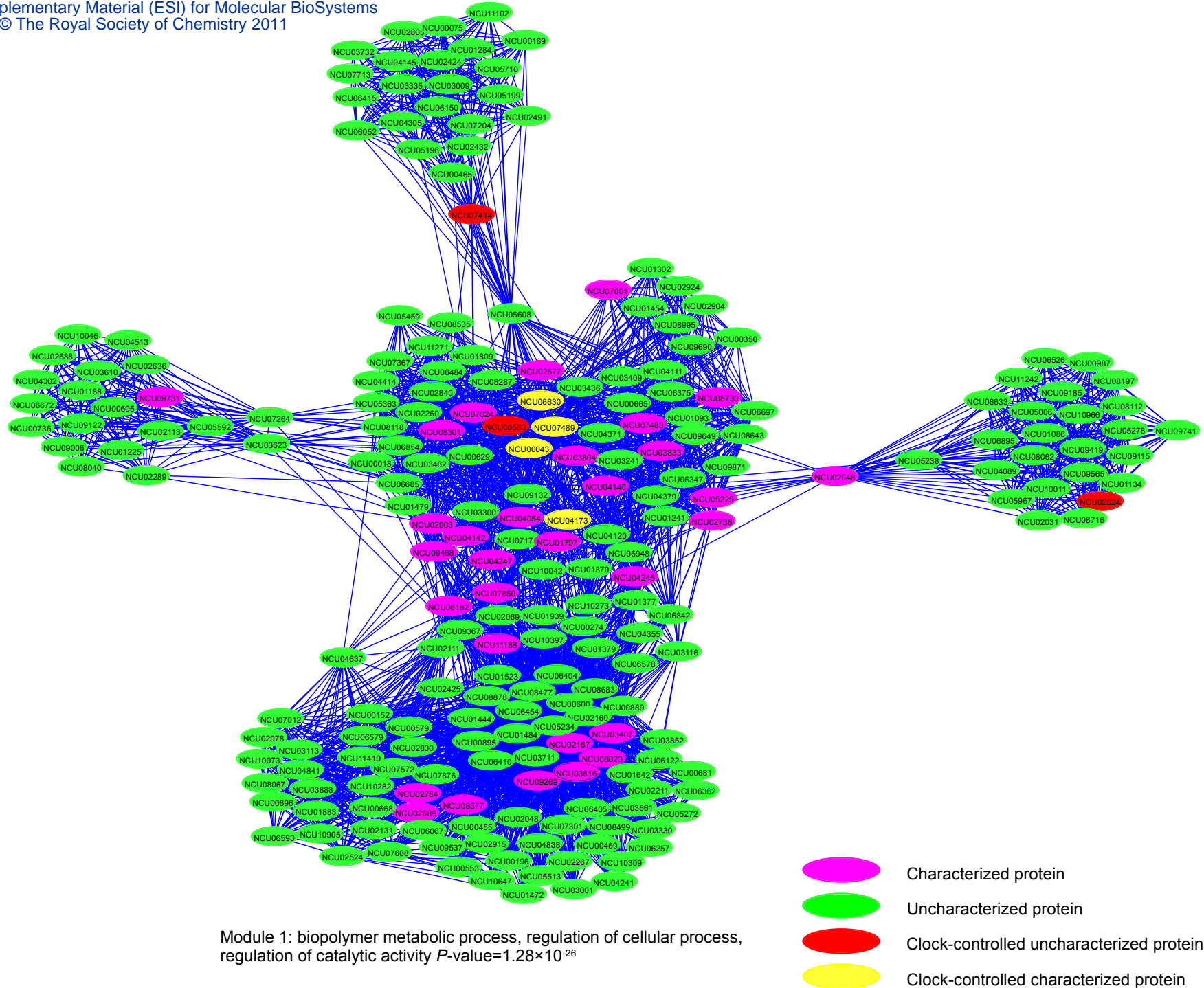
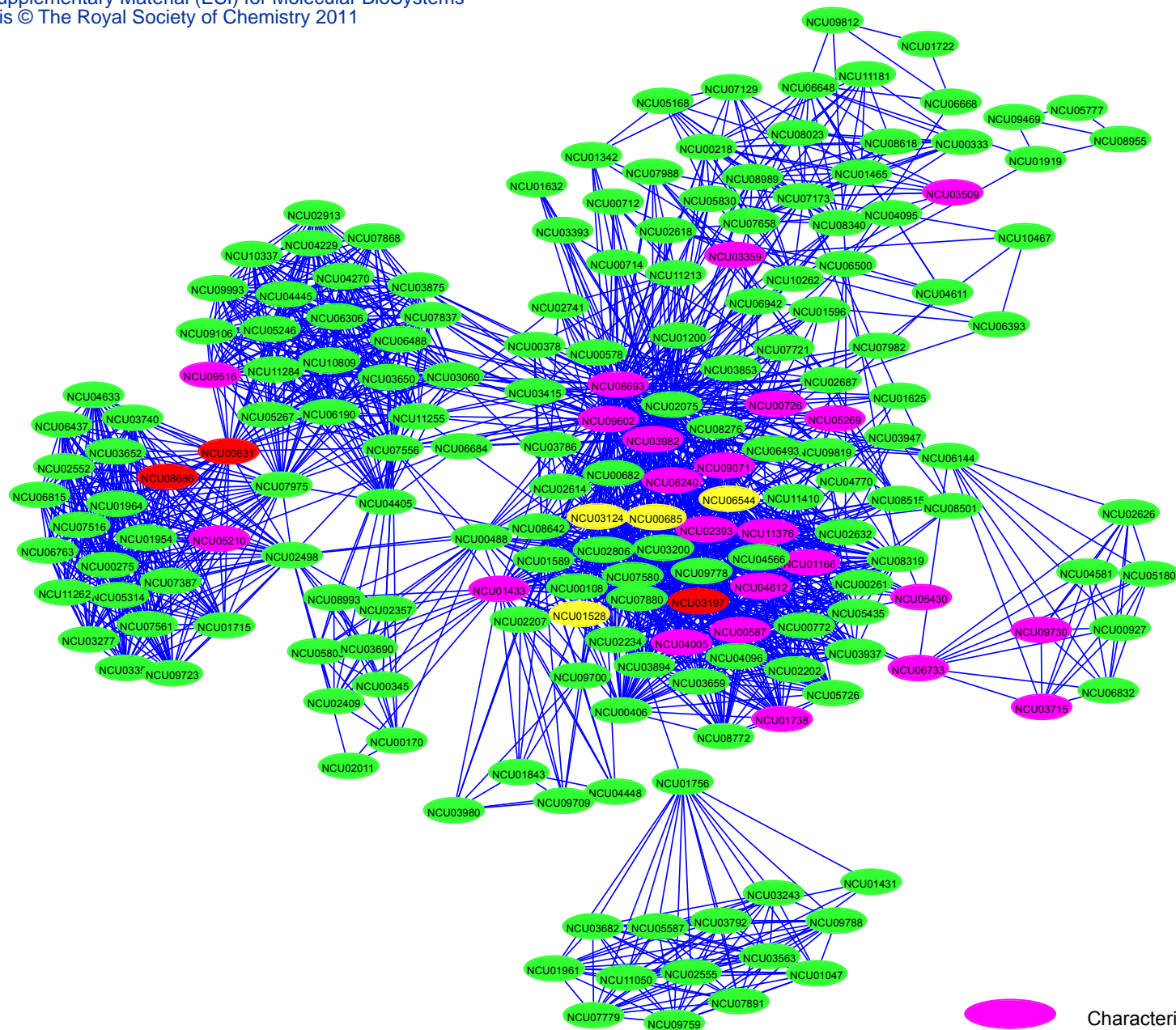


Figure S2: The clock-related modules, which were ranked as top six, with MCODE score outweigh 5 were identified in the predicted PPI network of *N. crassa*. Interestingly, three modules (Modules 3, 5 and 6) were also identified by CFinder (<http://www.cfinder.org>). The description alongside each module is the enriched GO term identified by Fisher's exact test followed by the q-value false discovery rate (FDR) correction (<http://genomics.princeton.edu/storeylab/qvalue/>) with a cut-off of 0.01, and the corresponding corrected *P*-value is also listed. Characterized proteins (fuchsia nodes), uncharacterized proteins (green nodes), clock-controlled uncharacterized proteins (red nodes) and clock-controlled characterized proteins (yellow nodes). You can zoom in for a clear view. Note that Module 3 is not presented in this file, since it was already shown in the main text (Figure 4).





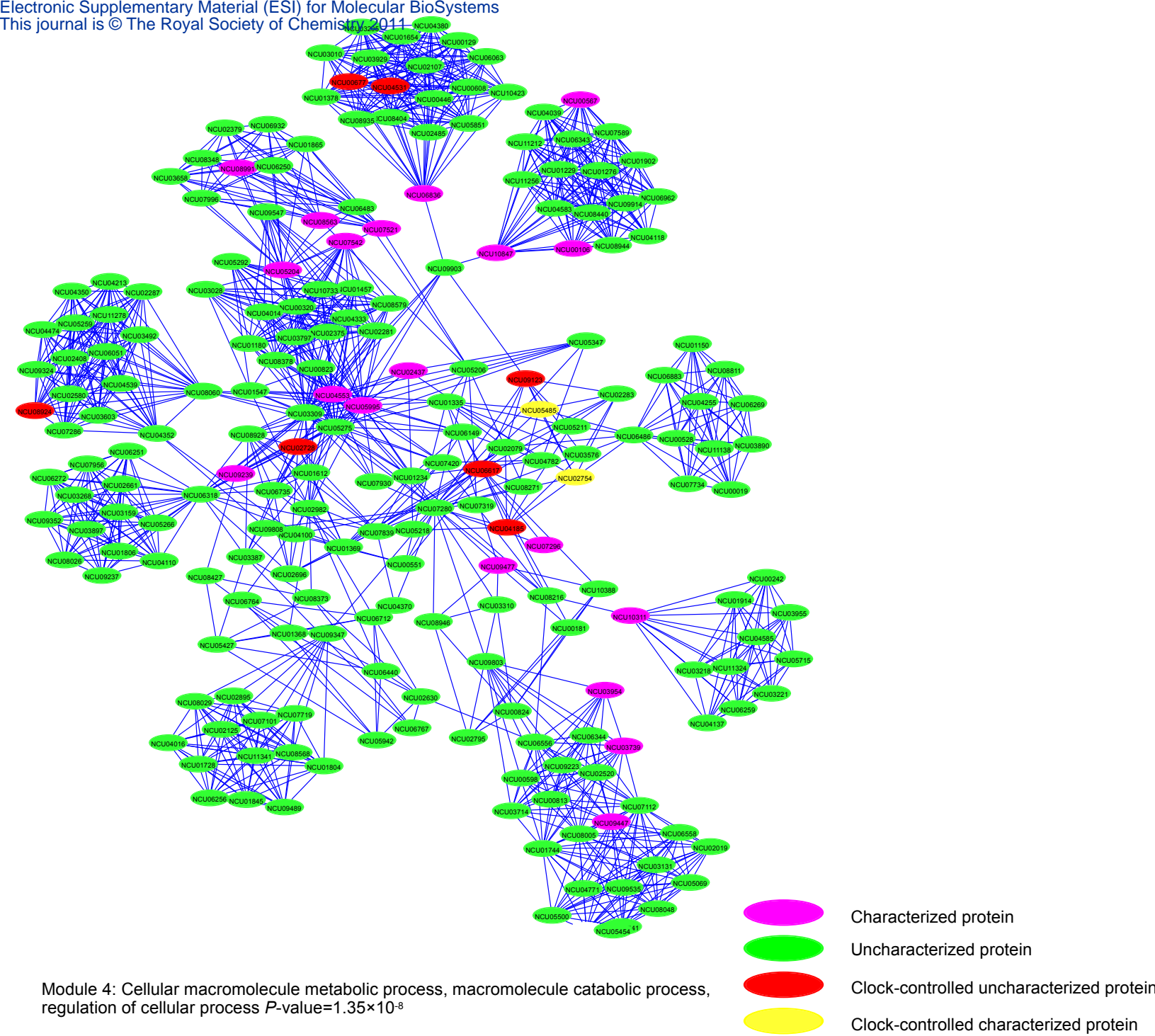
Module 2: Cellular macromolecule metabolic process,phosphorus metabolic process, biopolymer metabolic process P -value= 7.23×10^{-15}

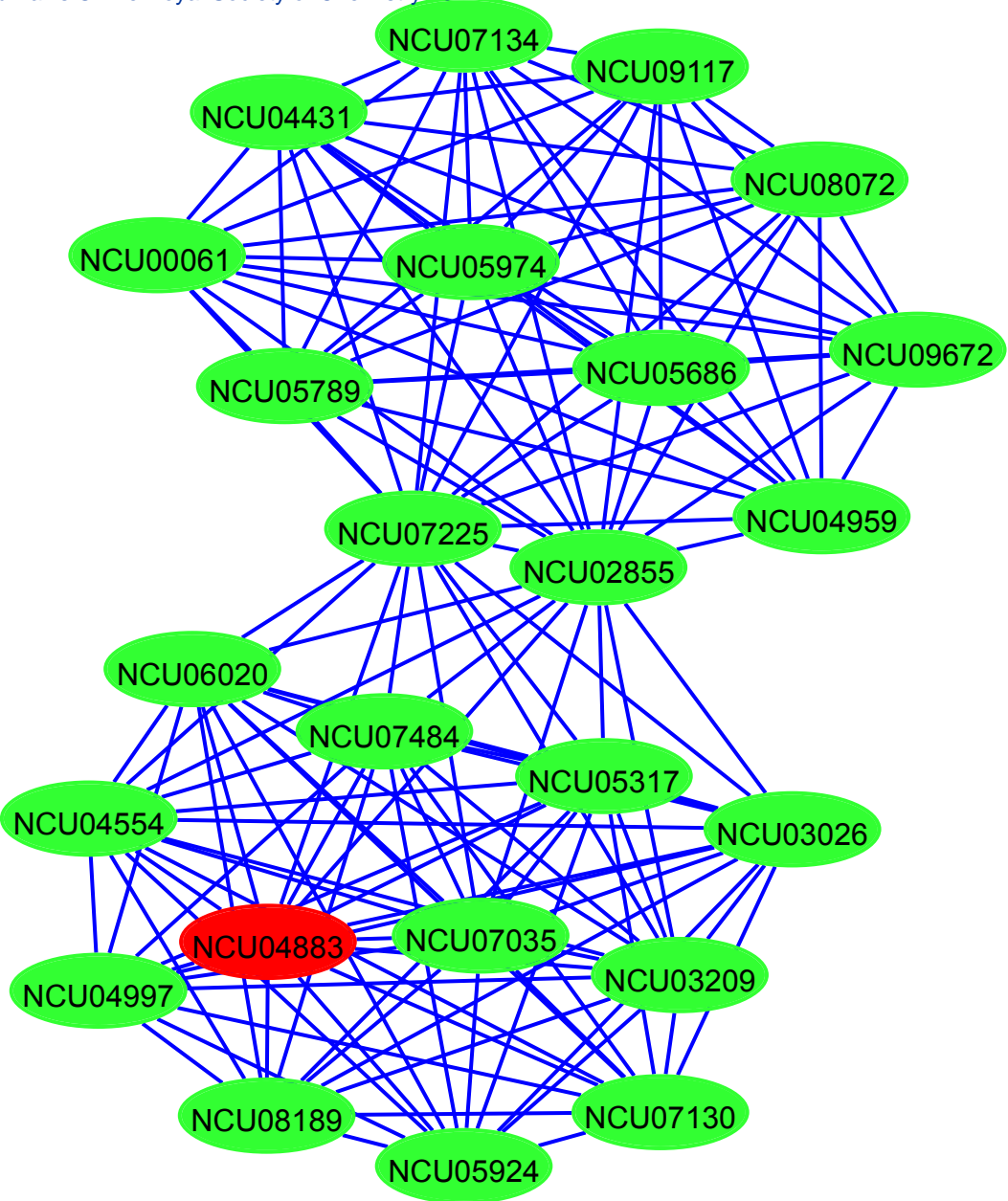
Characterized protein

Uncharacterized protein

Clock-controlled uncharacterized protein

Clock-controlled characterized protein





Module 5: Cell wall macromolecule metabolic process,
cell wall organization P -value= 1.30×10^{-7}

