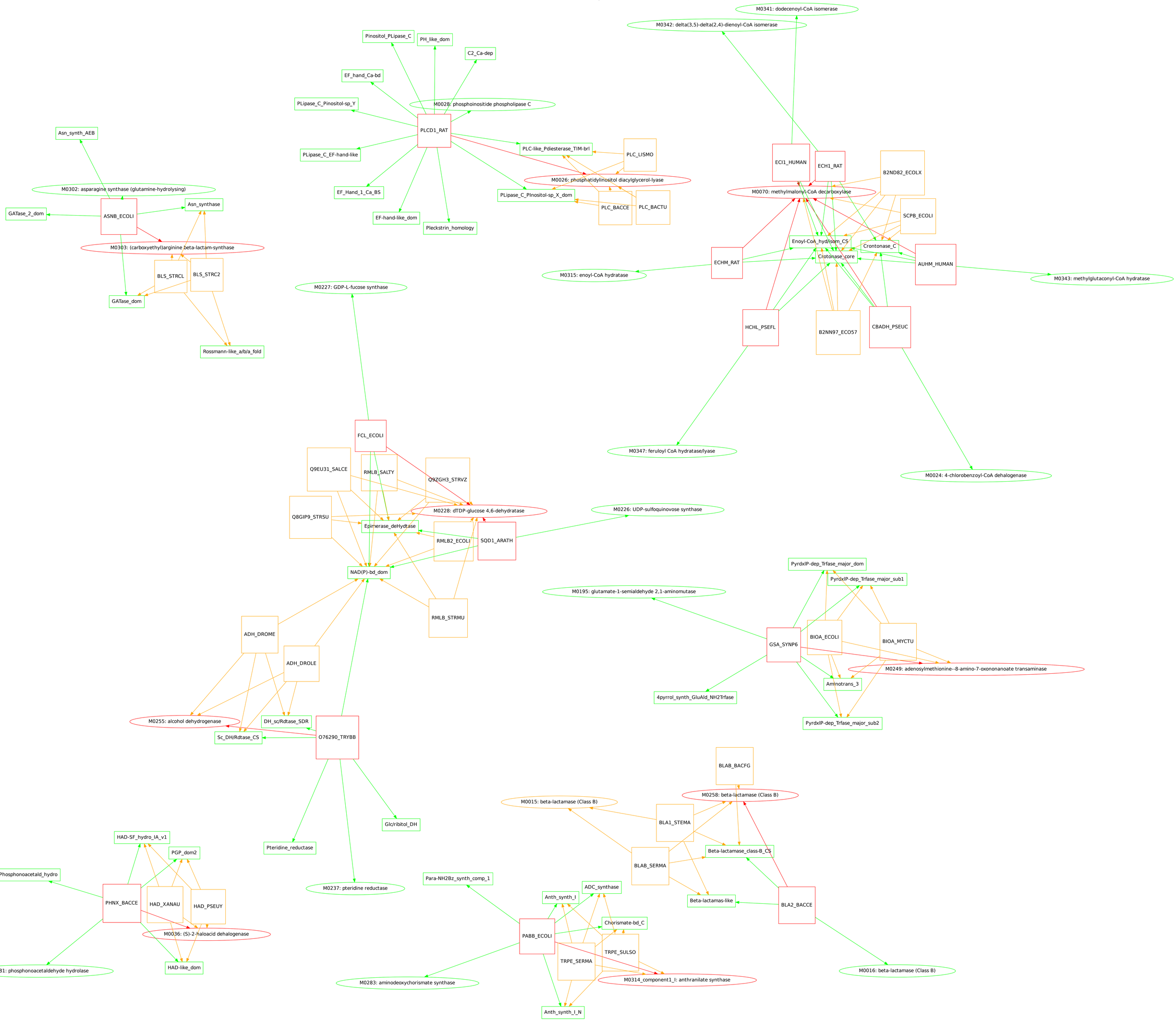This graph represents as red squares the proteins predicted as false positive when training on the mechanism dataset and testing on the negative set (using InterPro attributes, shown here as green rectangles).
The green oval represents the protein true mechanism, while the red oval is the mistaken prediction.
The yellow squares are neighbour proteins (proteins sharing some of the attributes) which caused the mis-prediction.
Authors: Luna De Ferrari and John Mitchell (2014)