Pichia pastoris is used for commercial production of human therapeutic proteins, and genome-scale models of P. pastoris metabolism have been generated in the past to study the metabolism and associated protein production by this yeast. A major challenge with clinical usage of recombinant proteins produced by P. pastoris is the difference in N-glycosylation of proteins produced by humans and this yeast. However, through metabolic engineering, a P. pastoris strain capable of producing humanized N-glycosylated proteins was constructed. The current genome-scale models of P. pastoris do not address native nor humanized N-glycosylation, and we therefore developed ihGlycopastoris, an extension to the iLC915 model with both native and humanized N-glycosylation for recombinant protein production, but also an estimation of N-glycosylation of P. pastoris native proteins. This new model gives a better prediction of protein yield, demonstrates the effect of the different types of N-glycosylation of protein yield, and can be used to predict potential targets for strain improvement. The model represents a step towards a more complete description of protein production in P. pastoris, which is required for using these models to understand and optimize protein production processes.