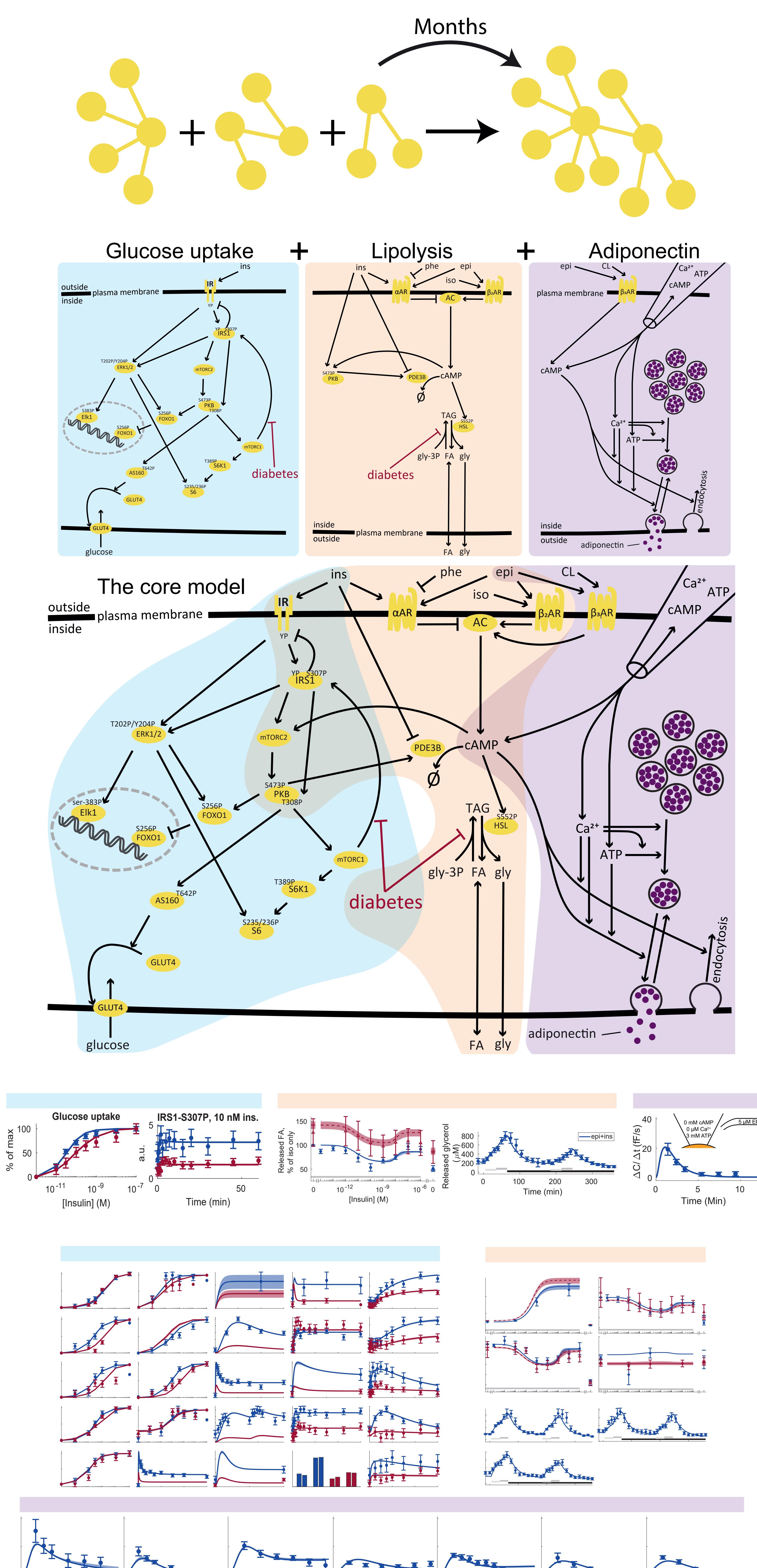


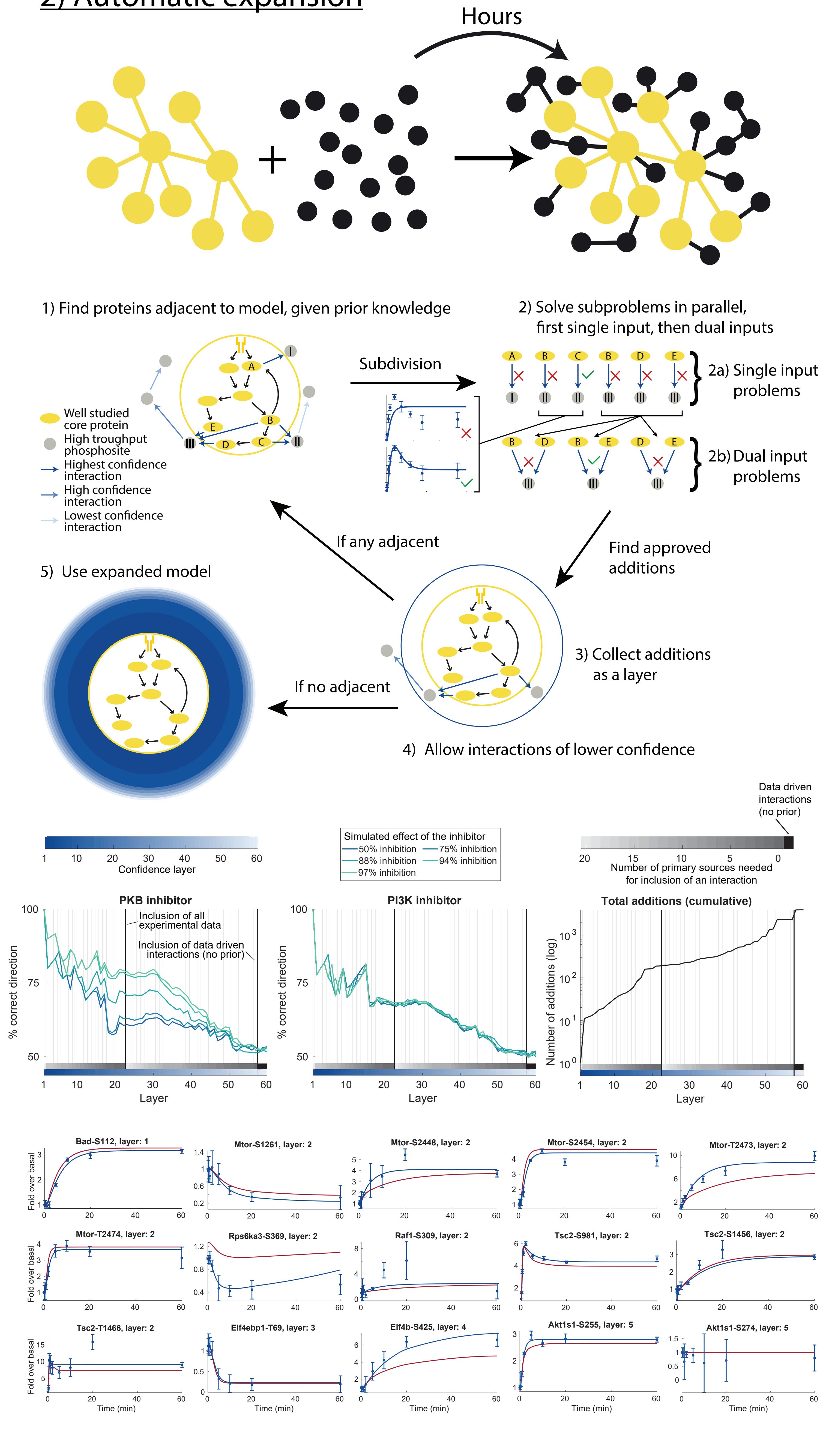
A comprehensive mechanistic model of adipocyte signaling - with layers of confidence

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1) Manual connection



2) Automatic expansion



Summary

We first connected three previously published models [1-3]. We then used the connected model as a core for further model expansion. This expansion was done by using prior knowledge in the form of database information on protein-protein interaction [4], and large-scale phosphoproteome data [5]. The expanded model could predict the effect of two inhibitors, and could propagate the effect of type 2 diabetes from the core model to the phosphoproteome scale.

A preprint of the work is available at bioRxiv [6].

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