Bioprocessing of the important Chinese hamster ovary (CHO) cell lines used for the production of biopharmaceuticals stands at the brink of several redefining events. In 2011, the field entered the genomics era, which has accelerated omics-based phenotyping of the cell lines. In this review we describe one possible application of this data: the generation of computational models for predictive and descriptive analysis of CHO cellular metabolism. We describe relevant advances in other organisms and how they can be applied to CHO cells. The immediate implications of the implementation of these methods will be accelerated development of the next generation of CHO cell lines and derived biopharmaceuticals.