Cancer cells reprogram metabolism to support rapid proliferation and survival. Energy metabolism is particularly important for growth and genes encoding enzymes involved in energy metabolism are frequently altered in cancer cells. A genome scale metabolic model (GEM) is a mathematical formalization of metabolism which allows simulation and hypotheses testing of metabolic strategies. It has successfully been applied to many microorganisms and is now used to study cancer metabolism. Generic models of human metabolism have been reconstructed based on the existence of metabolic genes in the human genome. Cancer specific models of metabolism have also been generated by reducing the number of reactions in the generic model based on high throughput expression data, e.g. transcriptomics and proteomics. Targets for drugs and bio markers for diagnostics have been identified using these models. They have also been used as scaffolds for analysis of high throughput data to allow mechanistic interpretation of changes in expression. Finally, GEMs allow quantitative flux predictions using flux balance analysis (FBA). Here we critically review the requirements for successful FBA simulations of cancer cells and discuss the symmetry between the methods used for modeling of microbial and cancer metabolism. GEMs have great potential for translational research on cancer and will therefore become of increasing importance in the future.