Recon 2.2 presents the most predictive model of human metabolism to date. Due to extensive manual curation Recon 2.2 now contains:
- 5,324 compartmentalized metabolites,
- of which 2,652 are unique chemical species,
- 7,785 reactions,
- and 1,675 associated genes.
All reactions in Recon 2.2 are mass and charge balanced, which allows for an accurate computational description of energy metabolism. Currently Recon 2.2 is the most complete and best-annotated consensus human metabolic reconstruction available.

Applications of Recon 2.2
Models are critical in the exploration and understanding of the complexity of the underlying human metabolism and have successfully been used:
- to predict biomarkers of inborn errors of metabolism,
- identify drug targets and off-target drug effects,
- to study cancer metabolism
- to improve understanding of microbial interactions with the host organism
Recently we developed a novel computational tool for rational prediction of minimal metabolic intervention strategies. We successfully tested its application for the design of optimal cell factories. We plan to use this tool together with a metabolic reconstruction of particular cancer tissues based on Recon 2.2 to predict optimal combination therapies with minimal side effects.

About acib
acib is a private, non-profit, research institution with 25+ years of experience. It is a multidisciplinary centre with research in disciplines: such as Organic Chemistry/Biocatalysis, Molecular-, Structural-, and Cell Biology, (Bio)Process Engineering, Bioinformatics and Synthetic Biology. In addition to its more than 200 employees, acib has framework contracts with several key universities in Austria, as well as across Europe and the world. Thus acib is able to provide this expertise and equipment to the industry and its research partners.

References