

## Publication

### A community effort towards a knowledge-base and mathematical model of the human pathogen *Salmonella Typhimurium* LT2

#### **JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)**

**ID** 749167

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**Year** 2011

**Title** A community effort towards a knowledge-base and mathematical model of the human pathogen *Salmonella Typhimurium* LT2

**Journal** BMC Systems Biology

**Volume** 5

**Number** 8

**Pages / Article-Number** 1-9

**BACKGROUND:** Metabolic reconstructions (MRs) are common denominators in systems biology and represent biochemical, genetic, and genomic (BiGG) knowledge-bases for target organisms by capturing currently available information in a consistent, structured manner. *Salmonella enterica* subspecies I serovar Typhimurium is a human pathogen, causes various diseases and its increasing antibiotic resistance poses a public health problem. **RESULTS:** Here, we describe a community-driven effort, in which more than 20 experts in *S. Typhimurium* biology and systems biology collaborated to reconcile and expand the *S. Typhimurium* BiGG knowledge-base. The consensus MR was obtained starting from two independently developed MRs for *S. Typhimurium*. Key results of this reconstruction jamboree include i) development and implementation of a community-based workflow for MR annotation and reconciliation; ii) incorporation of thermodynamic information; and iii) use of the consensus MR to identify potential multi-target drug therapy approaches. **CONCLUSION:** Taken together, with the growing number of parallel MRs a structured, community-driven approach will be necessary to maximize quality while increasing adoption of MRs in experimental design and interpretation.

**Publisher** BioMed Central

**ISSN/ISBN** 1752-0509

**edoc-URL** <http://edoc.unibas.ch/dok/A5844169>

**Full Text on edoc** Available;

**Digital Object Identifier DOI** 10.1186/1752-0509-5-8

**PubMed ID** <http://www.ncbi.nlm.nih.gov/pubmed/21244678>

**ISI-Number** WOS:000286822100001

**Document type (ISI)** Article