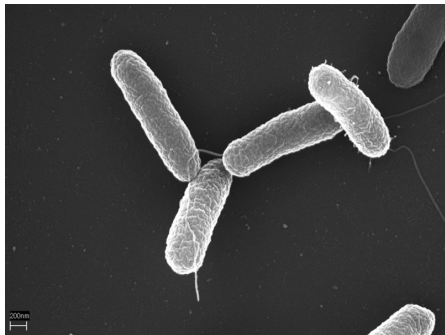
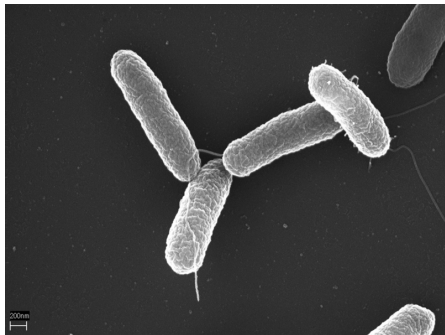


Salmonella typhimurium



- Gram negative enteric bacterium.
- Pathogen of Humans and other mammals.
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- Commonly used as a representative *Salmonella* model.

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Can we identify reactions whose inhibition will inhibit growth?

- Model constructed as an assembly of modules:
 - 816 Reactions extracted from BioCyc
 - 61 Transport reactions
 - 35 Additional reactions
- Final model consisting of 912 reactions and 783 metabolites

Method - FBA application to *Salmonella* metabolism

$$\begin{array}{ll} \text{minimise} & : |\mathbf{v}| \quad \leftarrow \text{objective} - \text{min. sum of fluxes} \\ \text{subject to} & \left\{ \begin{array}{l} \mathbf{N}\mathbf{v} = \mathbf{0} \quad \leftarrow \text{steady state constraint} \\ v_j = t_j \quad \leftarrow \text{output transporters fixed} \\ v_{\text{ATPase}} = J_{\text{ATPase}} \quad \leftarrow \text{ATP hydrolysis variable} \end{array} \right. \end{array}$$

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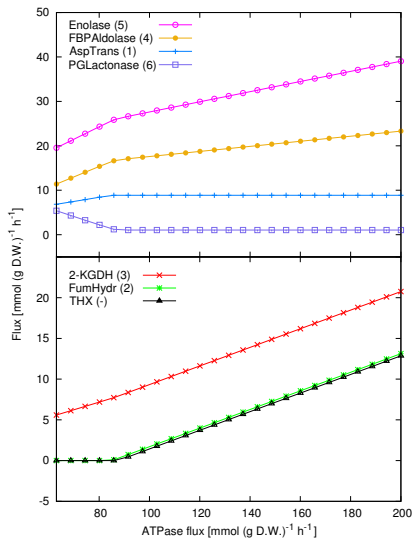
- Aerobic minimal media: Glucose, ammonia, sulphate, oxygen
- Fixed production rate of biomass precursors: Amino acids, DNA, RNA, cell envelope component
- Repeatedly solve with increasing ATP demand.

Results - general properties of flux solution

- 304 reactions, out of 912, required for biomass precursor synthesis

- 33 reactions responsive to ATP demand variation

Response to varying demand for ATP

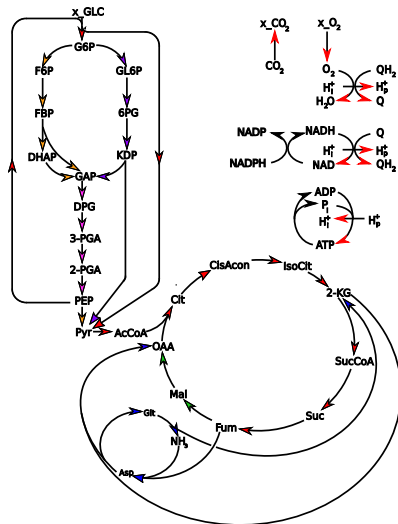


Application: Drug targets in *S. typhimurium*

- The reactions whose flux increases in response to increasing ATP demand form a single connected network:

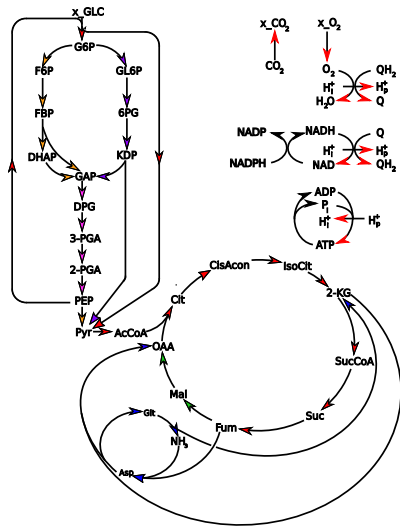
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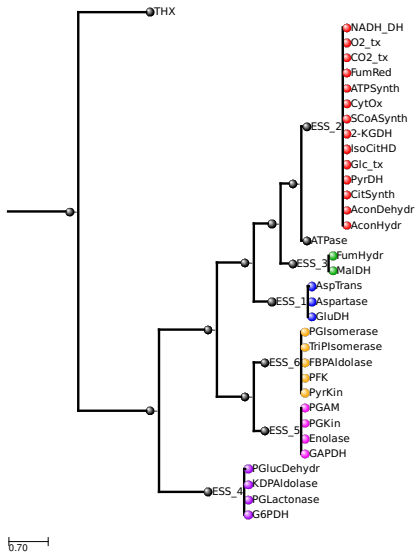
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- The reactions whose flux increases in response to increasing ATP demand form a single connected network:
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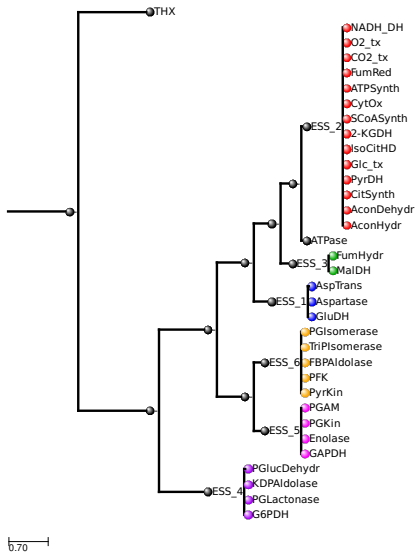
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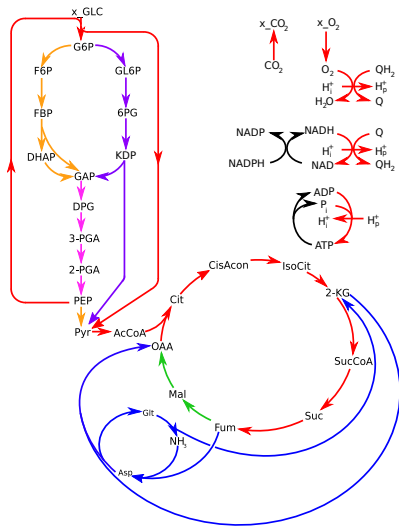
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- The reactions whose flux increases in response to increasing ATP demand form a single connected network:
- Reaction fluxes show different responses but these are correlated
- This identifies 6 sets of reactions with similar responses



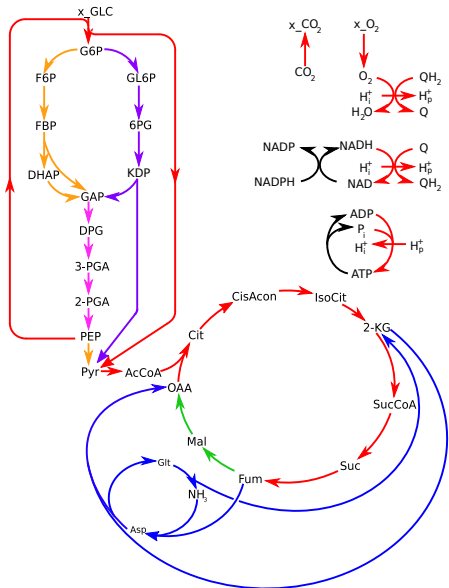
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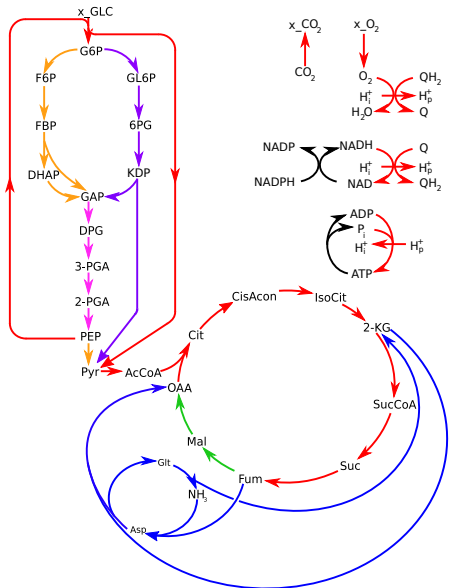
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- In the isolated catabolic core the correlated reactions form 6 subsets.



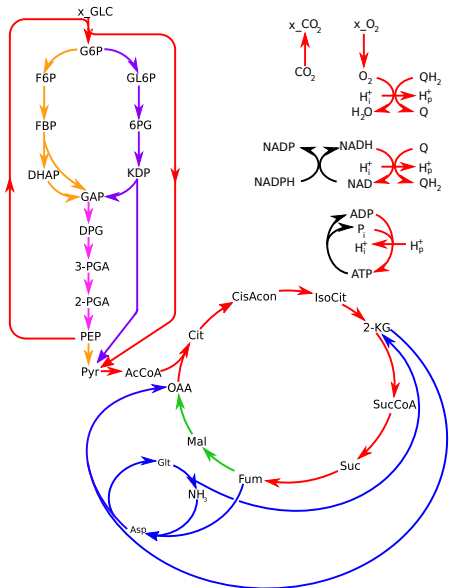
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- There are 5 elementary modes producing ATP.



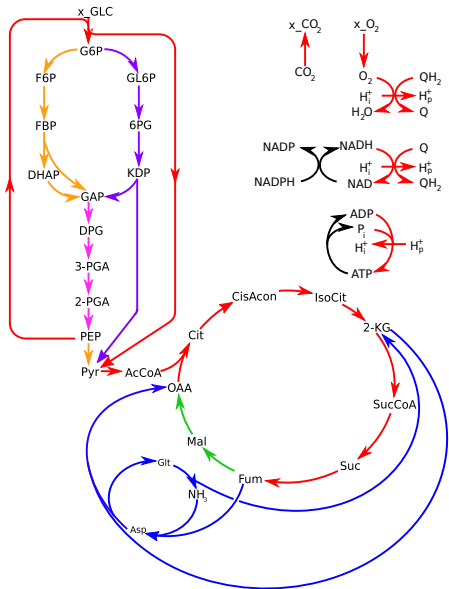
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- There are 5 elementary modes producing ATP.
- Note the involvement of nitrogen metabolism.

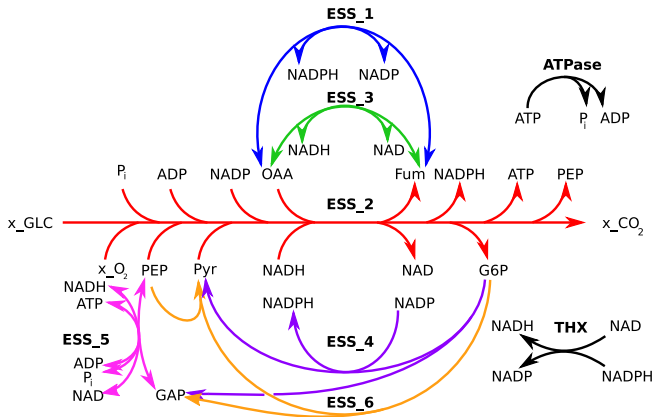


Application: Drug targets in *S. typhimurium*

- In the isolated catabolic core the correlated reactions form 6 subsets.
- There are 5 elementary modes producing ATP.
- Note the involvement of nitrogen metabolism.
- It is now easy catabolic core.



Results - catabolic core - as enzyme subsets



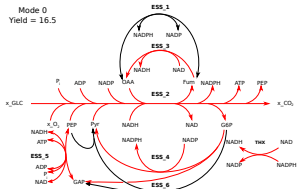
Results - elementary modes of the catabolic core

The six reaction subsets can be combined to generate a total of five elementary modes:

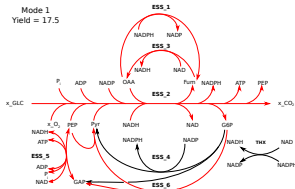
EM 1		1	2	3		5	
EM 2		1	2		4	5	
EM 3		1	2			5	6
EM 4			2	3	4	5	
EM 5			2	3		5	6

Results - catabolic core

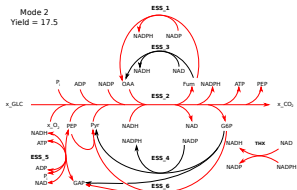
Mode 0
Yield = 16.5



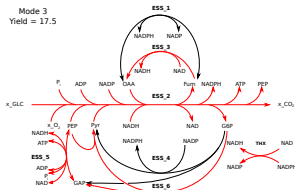
Mode 1
Yield = 17.5



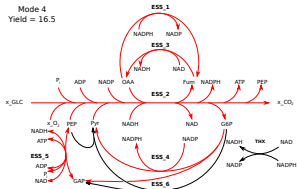
Mode 2
Yield = 17.5



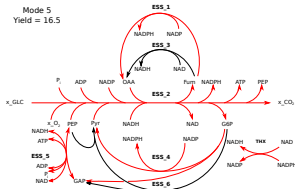
Mode 3
Yield = 17.5



Mode 4
Yield = 16.5



Mode 5
Yield = 16.5



From this we can identify:

- 1 Reactions whose removal, singly or in combination, abolish the production of ATP in the catabolic core.
- 2 Identify the impact this has on the *whole* model.
- 3 From 2 identify candidates for KO experiments.

Hartman *et al.* (2013), *Microbiology*,
Identification of potential drug targets in *Salmonella*
Typhimurium using metabolic modelling and experimental
validation., **vol**, pp pages.

Acknowledgements

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Martin Woodward Reading University
John Olsen University of Copenhagen
Anu Raghuthanan National Chemical Laboratory, Pune

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Identification of potential drug targets in *Salmonella*
Typhimurium using metabolic modelling and experimental
validation., **160**, pp 1252–1256.