

### Neurospora crassa Omics Pathway Table

Key to Omics Data Colors:


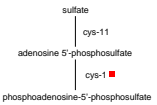
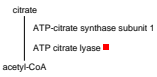


Pathways are ranked by Pathway Perturbation Score (PPS) for single-column datasets.  
Only the 10 top-scoring pathways are included in the table.

PPS: The PPS attempts to measure the overall extent to which a pathway is up- or down-regulated, by combining the activation levels of all reactions in the pathway. A Reaction Perturbation Score (RPS) is computed for each reaction as the maximum absolute value of all data values for objects associated with the reaction (e.g. genes for gene expression data, compounds for metabolomics data). If the data values are not already in log format, they are first converted to log values. For example, if a reaction has three associated genes with gene expression values -1.5, .3 and 1.2, the RPS would be 1.5.

To compute the **PPS**, we sum the squares of the **RPSs**  
for all reactions in the pathway for which data are available, divide by the number of  
reactions  
for which data are available, and take the square root of the result (we use the square of  
the  
**RPSs** instead of a traditional average in order to weight larger **RPSs** more heavily).  
For a pathway containing **N** reactions:

$$PPS = \sqrt{[(RPS_1^2 + RPS_2^2 + \dots + RPS_N^2)/N]}.$$

Pathway 	Pathway Diagram	PPS
sulfate activation for sulfonation		
acetyl-CoA biosynthesis (from citrate)		
geranylgeranyldiphosphate biosynthesis		
sulfate reduction I (assimilatory) - variant		
sulfate reduction I (assimilatory)		
sorbitol degradation I		
pentose phosphate pathway (oxidative branch)		
formaldehyde oxidation V (tetrahydrofolate pathway)		
acetate conversion to acetyl-CoA		
folate transformations		