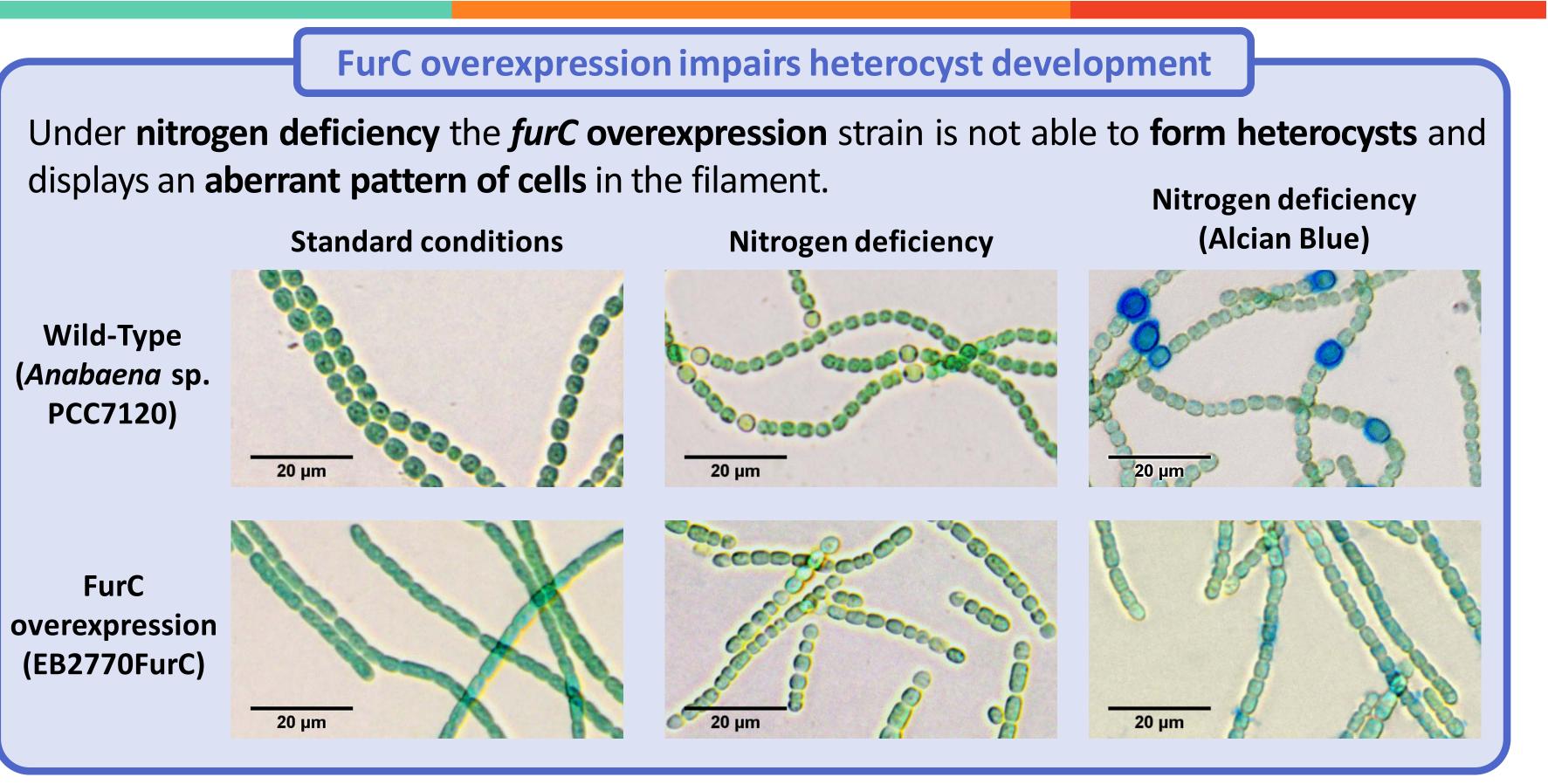
FurC (PerR) from Anabaena sp. PCC7120: a versatile transcriptional regulator Universidad engaged in the regulatory network of heterocyst development and nitrogen fixation Zaragoza Jorge Guío, Cristina Sarasa, M. Luisa Peleato, María F. Fillat and Emma Sevilla



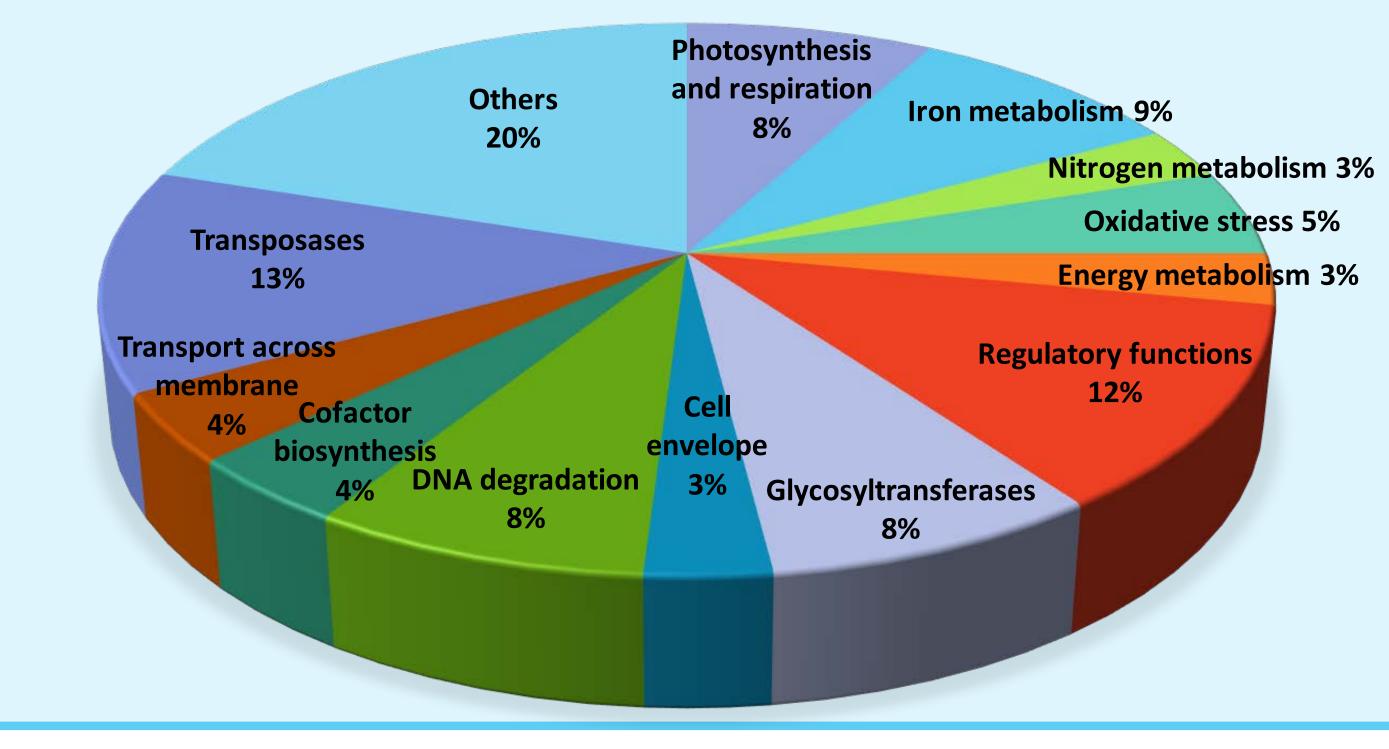
Department of Biochemistry and Molecular and Cell Biology and Institute for Biocomputation and Physics of Complex Systems, University of Zaragoza

FurC (PerR) from *Anabaena* sp. PCC 7120 was initially described as a key transcriptional regulator involved in setting off the oxidative stress response. In this work, the transcriptome of a *furC*-overexpressing strain was compared with that of a wild-type strain both under standard and nitrogen-deficiency conditions. Results showed that the overexpression of *furC* deregulates genes involved in several categories such as photosynthesis, iron transport and nitrogen metabolism. The novel FurC-direct targets included regulatory elements that control heterocyst development, genes involved in the heterocyst envelope formation and genes involved in nitrogen fixation. The relevance of FurC in these processes is brought out by the fact that the overexpression of *furC* impairs heterocyst development under nitrogen step-down conditions. In summary, this work reveals a new player in the complex regulatory network of heterocyst formation and nitrogen fixation.

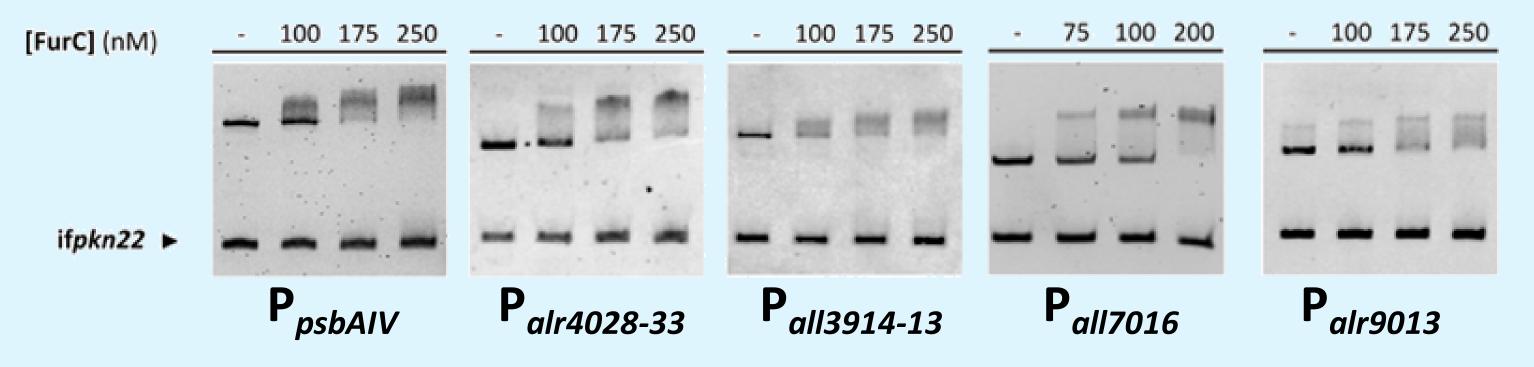


Differential transcriptomics under standard culture conditions

Under standard culture conditions, there are 75 genes with differential **expression** and **functional annotation** in the *furC* overexpression strain. These genes belong to a **wide variety** of functional categories



EMSA assays were used to analyse the binding of FurC to the promoter regions of genes with differential expression and find direct targets of this regulator



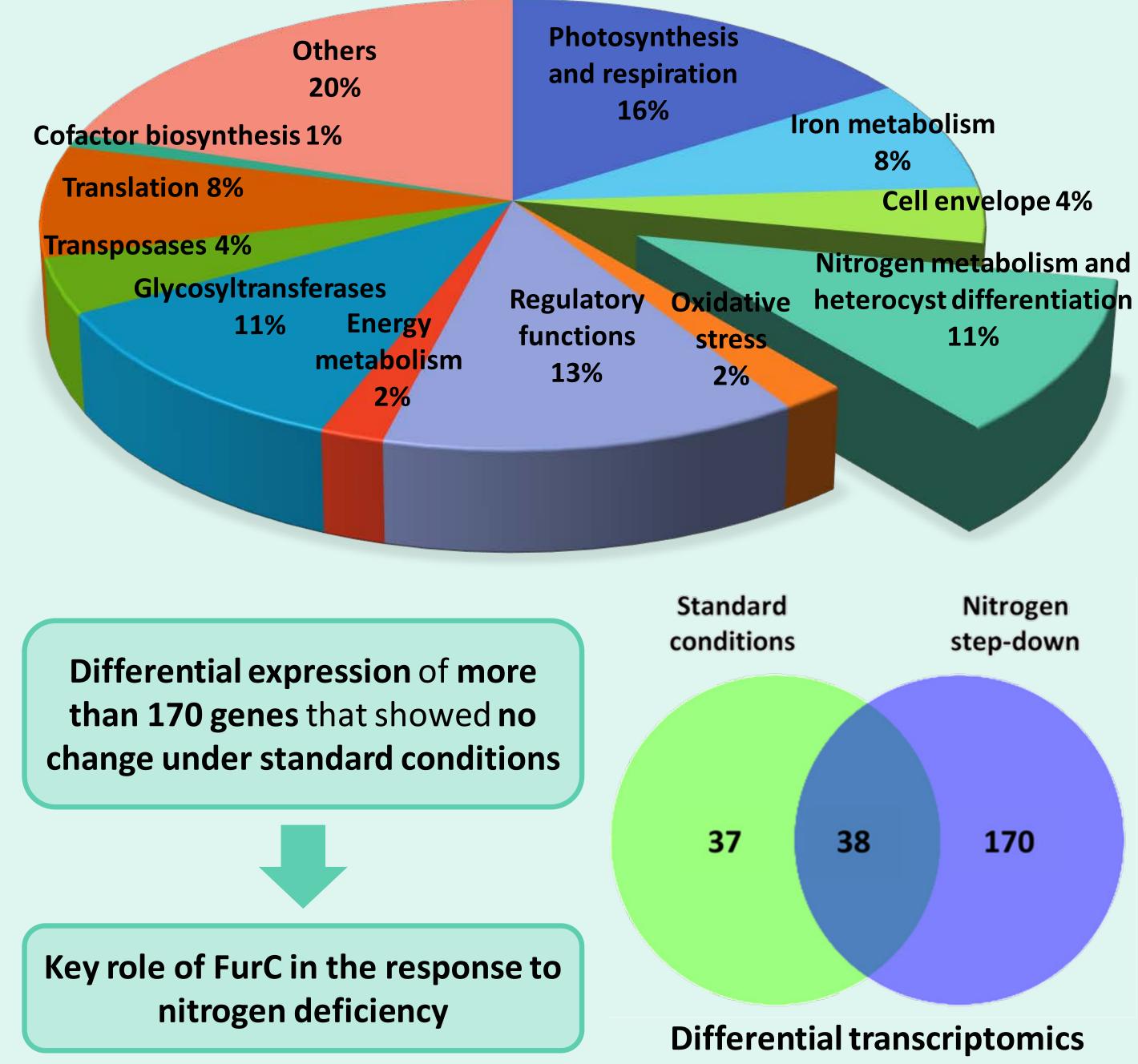
FurC directly regulates genes belonging to different functional categories

- Photosynthesis: Photosystem II P680 reaction center D1 protein (psbAIV)
- Iron metabolism: Fec system, uptake and transport of Fe³⁺-citrate (alr4028-33)
- **Energy metabolism**: Succinyl-CoA synthetase (*all3914-13*)
- <u>Regulatory functions</u>: Transcriptional regulator (*all7016*) Response regulator (*alr9013*)

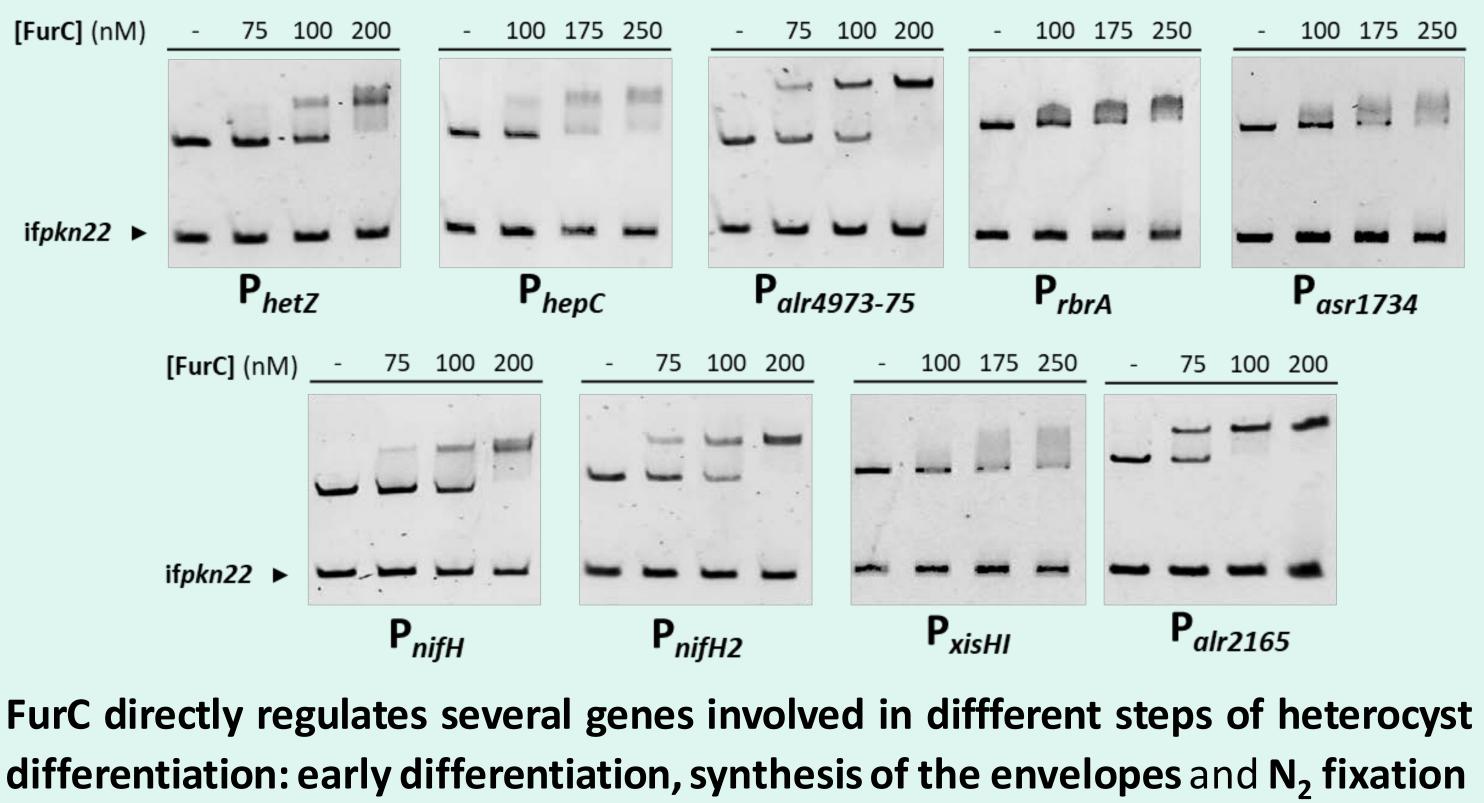
Differential transcriptomics under nitrogen deficiency

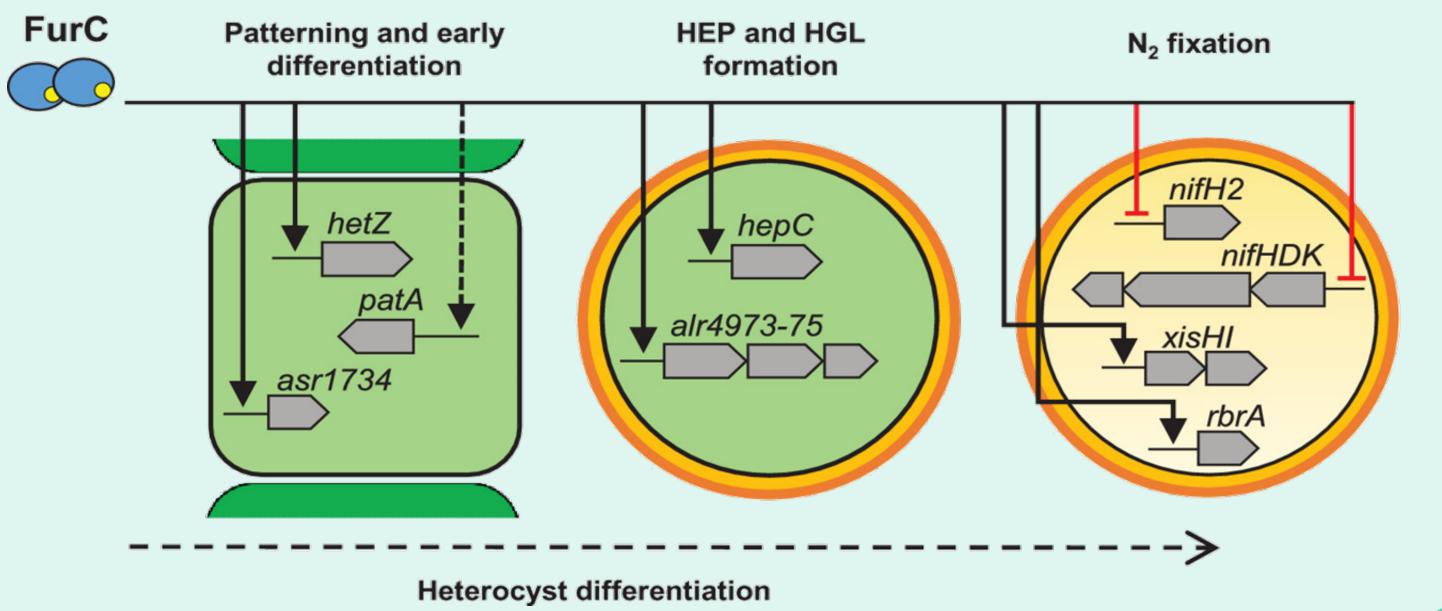
Under standard nitrogen deficiency, there are 208 genes with differential EMSA assays were used to analyse the binding of FurC to the promoter regions

expression and functional annotation in the *furC* overexpression strain.



of genes with differential expression and find direct targets of this regulator





EB2770FurC vs WT

CONCLUSIONS

FurC is a global regulator in *Anabaena* sp. PCC 7120 > The transcriptomic profile of the strain EB2770FurC vs WT changes drastically under nitrogen deficiency

> FurC plays a key role in heterocyst development

If you have any questions or are interested in our work please do not hesitate to contact me: jguio@unizar.es • Follow us on Twitter! @cyanofur

published in This study is Environmental Microbiology. If you are interested, you can find it here:



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