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In silico predicted transcriptional regulatory control of steroidogenesis in spawning female fathead minnows (*Pimephales promelas*)



D. Hala , J.A. Cullen , B. Hernout , I. Ivanov

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Highlights

- An integrated transcriptional-regulatory network (TRN) and flux balance analysis (FBA) model of steroidogenesis was constructed.
- The integrated model was used to study *in vivo* oogenesis in spawning female fathead minnows (*Pimephales promelas*).
- *In silico* simulations showed cycling for both steroidogenic enzyme gene expressions and associated steroid hormone productions during oogenesis.
- *In silico* predictions were in good agreement with trends observed *in vivo*.

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