An open challenge in developmental biology is to predict gene expression patterns from knowledge of the concentration dynamics of input transcription factors and their binding arrangement on regulatory DNA. While thermodynamic models can predict transcriptional regulation in bacteria, in eukaryotes chromatin accessibility and energy expenditure may call for a different framework. We systematically tested the predictive power of models of DNA accessibility based on the Monod-Wyman-Changeux (MWC) model of allostery, which posits that chromatin fluctuates between accessible and inaccessible states. We dissected the regulatory dynamics of *hunchback* by the activator Bicoid and the pioneer-like transcription factor Zelda in living *Drosophila* embryos and showed that no thermodynamic or non-equilibrium MWC model can recapitulate *hunchback* transcription. In contrast, a model where DNA accessibility is not the result of thermal fluctuations, but where accessibility is catalyzed by these transcription factors, can predict *hunchback* dynamics. Thus, our theory-experiment dialogue uncovered potential molecular mechanisms of governing transcriptional regulatory dynamics, a key step toward reaching a predictive understanding of developmental decision-making.