

The EcoTFs Database: *Escherichia Coli* Transcription Factors and Signals

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1 The EcoTFs database.

The EcoTFs web site (<http://EcoTFs.lanl.gov>) is dedicated to the assembly and dissemination of information about *Escherichia coli* transcription factors and the signals that control their activity.

This web site was established in November/December of 2003 to provide an online database of information about autoregulation of 50 transcription factors (TFs) in *E. coli* as supplementary material in support of a recently published review of gene circuit design [Wall et al., 2004].

Unique features of this database (currently an html table with links) include annotation of the signal(s) influencing the activities of each TF and classification of each TF based on 1) the response to a stimulus (induction or repression of regulated effector genes), 2) the mode of regulation at the promoters of regulated effector genes (repressor or activator control), and 3) the co-regulation of TF and effector gene products in response to signals. The information catalogued in the database allows the distribution of gene circuit types to be studied (Table 1).

The database was developed to help test theoretical predictions of classifications for elementary gene circuits [Hlavacek and Savageau, 1996; Wall et al., 2003]. A repressor mode of regulation at the TF (*i.e.*, negative autoregulation) is predicted when stability, robustness and responsiveness are important performance criteria, as is expected for many circuits such as those that control metabolic functions. The co-regulation of TF and effector gene products may be classified as direct coupling (TF and effector expression change in the same direction in response to signal), inverse coupling (TF and effector change in opposite directions), or uncoupled (TF expression does not change). Prediction of coupling type is related to the gain of effector gene products with signal (Table 2).

Over 100 TFs in *E. coli* have been studied experimentally (and there are more putative TFs based on the genome sequence), so the current version of the database is incomplete. We plan to add material until the database is as comprehensive as possible for *E. coli*. We also plan to extend the scope of the database to include information about well-studied TFs in other bacteria.

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2 Figures and tables.

Effector TU	Repressor mode of control at Regulator TU			Activator mode of control at Regulator TU			TF does not influence transcription of Regulator TU
	I	U	D	I	U	D	N/A
	Inducible (+)	4 ^b	3 ^c	4 ^d	0	0	5 ^e
Inducible (-)	0	0	9 ^g	0	0	0	4 ^h
Repressible (+)	0	3 ⁱ	0	0	0	0	2 ^j
Repressible (-)	0	1 ^k	9 ^l	0	0	0	1 ^m

Table 1: Distribution of system types among 49 surveyed *E. coli* TFs. The following footnotes indicate the sets of transcription factors that correspond to the table entries: ^b(AraC, IlvY, MetR, SoxS); ^c(CynR, SoxR, TorR); ^d(CysB, DsdC, MelR, RhaS); ^e(CpxR, IdnR, MarA, RhaR, XylR); ^f(MalT, MhpR, Rob, XapR); ^g(BetI, CytR, EmrR, GalS, MarR, NagC, PdhR, PutA, UxuR); ^h(GalR, GlpR, LacI, RbsR); ⁱ(AsnC, GcvA, PspF); ^j(FadR, FruR); ^k(TyrR); ^l(ArgR, DnaA, Fur, H-NS, IscR, MazEF, MetJ, PurR, TrpR); ^m(ModE). D – direct coupling, I – inverse coupling, U – uncoupled, N/A – no TF self-regulation.

Effector TU	Low Gain	Intermediate Gain	High Gain
Inducible (+)	I	U	D
Inducible (-)	D	U	I
Repressible (+)	I	D	D
Repressible (-)	D	U	I

Table 2: Predictions of coupling type for elementary gene circuits. (-) indicates a repressor mode of control, and (+) indicates an activator mode of control. Predictions depend on both the mode of control of effector expression and the magnitude of the steady-state gain of effector gene products with signal. The predictions for inducible and repressible systems are identical except for the case of activator control with intermediate gain. D – direct coupling, I – inverse coupling, U – uncoupled.

3 References and bibliography.

The EcoTFs web site is available at <http://EcoTFs.lanl.gov>

References

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