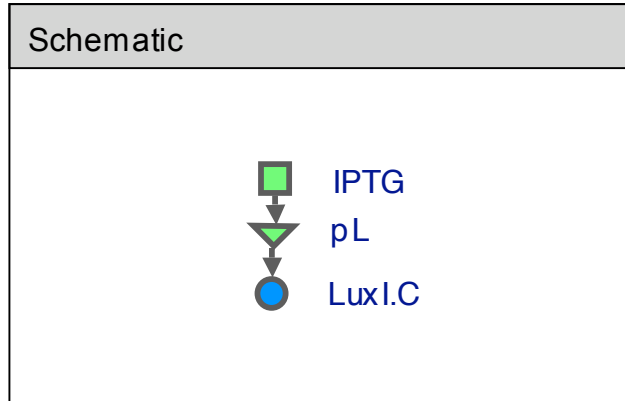


# [Trc-LIC] Inducible LuxI Expression Device

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|                          |  |
|--------------------------|--|
|                          | Host: Ecoli K12Z1  |
|                          | p1.lacI::p2.tetR   |
|                          | Part: [Trc-LIC]  |
|                          | pL.luxI.C  |
|                          | Small molecules  |
|                          | <ul style="list-style-type: none"> <li>•IPTG: Isopropyl β-D-1-thiogalactopyranoside.</li> </ul>  |
|                          | Promoters  |
|                          | <ul style="list-style-type: none"> <li>•p1: Constitutive LacIq promoter.</li> <li>•p2: Constitutive N25 promoter.</li> <li>•pL: Lac promoter.</li> </ul>   |
|                          | Proteins   |
|                          | <ul style="list-style-type: none"> <li>•LacI: Lac repressor, negative regulator of pL.</li> <li>•TetR: Tet repressor, negative regulator of pT.</li> <li>•LuxI: <i>V. fischeri</i> LuxI protein, synthesizes AHL.</li> <li>•C: Cyan fluorescent protein</li> </ul> |
|                          | Description  |
|                          | <p>IPTG drives the expression of the LuxI protein (monitored using polycistronic CFP). This in turn drives the synthesis of AHL, which is exported.</p>  |
|                          | Usage and compatibility  |
|                          | <p>This device can be used to drive expression from the promoter LuxpR in any AHL receiver device. It has not been tested with other devices.</p>  |
| Registry ID: BBa_I726031 |  |

Characteristics

Protocol: We grew cells overnight in LB. We then transferred them to Glu-M9 minimal medium containing the desired final concentration of IPTG, and allowed them to grow for 12h. The cell density at transfer was chosen so that the final OD600 was < 0.1. Cells were concentrated by centrifugation, and imaged on an epifluorescence microscope. We calculated the fluorescence per unit area of single cells, obtaining data from ~500 cells for each run. We then averaged these values in log space to obtain the final estimate of protein expression. The IPTG mesh was [0 5 10 50 100 500 1000] uM.

Sigmoidal fit:

$$y = a_0 + a_1 \frac{x^n}{K^n + x^n} \quad a_0 = 160; a_1 = 483; K = 158; n = 2;$$

Measurements and analysis were carried out by members of the NCBS iGEM 2007 team:  
Kiran, Krishna, Mukund, Navneet, Nilesch, Senthil, Shashanka, Sugat, Sushant, Varun, Vini, Vivek