

# Ann Hochschild Lab, Harvard Medical School

## Bacterial two-hybrid assay reagents

### Strain and plasmids

Strain	Relevant Details	Reference/Source
FW102 O <sub>L</sub> 2-62	Bacterial-two hybrid reporter strain. FW102 containing an F' Kan bearing the <i>plac</i> O <sub>L</sub> 2-62- <i>lacZ</i> fusion where the $\lambda$ CI operator is centered at position -62 upstream of the transcription start site	Deaconescu et al. 2002
Plasmids	Relevant Details	Reference/Source
pAC $\lambda$ CI	<i>P</i> <sub><i>lacUV5</i></sub> -directed synthesis of the $\lambda$ CI protein	Dove et al. 1997
pAC $\lambda$ CI- $\beta$ -flap (831-1057)	<i>P</i> <sub><i>lacUV5</i></sub> -directed synthesis of the $\lambda$ CI protein fused via three alanines to residues 831-1057 of the $\beta$ subunit of <i>E. coli</i> RNAP	Deighan et al. 2008
pBR $\alpha$	<i>P</i> <sub><i>lacUV5</i></sub> / <i>P</i> <sub><i>lpp</i></sub> -directed synthesis of the full length $\alpha$ subunit of <i>E. coli</i> RNAP	Dove et al. 1997
pBR $\alpha$ - $\sigma$ <sup>70</sup> D581G	<i>P</i> <sub><i>lacUV5</i></sub> / <i>P</i> <sub><i>lpp</i></sub> -directed synthesis of the $\alpha$ NTD (residues 1-248 of the $\alpha$ subunit of <i>E. coli</i> RNAP) fused directly to <i>E. coli</i> $\sigma$ <sup>70</sup> region 4 (residues 528-613 of $\sigma$ <sup>70</sup> ). The $\sigma$ <sup>70</sup> moiety also carries the D581G substitution.	Kuznedelov et al. 2002
pBR $\alpha$ - $\beta$ flap (831-1057)	<i>placUV5</i> - and <i>plpp</i> -directed synthesis of the $\alpha$ NTD (residues 1-248 of the $\alpha$ subunit of <i>E. coli</i> RNAP) fused via three alanines to residues 831-1057 of the $\beta$ subunit of <i>E. coli</i> RNAP.	Deighan et al. 2008

### User notes

- pAC $\lambda$ CI- $\beta$ -flap (831-1057) + pBR $\alpha$ - $\sigma$ <sup>70</sup> D581G = a positive control (about 800 MU  $\beta$ -gal activity in our hands with 20  $\mu$ M IPTG)
- pAC $\lambda$ CI- $\beta$ -flap (831-1057) + pBR $\alpha$  = a negative control (about 80 MU  $\beta$ -gal activity in our hands with 20  $\mu$ M IPTG)
- your pBR $\alpha$  fusion protein plasmid + pAC $\lambda$ CI = negative control 1
- pBR $\alpha$  + your pAC $\lambda$ CI fusion protein plasmid = negative control 2
- pBR $\alpha$ - $\beta$  flap (831-1057) and pAC $\lambda$ CI- $\beta$ -flap (831-1057) are the 'source plasmids' - digest these with NotI-BamHI to generate a NotI-BamHI backbone for cloning your gene (gene fragment) of interest: The  $\beta$ -flap fragment (831-1057) is 682bp.
- For the positive control we routinely grow the overnight cultures with 20  $\mu$ M IPTG and use 20  $\mu$ M IPTG in the sub-cultures. However, some fusion proteins may be toxic; for these we suggest growing the overnight cultures without IPTG and testing various IPTG concentrations (up to 200  $\mu$ M IPTG) in the sub-cultures.
- NotI is a 8bp cutter 5'-GCGGCCGC-3'. Since your protein of interest is going to be on the C-ter of the fusion proteins add an extra base onto the NotI site to maintain the reading frame (e.g., 'A'). This new NotI site, GCGGCCGCA, is translated into a 3 x Alanine linker.

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- The forward primer for cloning by PCR would look like: **5'-gaagGCGGCCGCA\_your seq in frame-3'**
- If cloning by PCR the reverse primer should incorporate a stop codon, and a BamHI recognition site (BstYI or BglII are also compatible and can be cloned into BamHI-digested pAC $\lambda$ CI- $\beta$ -flap or pBR $\alpha$ - $\beta$  flap backbones). The reverse primer would look like: **3'-your seq\_stop codon\_GGATCC\_gaag-5'**

### Sequencing primers

- pBR $\alpha$ \_F (approx 150bp upstream of NotI site in the pBR $\alpha$ -Y vector)  
**5'-gaacagcgtaccgacctggac-3'**
- pAC-cI\_F (approx 100bp upstream of NotI site in the pAC $\lambda$ CI-X vector)  
**5'-gatcagggatagcggtcagg-3'**

### References

- Dove, S. L., Joung, J. K., & Hochschild, A. (1997) Activation of prokaryotic transcription through arbitrary protein-protein contacts. *Nature* 386, 627-630
- Deaconescu, A. M., Chambers, A. L., Smith, A. J., Nickels, B. E., Hochschild, A., Savery, N. J., & Darst, S. A. (2006) Structural basis for bacterial transcription-coupled DNA repair. *Cell* 124, 507-520
- Deighan, P., Diez, C.M., Leibman, M., Hochschild, A., and Nickels, B.E. (2008) The bacteriophage  $\lambda$  Q antiterminator protein contacts the  $\beta$ -flap domain of RNA polymerase, *PNAS* 105: 15305-15310
- Kuznedelov, K., Minakhin, L., Niedziela-Majka, A., Dove, S. L., Rogulja, D., Nickels, B. E., Hochschild, A., Heyduk, T., & Severinov, K. (2002) A role for interaction of the RNA polymerase flap domain with the sigma subunit in promoter recognition. *Science* 295, 855-857