araC sequence :

plasmid number: 230726HV8303-8

araC forward primer: TCTGCAGAATGGCTGAAGCGCAAAATGATC

araC reversed primer: GTTATGCTAGTTATTGCTCAGCGGTGGCA

company: Sangon Biotech

tetR sequence:

plasmid number:230723PT6768-2

tetR forward primer: GCGGCCTGCAGAATGTCCAGATTAG

tetR reversed primer: GCTCAGCGGTGGCAGCAGCCAACTCA

company: Sangon Biotech

Shuffle T7-K12 competent cell：

Genotype： F′ lac, pro, laclQ /ρ(ara-leu)7697 araD139 fhuA2 lacZ::T7 gene1ρ(phoA) PvuII phoR ahpC∗ galE (or U) galK λatt::pNEB3-r1-cDsbC (Spec^R, laclq)ρtrxB rpsL150(Str^R)ρgorρ (malF)3

Company: Biomed

Enzyme:

The company of KpnI, XbaI , PstI, XhoI, NotI, SpeI, EcoRI, SalI: LABLEAD

The company of BlpI: Thermo SCIENTIFIC

The dataset:

http://webs.iiitd.edu.in/raghava/[1]

Reference

[1] Patiyal S, Dhall A, Raghava G P S. A deep learning-based method for the prediction of DNA interacting residues in a protein[J].Briefings in Bioinformatics, 2