araC sequence :
plasmid number: 230726HV8303-8
araC forward primer:TCTGCAGAatggctgaagcgcaaaatgatc
tetr 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