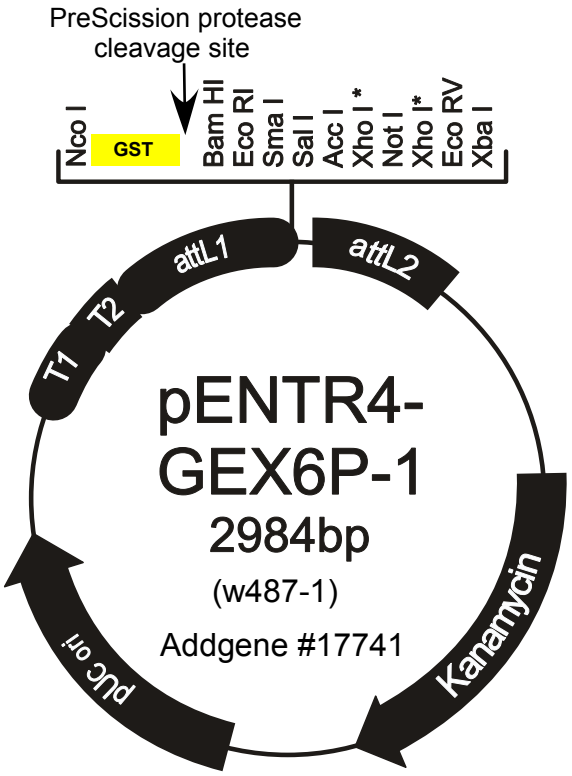


Nco I — PreScission protease cleavage site — Bam HI — Eco RI — Sma I — Sal I, Hinc II

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ACC ATG .GST.TTC CAG GGG CCC CTG GGA TCC CCG GAA TTC CCG GGT CGA
    Met       Phe Gln Gly Pro Leu Gly Ser Pro Glu Phe Pro Gly Arg
```

Xho I* — Not I — Xho I* — Eco RV — Xba I

```
CTC GAG CGG CCG CAC TCG AGA TAT CTA GACCCAGCTTTCTTGTACAAA
Leu Glu Arg Pro His Ser Arg Tyr Leu
```

Comment s for pENTR 4-GEX6P-1
2984 nucleotides

rrnB T1 transcription termination sequence: bases 106-149
rrnB T2 transcription termination sequence: bases 281-308
attL1:bases 358-457 (complementary strand)
glutathione S-transferase (GST): bases 463-1149
PreScission protease cleavage site: between bases 1155 and 1156
Multiple cloning site (MCS) bases 1163-1214
att L2: bases 1214-1314
Kanamycin resistance gene: bases 1436-2245
pUC origin: bases 2311-2983

Recommended E.coli strain for propagation: TOP10F' under kanamycin selection

NOTE: The position of the genetic elements are approximative.

Eric Campeau May 2008