

iGEM2021

2021-03-18

Team: UofUppsala

Subject : NanoFlex

- Description Biosensor Regulator Antiboy Variable region Cell Epitope
Marker
- Wiki : Team:UofUppsala
- Tag : Biosensor
- Part : UofUppsala:Parts

```
df2 = data.frame(df, ncol = 2) df2 paste('BBa_K34250', 01:12) paste('BBa_K34250', 01:12, sep="")
paste('BBa_K342500', 01:12, sep="") paste('BBa_K342500', 1:9, sep="") paste('BBa_K342500', 1:9,
sep="") + BBa_K3425010 paste('BBa_K342500', 1:9, sep="") 1:16 sprintf("%05d",1:16) sprintf("BBa_K3425%02d",1:16)
sprintf("BBa_K34250%02d",1:16) backborns = sprintf("BBa_K34250%02d",1:16) names <- paste('pSB3C',
11:14, sep="") names names <- c(paste('pSB3C', 11:14, sep=""),(paste('pSB3K0',1:4,sep=""))) names
names <- c(paste('pSB3C', 11:14, sep=""),(paste('pSB3K0',1:4,sep=""))) names <- c(paste('pSB3C', 11:14,
sep=""),(paste('pSB3K0',1:4,sep=""))) names <- paste('pSB3C', 11:14, sep="") names paste('pSB3K0',1:4,sep)
paste('pSB3K0', 1:4,sep="") names <- c(paste('pSB3C', 11:14, sep=""), paste('pSB3K0', 1:4,sep=""),
paste('pSB4K0', 1:4,sep=""), paste('pSB4A0', 1:4,sep=""), ) names <- c(paste('pSB3C', 11:14, sep=""),
paste('pSB3K0', 1:4,sep=""), paste('pSB4K0', 1:4,sep=""), paste('pSB4A0', 1:4,sep=""), ) names <-
c(paste('pSB3C', 11:14, sep=""), paste('pSB3K0', 1:4,sep=""), paste('pSB4K0', 1:4,sep=""), paste('pSB4A0',
1:4,sep="")) names kable(c(backborns, names)) library(knitr) kable(c(backborns, names)) data.frame(c(backborns,
names)) data.frame(backborns, names) kable(backborns, names) data.frame(backborns, names) df
<- data.frame(backborns, names) kable(df) knitr::kable(df, "pipe") knitr::kable(df, "simple") ?kable
t_names <- paste('Type IIS standard', c('Promoter, RBS, CDS, terminator), 'template' ) t_names <-
paste('Type IIS standard', c('Promoter, RBS, CDS, terminator)) t_names t_names t_names <- paste('Type
IIS standard', c('Promoter, RBS, CDS, terminator)) t_names <- paste('Type IIS standard', c('Promoter,
RBS, CDS, terminator)) t_names paste('A',1:5) paste("A",1:5) t_names <- paste("Type IIS standard",
c("Promoter", "RBS", "CDS", "terminator")) t_names <- paste("Type IIS standard", c("Promoter",
"RBS", "CDS", "terminator"), "template") t_names df_t <- data.frame(templates, t_names) Parts <-
paste('BBa_K335200',0:9,seq="") df_P <- data.frame(Parts,names) df <- data.frame(Parts, names, tag,
description, len) Parts <- c('BBa_K3669003','BBa_K3669004','BBa_K3669005','BBa_K3669006','BBa_K3669007','BBa_K
names <- c('gpdA3B box','amdS selectable marker','Pcox4 promoter','Pmin minimal gpdA pro-
moter','TcgrA Terminator','tetO7 binding site operator','ToxA Promoter','TtrpC Terminator','trpC Pro-
moter','sGFP','Nos Terminator','HygR selectable marker') tag <- c('Regulatory','CDS','Regulatory','Regulatory','Terminator',
description <- c('gpdA3B contains three copies of the gpdA box, which was discovered that when
removed transcription was significantly decreased. Therefore there is strong evidence that it is the
minimal promoter. Three copies of the gpdA box gave the highest levels of transcription, much higher
than the original single copy.','amdS is a dominant selective gene marker. Gene allows organism to use
acetamide as a carbon/nitrogen source for resource acquisition. Can be used in conjunction with ac-
etamide selective media.','Pcox4 constitutive promoter is comparable to gpdA in strength, good option
for high expression.','This DNA sequence encodes the 175 bp minimal gpdA promoter from Aspergillus
nidulans.','Terminator on plasmid p502. Can be used as a terminator gene in Aspergillus.','Seven
copies of tetO with spacers in between. Binds tTA to induce expression of some promoter. Used as a
binding site of tTA regulated by the amount of doxycycline in the system.','ToxA is a strong constitutive
```



```

<- data.frame(backborns, v_names) knitr::kable(df_v, "simple", caption = 'Vector') templates <-
paste('BBa_K34250',17:20, sep='') t_names <- paste("Type IIS standard", c("Promoter", "RBS", "CDS",
"terminator"), "template") df_t <- data.frame(templates, t_names) knitr::kable(df_t, "simple", caption =
"Template") Parts <- paste('BBa_K335200',0:9,sep='') names <- c('His-Tag / GS linker / SplintR Ligase',
'His-Tag / GS linker /  $\Phi$ 29 DNA polymerase', 'Extended RBS', 'T7 terminator', 'Strong Promoter /
Strong RBS / BBa_K3352000 / Double Terminator', 'Strong Promoter / Strong RBS / BBa_K3352001
/ Double Terminator', 'T7 Promoter / Strong RBS / BBa_K3352000 / Double Terminator', 'T7 Pro-
moter / Strong RBS / BBa_K3352001 / Double Terminator', 'pET 3a T7 Promoter UTR / Extended RBS /
BBa_K3352000 / T7 Terminator', 'pET 11a Promoter UTR / Extended RBS / BBa_K3352001 / T7 Termina-
tor') df_P <- data.frame(Parts,names) knitr::kable(df_P, "simple", caption = "Part Module") backborns <-
sprintf("BBa_K3482%02d",1:16) backborns backborns <- sprintf("BBa_K34820%02d", c(0,1,5:13,22))
backborns type <- c('Regulatory'*3) rep('Regulatory',3) rep('Regulatory',2,'A',3) rep('Regulatory',2)
parts <- sprintf("BBa_K34820%02d", c(4,14:18,20,30:38,40:44)) ls

```