iGEM2021

2021-03-18

Team: UofUppsala

Subject: NanoFlex

• Description Biosensor Regulator Antiboy Variable region Cell Epitope

Marker

• Wiki: Team: Uof Uppsala

• 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 $\langle -paste("pSB3C", 1:16) \rangle$ 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</p> 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_K3669006', 'BBa_K3669000', 'BBa_K366900', 'BBa_K366900', 'BBa_K366900', 'BBa_K366900', 'BBa_K366900', 'BBa_K366900', 'BBa_K366900', 'BBa_K36690', 'BBa_K36 names <- c('gpdA3B box', 'amdS selectable marker', 'Pcox4 promoter', 'Pmin minimal gpdA promoter', 'TcgrA Terminator', 'tetO7 binding site operator', 'ToxA Promoter', 'TtrpC Terminator', 'trpC Promoter', '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 acetamide 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

promoter, used to drive expression of a reporter gene.', Transcription terminator used to stop selective gene markers.', 'trpC promoter used to drive selectable marker gene resistance.', 'Variant of GFP, where a serine at position 65 is replaced with threonine. sGFP is a stronger reporter gene than normal GFP in filamentous fungi leading to greater fluorescence.', 'Nos Terminator used to stop transcription of reporter gene sGFP.', 'Confers resistance to the antibiotic hygromycin. Used for selectable markers in selectable media.', 'For selecting plasmids, one can use this gene in the presence of hygromycin.') len <c('171bp','1647bp','1500bp','175bp','278bp','271bp','265bp','763bp','351bp','720bp','253bp','1026bp') df <- data.frame(Parts, names, tag, description, len) Parts <- c('BBa_K3669003','BBa_K3669004','BBa_K3669005','BBa_I names <- c('gpdA3B box', 'amdS selectable marker', 'Pcox4 promoter', 'Pmin minimal gpdA promoter', 'TcgrA Terminator', 'tetO7 binding site operator', 'ToxA Promoter', 'TtrpC Terminator', 'trpC Promoter', '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. 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For selecting plasmids, one can use this gene in the presence of hygromycin.') len <c('171bp','1647bp','1500bp','175bp','278bp','271bp','265bp','763bp','351bp','720bp','253bp','1026bp') df <- data frame(Parts, names, tag, description, len) knitr∷kable(df_P, "simple", caption = "Part List") df <- data frame(Parts, names, tag, description, len) knitr∷kable(df, "simple", caption = "Part List") library(knitr) backborns <- sprintf("BBa_K34250%02d",1:16) v_names <- c(paste('pSB3C', 11:14, sep="), paste('pSB3K0', 1:4,sep="), paste('pSB4K0', 1:4,sep="), paste('pSB4A0', 1:4,sep=")) df_v

<- 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,seq=") names <- c('His-Tag / GS linker / SplintR Ligase', 'His-Tag / GS linker / Φ29 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 Promoter / Strong RBS / BBa_K3352001 / Double Terminator', 'pET 3a T7 Promoter UTR / Extended RBS / BBa_K3352001 / T7 Terminator') 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)) Is</p>