Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : SpYFH32A08

Lot # :6107_B4Lb

Vector : pDual-YFH1c

Systematic Name	SPBC16E9.01c
ORF length	888 bp

● Plasmid DNA purification

Date : 2024/12/12 Culture : LB (100 ug/ml Ampicillin) 5 ml -> 37℃ O/N

Date : 2024/12/13 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2024/12/13

DNA concentration (O.D.): 418 ng/ul

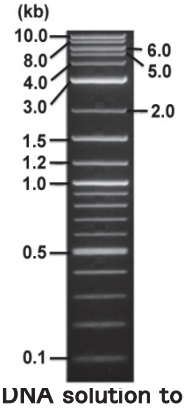
DNA	0.25 ul
Enzyme (SalI + BglII)	0.5 + 0.5 ul
Buffer H	1 ul
dH_2O	7.75 ul
Total	10 ul

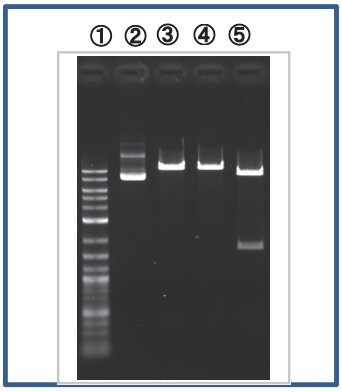
< Size of fragment expected from this clone >

SalI		10.8 kb
BglII		10.8 kb
SalI + BglII	9.1,	1.7 kb

Erectrophoresis : 1% agarose gel, 1x TAE Buffer

Marker : 2-Log DNA Ladder (NEB#N3200L)





①:Marker
②:uncut
③:SalI
④:BglII
⑤:SalI+BglII

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/01/10

DNA (418 ng/ul)	84 ul
10x TE	140 ul
dH_2O	1,180 ul
Total	1,404 ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ng/μl, Volume : μl

APPROVED BY :

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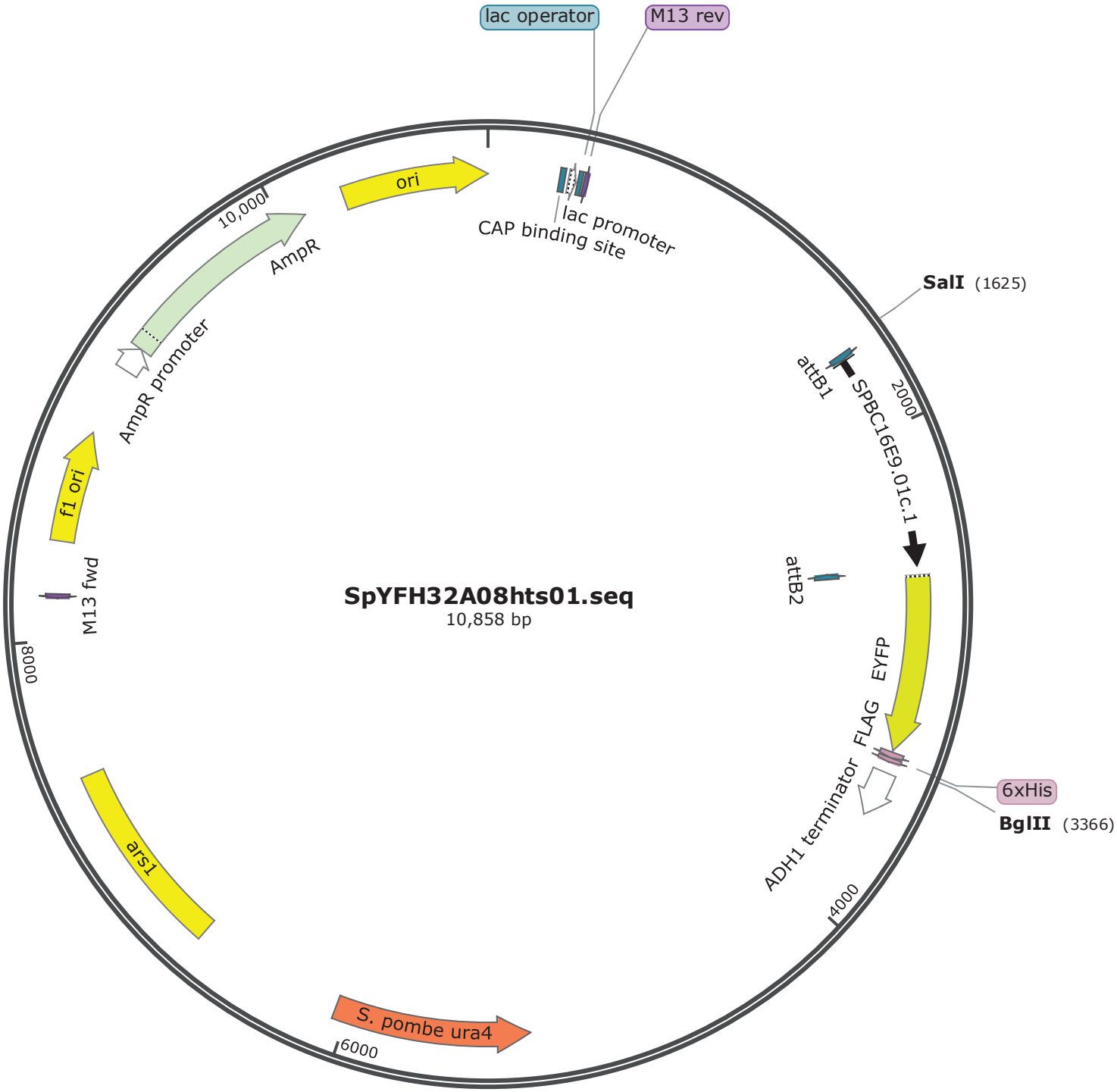

lac operator
M13 rev
ori
lac promoter
CAP binding site
10,000
AmpR
AmpR promoter
SalI (1625)
attB1
SPBC16E9.01c.1
2000
f1 ori
M13 fwd
attB2
SpYFH32A08hts01.seq
10,858 bp
EYFP
FLAG
6xHis
BglII (3366)
ADH1 terminator
4000
8000
ars1
S. pombe ura4
6000

BLAST Results

Questions/comments

Blast 2 sequences

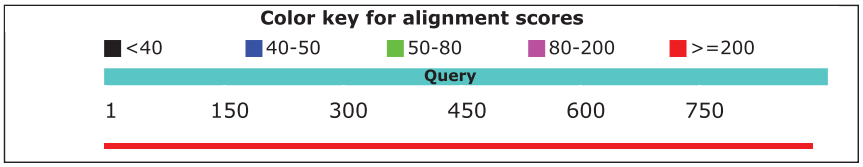
Job title: Nucleotide Sequence

RID P4JMPWEE114 (Expires on 12-19 11:07 am)

Query ID	lcl|Query_4788227	**Subject ID**	lcl|Query_4788229
Description	None	**Description**	None
			See details
Molecule type	dna	**Molecule type**	dna
Query Length	888	**Subject Length**	10858
	SPBC16E9.01c.1	**Program**	BLASTN 2.16.1+
			SpYFH32A08hts01.seq

Graphic Summary

Distribution of the top 1 Blast Hits on 1 subject sequences



Dot Matrix View

Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
None provided	1639	1639	99%	0.0	100.00%	Query_4788229

Alignments

Sequence ID: Query_4788229 Length: 10858 Number of Matches: 1
Range 1: 1681 to 2567

Score	Expect	Identities	Gaps	Strand	Frame
1639 bits(887)	0.0()	887/887(100%)	0/887(0%)	Plus/Plus	

Features:

```
Query  1     ATGGAATCGTCTAAAAGTCCATCGGAAGTGGAAAAATCATCTTCTGCTTCTCCAGCACCT  60
Sbjct  1681  ............................................................  1740

Query  61    CAAAAGCCGATGATTCGCGTCTCTAAACAATGGGTTGTTCCTCCTCGTCCCAAACCAGGA  120
Sbjct  1741  ............................................................  1800

Query  121   AGGAAACCTGCGTTAGATGCTCTGGGAAGAAGAAAGGCACCTATTAAACCAAGACCTGGG  180
Sbjct  1801  ............................................................  1860

Query  181   CCGACTTCAGCTTTGTCGGTCGAGGAAGCCAAATTCCGTGTTCGTGAAAAACAATATCAG  240
Sbjct  1861  ............................................................  1920

Query  241   GATACGATCGGAAAGTTACAGAAGGAGAACAACGAGCTGCTTGAGCAGTTGGAGATGCTG  300
Sbjct  1921  ............................................................  1980

Query  301   CAGGCTCAGTTGAAGAATTCTACTTTGGATAGCCCCAAGGAAGTCGAAGTAAACTCTGAA  360
Sbjct  1981  ............................................................  2040

Query  361   GTTGTCAAGCCAGATTCTGCGACTACTGAGAATGAAAACCGTTATGTAAATCAGTACAAT  420
Sbjct  2041  ............................................................  2100

Query  421   TATCCGGTCGAGCCGCCCTGTGCTAAGAATGCCGTTTATACAGAGATTCCCATTGAGCTA  480
Sbjct  2101  ............................................................  2160
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Query  481   GATCCTCATGCCTTCTTGGGTGATTCGGCCAAGAGAATTCGTGTGGATAGTGACAGTAAA  540
Sbjct  2161  ............................................................  2220

Query  541   GATGCAAAGTCCGTTCCATCCGAAAATGGAAGAATTCGTGTATCTATGTCTCCCCAAAAC  600
Sbjct  2221  ............................................................  2280

Query  601   GAAATTAATTTTACACCTGAAAACCCAGCAGTAATGGAGAAGATACGTAAACGTGGTGTT  660
Sbjct  2281  ............................................................  2340

Query  661   TGCAATAGTGTAGAAGGATGTTTGTACTCTGGAAGCCCTAAATCTGTTAAACGTGTCCGT  720
Sbjct  2341  ............................................................  2400

Query  721   GAATCCGAGGAAACCAAGGTTTATGCTCAACTACTTATTGACTTACACAAGTCCTCGAAG  780
Sbjct  2401  ............................................................  2460

Query  781   TCTGCTCCGATGTTAAAGGCAGGTCCTTCAATCGCCTTCAAACTTCCTACCATGGAACCA  840
Sbjct  2461  ............................................................  2520

Query  841   AATTTTAACGATGTTCGTCCCGTCACTTCCATATCCTCTTCTTCCTA  887
Sbjct  2521  ..........................................  2567
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