Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : SpFFH03G06

Lot # :6106_B5Aa

Vector : pDual-FFH1c

Systematic Name	SPBC20F10.09
ORF length	438 bp

● Plasmid DNA purification

Date : 2025/01/14 Culture : LB (100 ug/ml Ampicillin) 5 ml -> 37℃ O/N

Date : 2025/01/15 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/01/15

DNA concentration (O.D.): 419 ng/ul

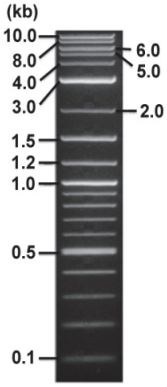
DNA	0.25 ul
Enzyme (SalI + BglII)	0.5 + 0.5 ul
Buffer H	1 ul
dH_2O	7.75 ul
Total	10 ul

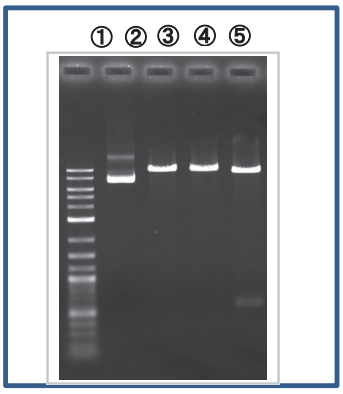
< Size of fragment expected from this clone >

SalI		9.7 kb
BglII		9.7 kb
SalI + BglII	9.1,	0.6 kb

Erectrophoresis : 0.8% 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 : 2025/01/21

DNA (419 ng/ul)	84 ul
10x TE	141 ul
dH_2O	1,183 ul
Total	1,408 ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ng/μl, Volume : μl

APPROVED BY :

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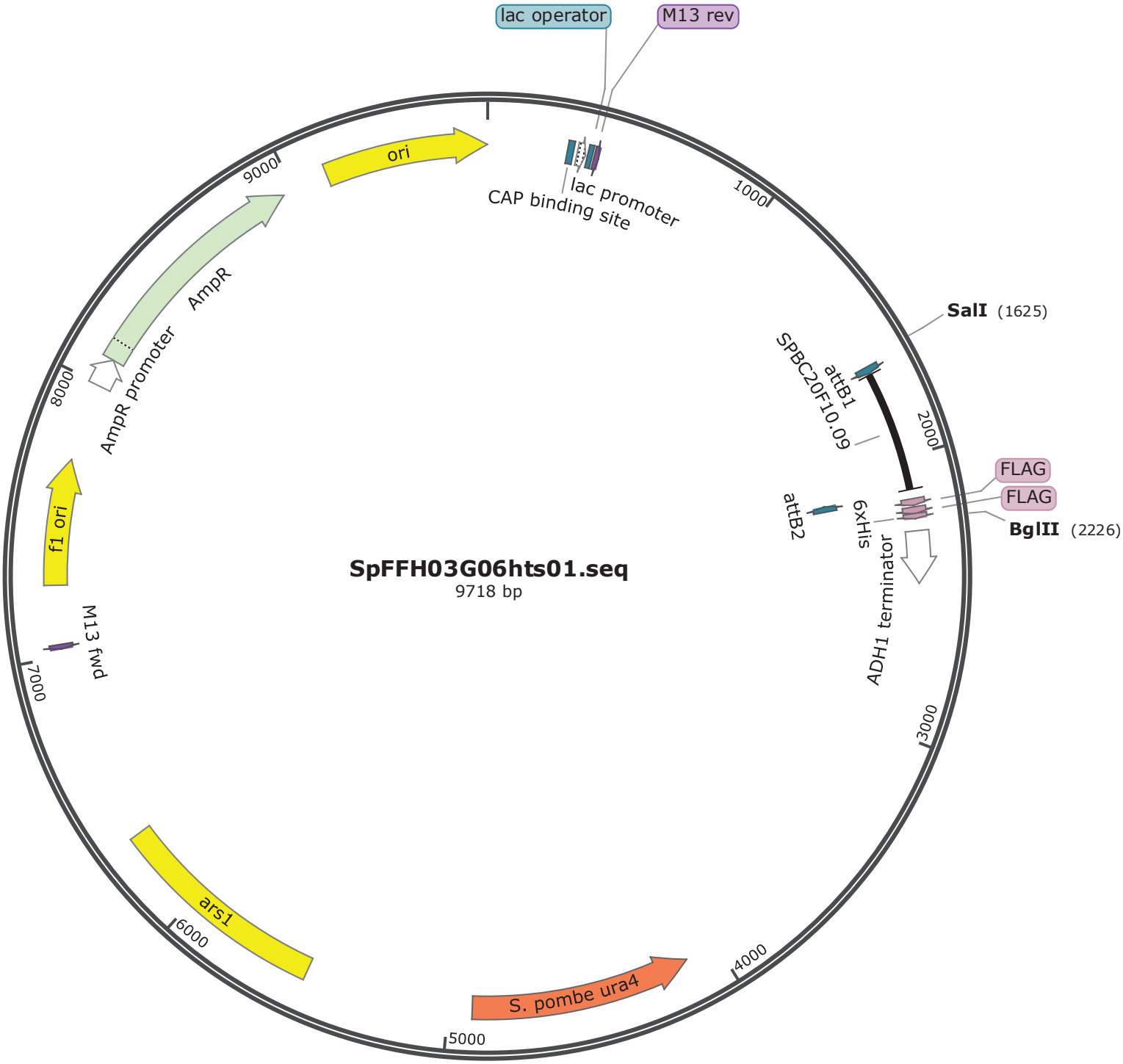

lac operator
M13 rev
ori
lac promoter
CAP binding site
1000
SalI (1625)
SPBC20F10.09
attB1
2000
FLAG
FLAG
attB2
6xHis
BglII (2226)
ADH1 terminator
3000
4000
5000
S. pombe ura4
6000
ars1
7000
M13 fwd
f1 ori
8000
AmpR promoter
AmpR
9000
SpFFH03G06hts01.seq
9718 bp

BLAST Results

Questions/comments

Blast 2 sequences

Job title: Nucleotide Sequence

RID SV7SN0VH114 (Expires on 01-21 07:55 am)

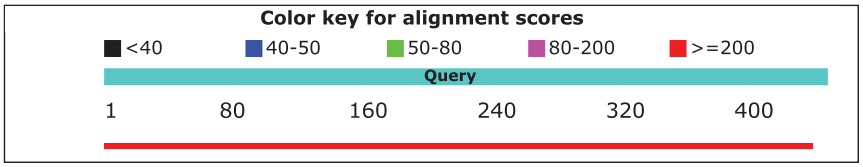
Query ID	lcl|Query_1024547	**Subject ID**	lcl|Query_1024549
Description	None	**Description**	None
			See details
Molecule type	dna	**Molecule type**	dna
Query Length	438	**Subject Length**	9718
		Program	BLASTN 2.16.1+

SPBC20F10.09

SpFFH03G06hts01.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	808	808	100%	0.0	100.00%	Query_1024549

Alignments

Sequence ID: Query_1024549 Length: 9718 Number of Matches: 1
Range 1: 1681 to 2117

Score	Expect	Identities	Gaps	Strand	Frame
808 bits(437)	0.0()	437/437(100%)	0/437(0%)	Plus/Plus	

Features:

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

Query  61    CATAATAAGAAAAGGGAAAAATTATTGATTTATGCCCTGGGTAAATCTGTTCATGCTAAC  120
Sbjct  1741  ............................................................  1800

Query  121   AAGCAGAATTAATTGATAAATGCATTGGATCAAACTTATGGGTGATCATGAAAAGTGAAC  180
Sbjct  1801  ............................................................  1860

Query  181   GCGAATTTGCGGGGACACTTGTTGGATTCGATGATTATGTGAATATTGTTCTAAAAGATG  240
Sbjct  1861  ............................................................  1920

Query  241   TTACAGAATAGTATGAAATATAATAACTTTAATTATCTTTGCTAATTTCTATGAAGTGAT  300
Sbjct  1921  ............................................................  1980

Query  301   ACTGTTACCGGCGTTACCGAAAAACACTCTGAAATGCTTTTGAACGGAAATGGGATGTGC  360
Sbjct  1981  ............................................................  2040

Query  361   ATGGTATGTCAATGAAAATAATAAAGGAATTTTTGTACACTAACTATCTAGTTGATTCCT  420
Sbjct  2041  ............................................................  2100

Query  421   GGTGGAAAACCCGAATA  437
Sbjct  2101  .................  2117
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