

Optimization Report

Sequence optimization information:

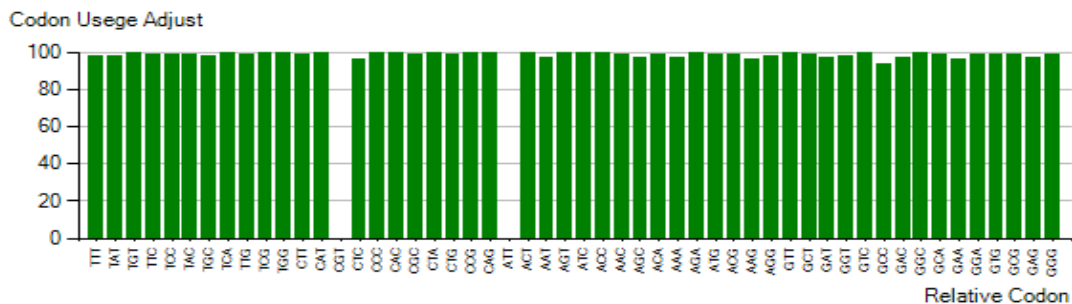
Gene Name: BAD10112021

Expression System: *Escherichia coli*

Gene Length: 459 (bp)

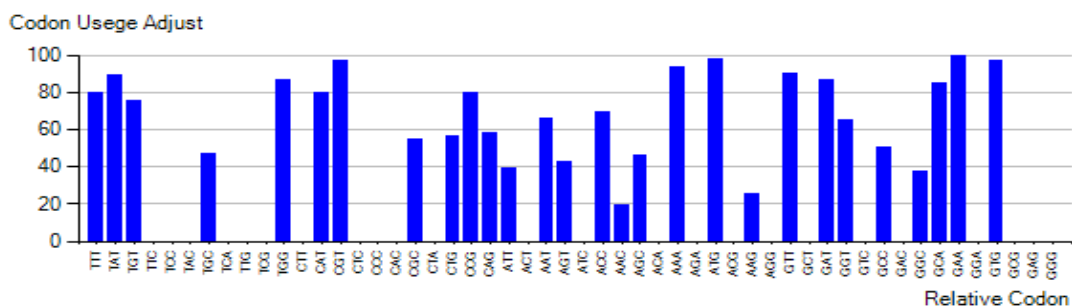
1. Codon Used Adjustment

The best value is 1 for sequence optimization.



CAI: 0.68

Before Codon Adjustment



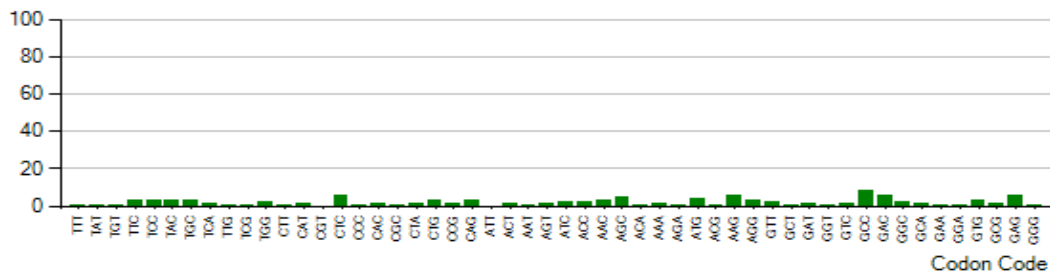
CAI: 0.98

After Codon Adjustment

2. Codon Used Distribution

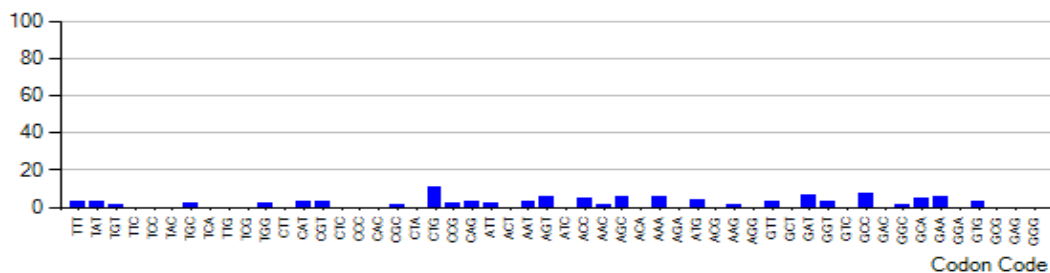
Show the relative codon used distribution

Original Sequence Codon



Before Optimization

Optimized Sequence Codon

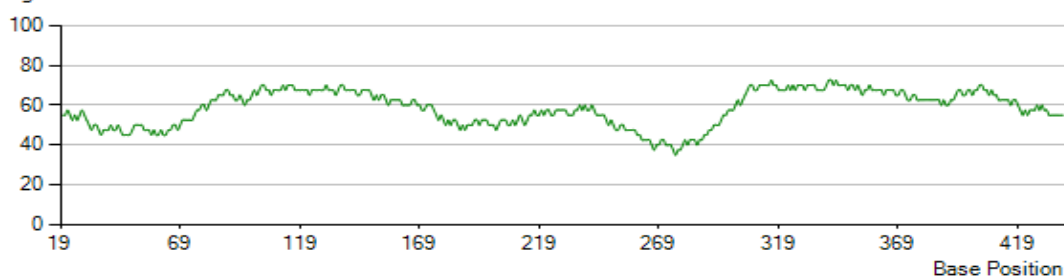


After Optimization

3.GC Content:

The comparison of GC content between original sequence and optimized sequence

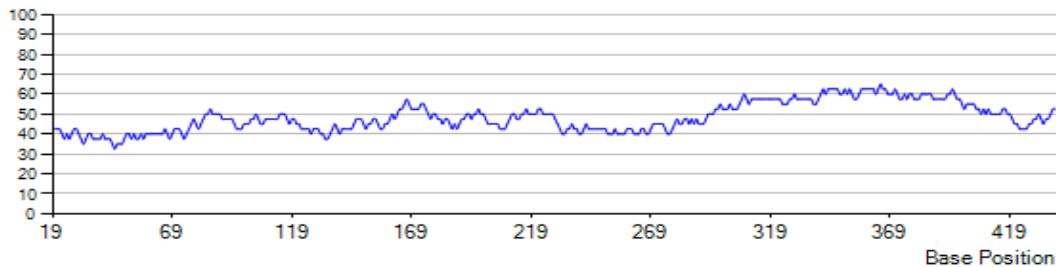
Original GC Content



GC: 0.58

Before Optimization

Optimized GC Content



GC: 0.49

After Optimization

4.Restriction Enzyme And Avoid Sequence

Restriction Name	Original	Optimization
BamHI	0	0
HindIII	0	0

Removed	Original	Optimization
GGTAAG	0	0
GGTGAT	0	0
AATAAA	0	0
ATTAAA	0	0
ATTTA	0	0
TTTTTT	0	0
AAAAAAA	0	0

5.Removed Repeats

Before Optimization

After Optimization

6.Optimized Sequence

ATGCTGATTGCCAAAGATCTGATGCAGAAAGGTGCAGATAATAAGACCTATTGCATTAGCATTAACCTGGCAGTGCTGAAATTGCAACCAATACC
 GGTAGCCTGAGTCTGAGTAATGGTAGTCATTGCGATAGCGAAGATGAAGTTGCATATAGCGAAGTGTGCCAGATGAGCAATGCCGTGCCGTTTA
 TGATATGAATTGGATGACCGCCAGTCTGAAAGCCAGTCGAAACTGTATACCTTTGAAAAAGCCGAAATGCTGCTGAGCAAAGTTCTGTTTCTGAA

AGCATGGTTTCCGAGCCTGTGTGTGGCAGCCTTTCATGCCGAACCTGGATACCGTGGATCGCGAAGCCTGTCCGCAGAGCGAACAGTATGCCCGTC
TGCTGAGTGTTCGTCTGGCCTGGATAGTGCAGTTCATGGTGAAAGTCATTGGCGTAAAGATGCCACCGATGGCGCC

7. Protein Alignment

Original Protein

MLIAKDLMQKGADNKTYCISINLAVLK FATNTGSLSLNNGSHCDSEDEVAYSEVCQMSNAVPVYDMNWM TATSLKASRKLYTFEKAEMLLSKVFLKA
WFPSLCVA AFHAE LDTVDREAC PQSEQYARLLSVRRGLDS AVHGESHW RKDATDGA

Optimized Protein

MLIAKDLMQKGADNKTYCISINLAVLK FATNTGSLSLNNGSHCDSEDEVAYSEVCQMSNAVPVYDMNWM TATSLKASRKLYTFEKAEMLLSKVFLKA
WFPSLCVA AFHAE LDTVDREAC PQSEQYARLLSVRRGLDS AVHGESHW RKDATDGA

8. DNA Alignment

Original DNA

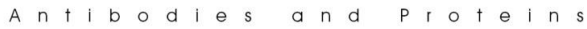
ATGCTGATCGCCAAGGATCTGATGCAGAAAGGCGCGACAACAAGACGTATTGTATCAGCATCAATCTGGCCGTGCTCAAGTTCGCCACCAACAC
CGGCAGCCTCAGCCTCTCCAACGGCAGCCACTGCGACTCGGAGGACGAGGTCGCCTACTCCGAGGTGTGCCAGATGAGCAACGCTGTTCCCGTC
TACGATATGAACTGGATGACTGCGTCACTCAAGGCCAGCAGGAAGCTCTACACCTTCGAGAAGGCCGAGATGTTGCTTTCAAAGTTCTATTCTTA
AAGGCATGGTTCCCGAGTCTCTGCGTGGCCGCCTTCCACGCCGAGCTGGACACTGTGGACAGGGAGGCCTGCCCGCAGTCCGAGCAGTACGCA
AGACTGCTCAGCGTTCGAGGGGACTCGACTCCGCCGTGCATGGGGAAAGTCATTGGAGGAAAGACGCCACAGACGGTGCC

Optimized DNA

ATGCTGATGCCAAAGATCTGATGCAGAAAGGTGCAGATAATAAGACCTATTGCATTAGCATTAACTGGCAGTGCTGAAATTGCAACCAATACC
GGTAGCCTGAGTCTGAGTAATGGTAGTCATTGCGATAGCGAAGATGAAGTTGCATATAGCGAAGTGTGCCAGATGAGCAATGCCGTGCCGGTTTA
TGATATGAATTGGATGACCGCAGTCTGAAAGCCAGTCGAACTGTATACCTTTGAAAAGCCGAAATGCTGCTGAGCAAAGTTCTGTTTCTGAA
AGCATGGTTCCGAGCCTGTGTGTGGCAGCCTTTCATGCCGAACCTGGATACCGTGGATCGCGAAGCCTGTCCGCAGAGCGAACAGTATGCCCGTC
TGCTGAGTGTTCTGTCGTGGCCTGGATAGTGCAGTTCATGGTGAAAGTCATTGGCGTAAAGATGCCACCGATGGCGCC

9. Codon Used Table

TTT [56791]	TCT [30494]	TAT [50400]	TGT [13662]
TTC [32513]	TCC [22637]	TAC [27239]	TGC [12777]
TTA [40627]	TCA [30502]	TAA [4664]	TGA [2674]
TTG [30084]	TCG [19071]	TAG [751]	TGG [31207]
CTT [33816]	CCT [22121]	CAT [28919]	CGT [37134]
CTC [22074]	CCC [14379]	CAC [17117]	CGC [32720]
CTA [12951]	CCA [21237]	CAA [33607]	CGA [11216]
CTG [87261]	CCG [33795]	CAG [62329]	CGG [18434]



ATT [68942]	ACT [30518]	AAT [68348]	AGT [30749]
ATC [45213]	ACC [44139]	AAC [47233]	AGC [33255]
ATA [31065]	ACA [35293]	AAA [86726]	AGA [16583]
ATG [55356]	ACG [31794]	AAG [35652]	AGG [9238]
GTT [50261]	GCT [44034]	GAT [78663]	GGT [55283]
GTC [30515]	GCC [50411]	GAC [41619]	GGC [47962]
GTA [30461]	GCA [53619]	GAA [81727]	GGA [31729]
GTG [46309]	GCG [49169]	GAG [45154]	GGG [28720]

Sequence Secondary Structure information as below:

One Line

[illegible]

