GenScript Rare Codon Analysis Report

If your sequence was not optimized for protein expression in the host you selected, please request a free quote for gene synthesis with codon optimization that designed by GenScript's patented OptimumGene™ algorithm now. Or you can use online GenSmart Codon Optimization tool geared up with newly developed algorithm to optimize by yourself.

Basic Information	
Host Organism	*Yeast*
Origin Organism	other
CDS length	1251

Sequence:

ATGTCTTTATCTTCAAAGTTGTCTGTCCAAGATTTGGACTTGAAGGACAAGCGTGTCTTCATCAGAGTTGACTTCAACGT
CCCATTGGACGGTAAGAAGATCACTTCTAACCAAAGAATTGTTGCTGCTTTGCCAACCATCAAGTACGTTTTGGAACACC
ACCCAAGATACGTTGTCTTGGCTTCTCACTTGGGTAGACCAAACGGTGAAAGAAACGAAAAATACTCTTTGGCTCCAGTT
GCTAAGGAATTGCAATCATTGTTGGGTAAGGATGTCACCTTCTTGAACGACTGTGTCGGTCCAGAAGTTGAAGCCGCTGT
CAAGGCTTCTGCCCCAGGTTCCGTTATTTTGTTGGAAAACTTGCGTTACCACATCGAAGAAGAAGGTTCCAGAAAGGTCG
ATGGTCAAAAGGTCAAGGCTTCCAAGGAAGATGTTCAAAAGTTCAGACACGAATTGAGCTCTTTGGCTGATGTTTACATC
AACGATGCCTTCGGTACCGCTCACAGAGCTCACTCTTCTATGGTCGGTTTCGACTTGCCACAACGTGCTGCCGGTTTCTT
GTTGGAAAAGGAATTGAAGTACTTCGGTAAGGCTTTGGAGAACCCAACCAGACCATTCTTGGCCATCTTAGGTGGTGCCA
AGGTTGCTGACAAGATTCAATTGATTGACAACTTGTTGGACAAGGTCGACTCTATCATCATTGGTGGTGGTATGGCTTTC
ACCTTCAAGAAGGTTTTGGAAAACACTGAAATCGGTGACTCCATCTTCGACAAGGCTGGTGCTGAAATCGTTCCAAAGTT
GATGGAAAAGGCCAAGGCCAAGGGTGTCGAAGTCGTCTTGCCAGTCGACTTCATCATTGCTGATGCTTTCTCTGCTGATG
CCAACACCAAGACTGTCACTGACAAGGAAGGTATTCCAGCTGGCTGGCAAGGGTTGGACAATGGTCCAGAATCTAGAAAG
TTGTTTGCTGCTACTGTTGCAAAGGCTAAGACCATTGTCTGGAACGGTCCACCAGGTGTTTTCGAATTCGAAAAGTTCGC
TGCTGGTACTAAGGCTTTGTTAGACGAAGTTGTCAAGAGCTCTGCTGCTGGTAACACCGTCATCATTGGTGGTGGTGACA
CTGCCACTGTCGCTAAGAAGTACGGTGTCACTGACAAGATCTCCCATGTCTCTACTGGTGGTGGTGCTTCTTTGGAATTA
TTGGAAGGTAAGGAATTGCCAGGTGTTGCTTTCTTATCCGAAAAGAAATAA

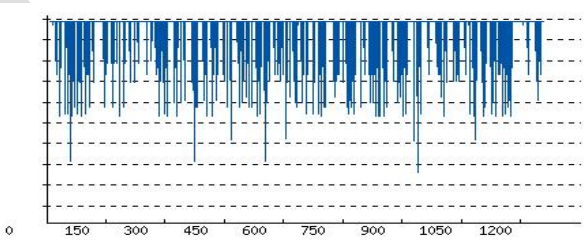
Protein Seuence:

MSLSSKLSVQDLDLKDKRVFIRVDFNVPLDGKKITSNQRIVAALPTIKYVLEHHPRYVVLASHLGRPNGERNEKYSLAPV
AKELQSLLGKDVTFLNDCVGPEVEAAVKASAPGSVILLENLRYHIEEEGSRKVDGQKVKASKEDVQKFRHELSSLADVYI
NDAFGTAHRAHSSMVGFDLPQRAAGFLLEKELKYFGKALENPTRPFLAILGGAKVADKIQLIDNLLDKVDSIIIGGGMAF
TFKKVLENTEIGDSIFDKAGAEIVPKLMEKAKAKGVEVVLPVDFIIADAFSADANTKTVTDKEGIPAGWQGLDNGPESRK
LFAATVAKAKTIVWNGPPGVFEFEKFAAGTKALLDEVVKSSAAGNTVIIGGGDTATVAKKYGVTDKISHVSTGGGASLEL
LEGKELPGVAFLSEKK*

Rare Codon Analysis Result			
	Index	**Parameter**	**Suggestion**
CAI	0.82	0.8 - 1.0	• A CAI of 1.0 is considered ideal. • The lower the number, the higher the chance that your gene will be expressed poorly. • GenScript's OptimumGene™ codon optimization tool can typically improve your sequence.
GC Content	46.65%	30% - 70%	• The ideal percentage range of GC content is between 30% and 70%.
CFD	The percentage of low frequency (<30%) codons based on your target host organism is 0%	<30%	• This un-optimized gene employs tandem rare codons that can reduce the efficiency of translation or even disengage the translational machinery. • GenScript's OptimumGene™ can give you the option to solve this problem.

Codon Adaptation Index (CAI)

Yeast

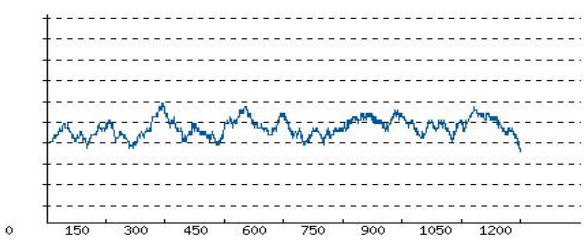


CAI: 0.82

Figure 1. The distribution of codon usage frequency along the length of your CDS to be expressed in your target host organism. Possibility of high protein expression level is correlated to the value of CAI - a CAI of 1.0 is considered to be ideal while a CAI of >0.8 is rated as good for expression in the desired expression organism. GenScript's OptimumGeneTM codon optimization tool can typically improve your sequence to reach a CAI of higher than 0.8 thus better chance of high level protein expression.

GC Content Adjustment

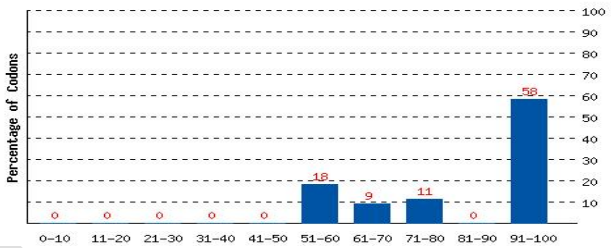
GC curve



Average GC content: 46.65%

Figure 2. The ideal percentage range of GC content is between 30% to 70%. Any peaks outside of this range will adversely affect transcriptional and translational efficiency.

Codon Frequency Distribution(CFD)



Yeast

Figure 3. The percentage distribution of codons in computed codon quality groups. The value of 100 is set for the codon with the highest usage frequency for a given amino acid in the desired expression organism. Codons with values lower than 30 are likely to hamper the expression efficiency.

Analysis of negative CIS elements and repeat sequences	
Negative CIS elements	Negative repeat elements
4	0

NOTE: CAI (codon adaptation index) result from this tool is only for evaluation. It will not necessarily be the same as the one in our optimization report, since we might use different codon bias table for gene optimization.

Summary:

- Codon Adaptation Index (CAI) of your gene is 0.82. A CAI of 1.0 is considered ideal while a CAI of >0.8 is rated as good for expression in the desired expression organism. The lower the number, the higher the chance that your gene will be expressed poorly. GenScript's OptimumGeneTM codon optimization tool can typically improve your sequence to reach a CAI of higher than 0.8.
- The GC content of your gene is 46.65%. The ideal percentage range of GC content is between 30% **and** 70%. Any peaks outside of this range will adversely affect transcriptional and translational efficiency. OptimumGene™ can give you the option to solve this problem.
- The percentage of low frequency (<30%) codons based on your target host organism is 0% . This un-optimized gene employs tandem rare codons that can reduce the efficiency of translation or even disengage the translational machinery.
- GenScript's proprietary gene design and synthesis technology can improve all the essential parameters analyzed above, and other parameters involved in RNA secondary structure and the protein folding.

http://www.genscript.com/
Phone: 1 - 732 - 885 - 9188
Toll - Free: 1 - 877 - 436 - 7274
Fax: 1 - 732 - 885 - 5878
Email: order@genscript.com