

# GenRCA Rare Codon Analysis Report

Gene Name: *Insulin*

Reference Source: Codon Usage Database - Kazusa

Expression Host Organism: *Pichia pastoris* (budding yeasts)

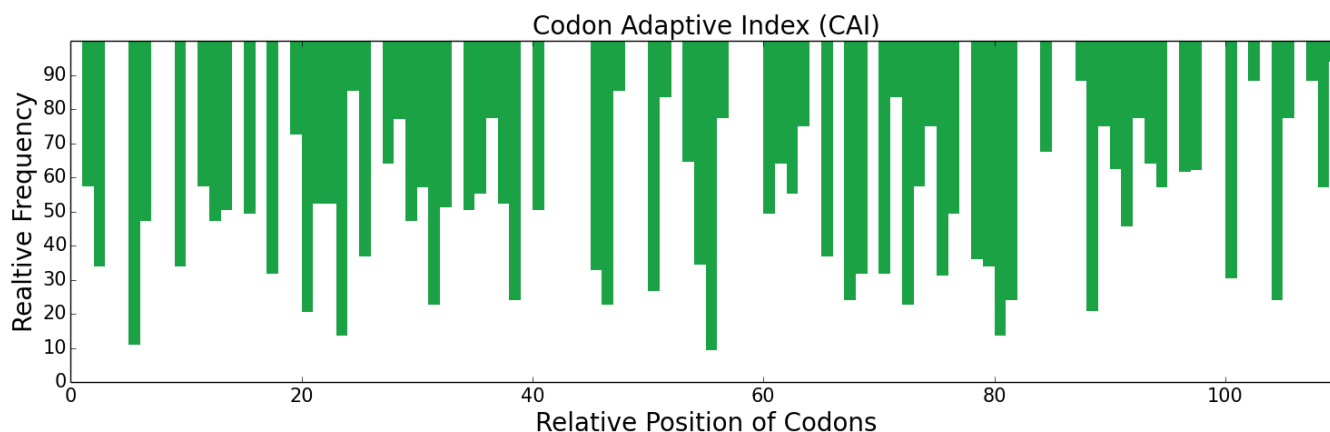
DNA Sequence Length: 330

## DNA Sequence:

```
ATGGCCCTATGGATGCGCCTGTTGCCACTATTGGCCCTGCTTGCTTTATGGGGCCCAGAC
CCGGCAGCAGCGTTTCGTAAACCAGCACCTGTGCGGGAGTCATCTTGTGAGGCACTCTAC
CTTGTTTGTGGTGAAAGGGGGTTCTTTTACACGCCCTAAGACCCGTCGGGAGGCTGAAGAT
TTACAGGTCGGACAAGTAGAACTCGGCGGTGGCCCTGGGGCCGGAAGCTTACAACCCCTA
GCGCTCGAAGGTTCTTGC AAAACGAGGAATCGTGGAGCAGTGCTGTACATCAATTTGT
TCGTTGTATCAACTCGAGAACTATTGCAAT
```

## Protein Sequence:

```
MALWMRLPLLLALLALWGPDPAAAFVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAED
LQVGQVELGGGPGAGSLQPLALEGSLQKRGIVEQCCTSICSLYQLENYCN
```



Negative CIS Elements	Negative repeat Elements
0	0

Indices based on non-uniform usage of synonymous codon				
Index	Description	Range	Value	Reference
RSCU	Relative Synonymous Codon Usage	0~6	1.03	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	61	<a href="#">[2, 3]</a>

RCBS	Relative Codon Bias Strength	$\geq 0$	0.2	<a href="#">[4]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.53	<a href="#">[5]</a>
CDC	Codon Deviation Coefficient	0~1	0.12	<a href="#">[6]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.83	<a href="#">[7]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.04	<a href="#">[8]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.03	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.93	<a href="#">[11]</a>
P	Codon Preference	$\geq 1$	1.05	<a href="#">[12]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.04	<a href="#">[13]</a>

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.57	<a href="#">[1]</a>
CFD	Codon Frequency Distribution	0~1	0.13	<a href="#">[2]</a>
FOP	Frequency of Optimal Codons	0~1	0.3	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.18	<a href="#">[5]</a>
COUSIN18			0.35	
CBI	Codon Bias Index	-1~1	-0.02	<a href="#">[6]</a>
Dmean	Mean Dissimilarity-based Index	0~2	1.1	<a href="#">[7]</a>
RCA	Relative Codon Adaptation	$\geq 0$	1.03	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.29	<a href="#">[9]</a>
B	Codon Usage Bias	0~2	0.36	<a href="#">[10]</a>

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	0~1	0.42	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	0~1	0.48	<a href="#">[2]</a>
P2	P2 Index	0~1	0.54	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
GC3	GC Content at the Third Position of Synonymous Codons	0~1	0.54	<a href="#">[1]</a>
GC	GC Content		0.54	
GC1	GC Content at the First Position of Synonymous Codons		0.64	

GC2	GC Content at the Second Position of Synonymous Codons		0.45	
ENcp	Effective Number of Codon Pairs	20~61	61	<a href="#">[2]</a>
CPS	Codon Pair Score	-1~1	-0.02	<a href="#">[3, 4]</a>
Codon Volatility	Codon Volatility	0.5~1	0.74	<a href="#">[5]</a>

**Gene Name:** Somatotropin

**Reference Source:** Codon Usage Database - Kazusa

**Expression Host Organism:** Pichia pastoris (budding yeasts)

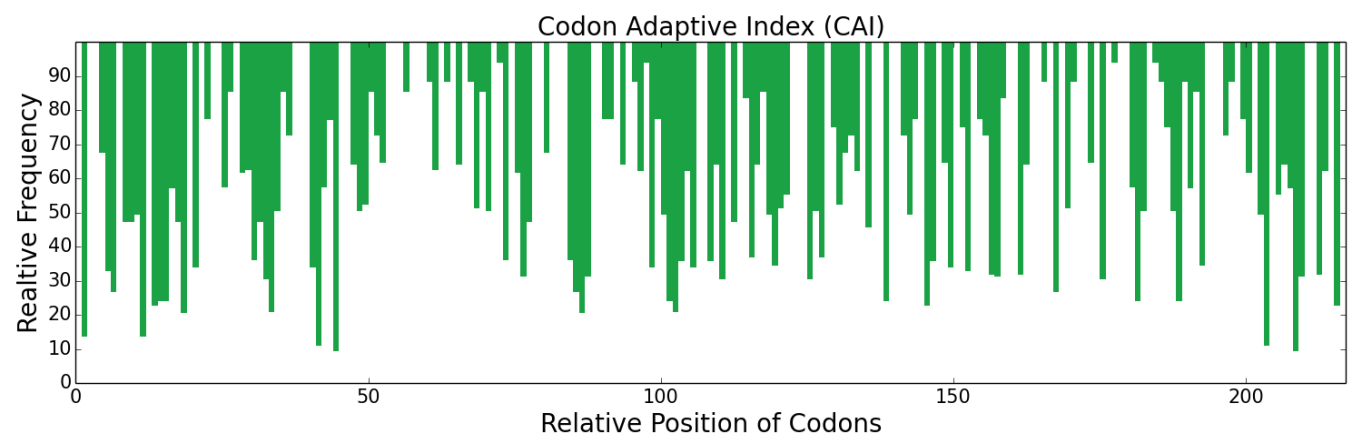
**DNA Sequence Length:** 651

**DNA Sequence:**

```
ATGGCGACTGGTTCCAGGACGTCTCTGCTGTTAGCGTTTGGGCTCCTCTGCCTGCCGTGG
CTACAAGAGGGTTCTGCCTTCCCAACAATCCCCCTGTCGCGACTTTTCGACAACGCTATG
CTACGCGCCACCAGGTTGCATCAGCTTGCATTTCGACACCTACCAAGAATTCGAAGAAGCT
TATATCCCAAAAAGAACAGAAGTATAGTTTCCCTTCAAAAATCCCCAAACAAGCCTGTGTTTT
TCCGAATCTATTCCCACGCCGAGCAACAGAGAGGAGACTCAGCAAAAATCAAATCTAGAG
TTACTCCGAATATCACTATTGTTGATACAGTCGTGGCTGGAACCTGTACAGTTCTTACGT
AGTGTCTTTGCTAACTCGCTTGTATACGGAGCATCCGACTCAAACGTGTACGATCTCTTG
AAGGACTTAGAGGAAGGGATACAAACCCTAATGGGAAGGTTGGAGGACGGCAGCCCTAGA
ACTGGCCAGATTTTTTAAACAAACGTACAGTAAATTTGATACCAACTCGCATAATGATGAT
GCCCTCCTTAAGAATTATGGACTTCTCTATTGCTTCCGTAAGGATATGGACAAAGTTGAG
ACATTTTTTACGCATTGTCCAGTGCCGGAGCGTTGAAGGCTCATGTGGGTTT
```

**Protein Sequence:**

```
MATGSRTSLLLAFLGLCLPWLQEGSAFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEA
YIPKEQKYSFLQNPQTSLCFSESIPTSPNREETQQKSNLELLLRISLLLIQSWLEPVQFLR
SVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHNDD
ALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF
```



Negative CIS Elements	Negative repeat Elements
0	0

Indices based on non-uniform usage of synonymous codon				
Index	Description	Range	Value	Reference

RSCU	Relative Synonymous Codon Usage	0~6	0.99	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	61	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.13	<a href="#">[4]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.39	<a href="#">[5]</a>
CDC	Codon Deviation Coefficient	0~1	0.07	<a href="#">[6]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.68	<a href="#">[7]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.01	<a href="#">[8]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.01	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.97	<a href="#">[11]</a>
P	Codon Preference	$\geq 1$	1.01	<a href="#">[12]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.02	<a href="#">[13]</a>

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.61	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.1	<a href="#">[2]</a>
FOP	Frequency of Optimal Codons	0~1	0.33	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.07	<a href="#">[5]</a>
COUSIN18			0.19	
CBI	Codon Bias Index	-1~1	-0.01	<a href="#">[6]</a>
Dmean	Mean Dissimilarity-based Index	0~2	1.09	<a href="#">[7]</a>
RCA	Relative Codon Adaptation	$\geq 0$	1.05	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.2	<a href="#">[9]</a>
B	Codon Usage Bias	0~2	0.31	<a href="#">[10]</a>

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	0~1	0.44	<a href="#">[11]</a>
gtAI	Genetic tRNA Adaptation Index	0~1	0.51	<a href="#">[2]</a>
P2	P2 Index	0~1	0.48	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
GC3	GC Content at the Third Position of Synonymous Codons	0~1	0.51	<a href="#">[11]</a>
GC	GC Content		0.47	

GC1	GC Content at the First Position of Synonymous Codons		0.51	
GC2	GC Content at the Second Position of Synonymous Codons		0.38	
ENcp	Effective Number of Codon Pairs	20~61	20	<a href="#">[2]</a>
CPS	Codon Pair Score	-1~1	0.03	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	0.5~1	0.76	<a href="#">[5]</a>

**Gene Name:** Erythropoietin

**Reference Source:** Codon Usage Database - Kazusa

**Expression Host Organism:** Pichia pastoris (budding yeasts)

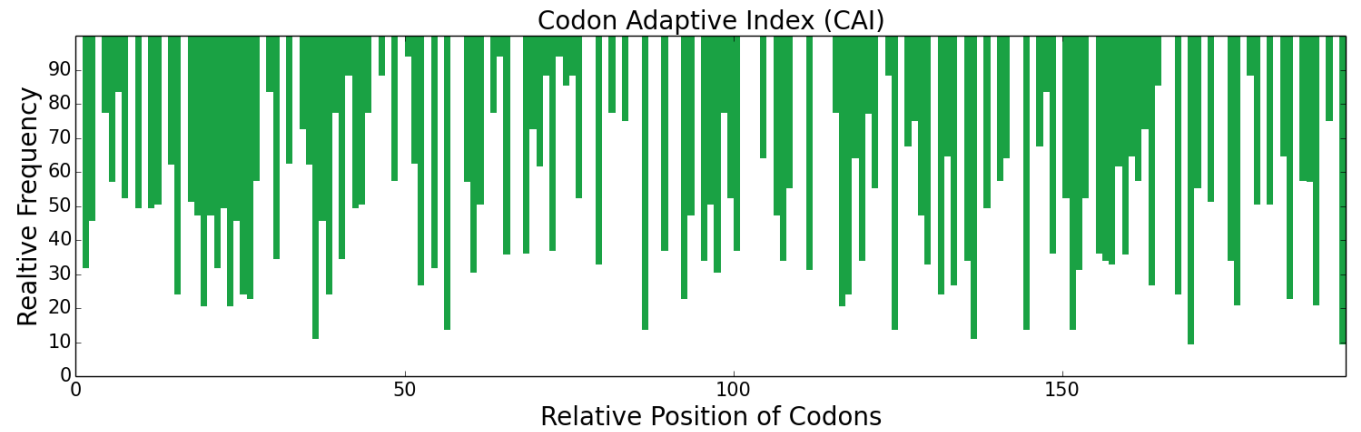
**DNA Sequence Length:** 579

**DNA Sequence:**

ATGGGCGTGCATGAGTGCCCTGCATGGTTATGGTTACTTTTGTCACTCTTGAGTCTGCCG  
CTGGGCTTACCGGTGCTCGGGGCCCCACCTCGTTTGATCTGTGACTCACGCGTGCTCGAG  
CGTTATTTACTTGAGGCTAAAGAAGCCGAAAAATATCACGACTGGCTGTGCGGAACATTGC  
TCGCTTAACGAGAATATAACTGTTCCCCGACACAAAAAGTAAATTTCTATGCATGGAAGAGG  
ATGGAGGTTGGACAACAAGCGGTTGAAGTATGGCAAGGGCTGGCTCTACTTTCGGAGGCA  
GTATTGAGAGGTCAGGCTCTGCTAGTCAACTCTAGCCAACCATGGGAGCCGCTCCAGCTA  
CACGTCGATAAAGCGGTTTCCGGACTGAGGTCTCTCACCACGTTGCTACGCGCTTTAGGT  
GCCCAGAAGGAAGCGATTTCCCTCCCGATGCAGCGAGCGCAGCTCCCCTAAGGACAATA  
ACCGCCGACACGTTTCAGAAAGCTCTTTCGGGTCTACAGTAACTTTCTACGAGGTAACTT  
AAGCTTTACACCGGGGAAGCCTGCCGAAGTGGAGATCGG

**Protein Sequence:**

MGVHECPAWLWLLLSLLSLPLGLPVLGAPPRLICDSRVLERYLLEAKEAENITTGCAEHC  
SLNENITVPDTKVNFYAWKRMEVGGQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQL  
HVDKAVSGLRSLTTLRLALGAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKL  
KLYTGEACRTGDR



Negative CIS Elements	Negative repeat Elements
0	0

Indices based on non-uniform usage of synonymous codon				
Index	Description	Range	Value	Reference
RSCU	Relative Synonymous Codon Usage	0~6	0.98	<a href="#">[11]</a>

ENC	Effective Number of Codons	20~61	61	[ <a href="#">2</a> , <a href="#">3</a> ]
RCBS	Relative Codon Bias Strength	$\geq 0$	0.11	<a href="#">[4]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.39	<a href="#">[5]</a>
CDC	Codon Deviation Coefficient	0~1	0.06	<a href="#">[6]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.71	<a href="#">[7]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.01	<a href="#">[8]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.01	[ <a href="#">9</a> , <a href="#">10</a> ]
Ew	Weighted Sum of Relative Entropy	0~1	0.96	<a href="#">[11]</a>
P	Codon Preference	$\geq 1$	1.01	<a href="#">[12]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.01	<a href="#">[13]</a>

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.56	<a href="#">[1]</a>
CFD	Codon Frequency Distribution	0~1	0.13	<a href="#">[2]</a>
FOP	Frequency of Optimal Codons	0~1	0.3	[ <a href="#">3</a> , <a href="#">4</a> ]
COUSIN59	Codon Usage Similarity Index	$\infty$	-0.02	<a href="#">[5]</a>
COUSIN18			0.07	
CBI	Codon Bias Index	-1~1	-0.01	<a href="#">[6]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.95	<a href="#">[7]</a>
RCA	Relative Codon Adaptation	$\geq 0$	1	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.2	<a href="#">[9]</a>
B	Codon Usage Bias	0~2	0.34	<a href="#">[10]</a>

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	0~1	0.41	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	0~1	0.48	<a href="#">[2]</a>
P2	P2 Index	0~1	0.51	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
GC3	GC Content at the Third Position of Synonymous Codons	0~1	0.52	<a href="#">[1]</a>
GC	GC Content		0.53	
	GC Content at the First Position			



GC1	of Synonymous Codons		0.6	
GC2	GC Content at the Second Position of Synonymous Codons		0.46	
ENcp	Effective Number of Codon Pairs	20~61	39.72	<a href="#">[2]</a>
CPS	Codon Pair Score	-1~1	0.02	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	0.5~1	0.73	<a href="#">[5]</a>

**Gene Name:** Interferon alpha

**Reference Source:** Codon Usage Database - Kazusa

**Expression Host Organism:** Pichia pastoris (budding yeasts)

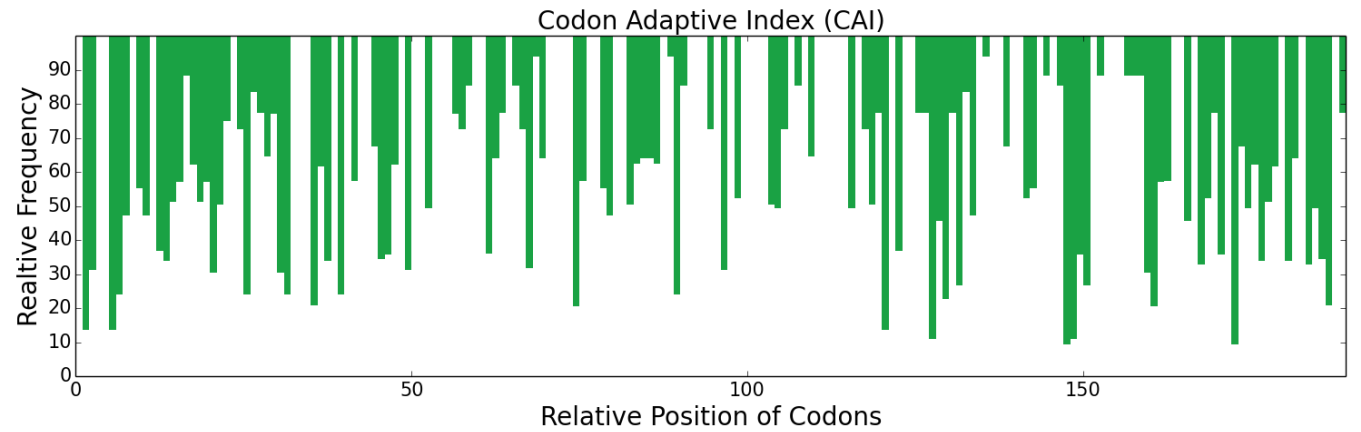
**DNA Sequence Length:** 567

**DNA Sequence:**

ATGGCGAGCCCATTGCGCTCCTGATGGTCTGGTTGTACTAAGTTGCAAATCAAGTTGC  
TCGCTTGGATGTGACCTCCCTGAGACCCACTCGCTCGATAACAGACGAACACTAATGCTC  
TTGGCCCAAATGTCCCGTATATCACCAAGCTCTTGTTTAATGGATAGACACGACTTCGGT  
TTTCCCCAGGAGGAATTCGACGGCAATCAGTTTCAAAAGGCTCCGGCCATTTCTGTCCTG  
CATGAAC TTATCCAGCAGATCTTTAATCTCTTCACTACTAAGGACTCTAGCGCTGCATGG  
GATGAAGATCTTTTAGACAAGTTCTGTACCGAATTGTACCAACAATTAAACGACCTTGAG  
GCGTGTGTAATGCAAGAGGAGCGCGTGGGGGAGACGCCTCTGATGAATGCTGATTCCATT  
TTGGCAGTCAAGAAATACTTCCGGCGCATAACGTTGTATTTGACTGAAAAAAAAATATTCG  
CCGTGCGCCTGGGAAGTGGTTAGGGCAGAGATAATGCGGTCCTTATCACTAAGTACAAAC  
CTACAGGAAAGGTTACGTGCAAAGGAG

**Protein Sequence:**

MASPFALLMVLVVLSCKSSCSLGC DLPETHSLDNRR TLMLLAQMSRISPSSCLMDRHDFG  
FPQEEFDGNQFQKAP AISVLHELIQQIFNLFTTKDSSAAWDEDLLDKFCTELYQQ LNDLE  
ACVMQEERVGETPLMNAD SILAVKKYFR RITLYLTEKKYSPCAWEVVRAEIMRSLSLSTN  
LQERLRRKE



Negative CIS Elements	Negative repeat Elements
1	0

Indices based on non-uniform usage of synonymous codon				
Index	Description	Range	Value	Reference
RSCU	Relative Synonymous Codon Usage	0~6	0.96	<a href="#">[11]</a>

ENC	Effective Number of Codons	20~61	61	[2, 3]
RCBS	Relative Codon Bias Strength	$\geq 0$	0.14	[4]
DCBS	Directional Codon Bias Score	$\geq 1$	1.45	[5]
CDC	Codon Deviation Coefficient	0~1	0.08	[6]
MILC	Measure Independent of Length and Composition	-1~1	-0.71	[7]
ICDI	Intrinsic Codon Deviation Index	0~1	0.01	[8]
SCUO	Synonymous Codon Usage Order	0~1	0.01	[9, 10]
Ew	Weighted Sum of Relative Entropy	0~1	0.94	[11]
P	Codon Preference	$\geq 1$	1.01	[12]
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.01	[13]

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.6	[1]
CFD	Codon Frequency Distribution	0~1	0.1	[2]
FOP	Frequency of Optimal Codons	0~1	0.33	[3, 4]
COUSIN59	Codon Usage Similarity Index	$\infty$	-0.06	[5]
COUSIN18			-0.14	
CBI	Codon Bias Index	-1~1	-0	[6]
Dmean	Mean Dissimilarity-based Index	0~2	1.01	[7]
RCA	Relative Codon Adaptation	$\geq 0$	1.04	[8]
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.19	[9]
B	Codon Usage Bias	0~2	0.29	[10]

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	0~1	0.44	[1]
gtAI	Genetic tRNA Adaptation Index	0~1	0.51	[2]
P2	P2 Index	0~1	0.53	[3]

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
GC3	GC Content at the Third Position of Synonymous Codons	0~1	0.53	[1]
GC	GC Content		0.47	
	GC Content at the First Position			

GC1	of Synonymous Codons		0.51	
GC2	GC Content at the Second Position of Synonymous Codons		0.38	
ENcp	Effective Number of Codon Pairs	20~61	22.2	<a href="#">[2]</a>
CPS	Codon Pair Score	-1~1	0	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	0.5~1	0.76	<a href="#">[5]</a>

**Gene Name:** Interferon omega-1

**Reference Source:** Codon Usage Database - Kazusa

**Expression Host Organism:** Pichia pastoris (budding yeasts)

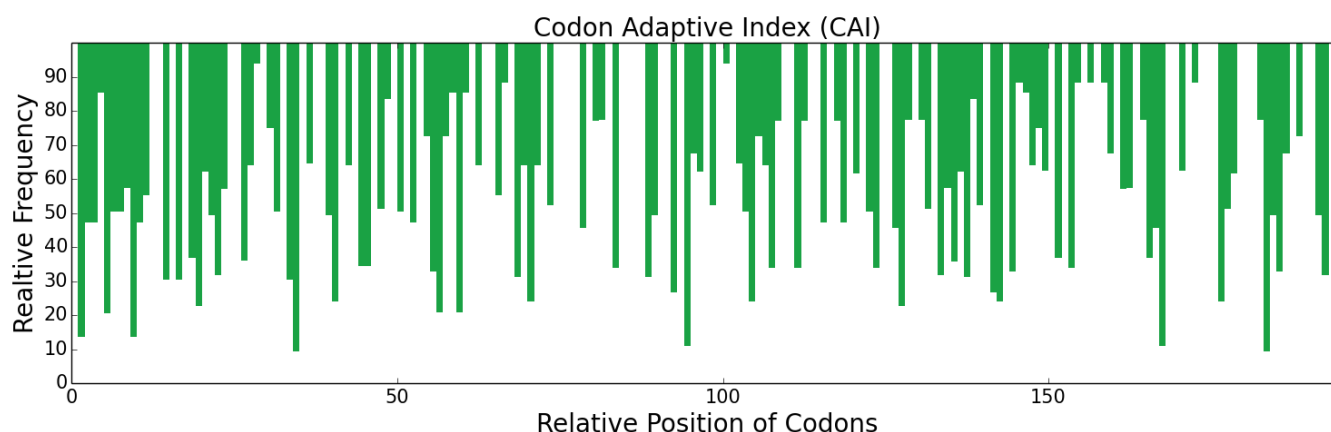
**DNA Sequence Length:** 585

#### DNA Sequence:

```
ATGGCGCTGCTGTTCCCGCTTCTTGCCGCGCTGGTCATGACTTCGTACTCGCCAGTAGGG
TCATTAGGCTGCGATTTGCCCCAGAATCATGGACTTTTGTGCGGGAACACCTTGGTTTTA
CTCCATCAGATGCGTCGTATTAGTCCTTTTCTTTGTCTGAAGGACAGGCGAGACTTCCGA
TTCCCACAGGAAATGGTCAAAGGTAGCCAGCTCCAGAAGGCACATGTTATGTCTGTGTTG
CACGAGATGCTACAACAAATTTTGTAGCTTATTTTCATACGGAACGCTCCTCAGCTGCATGG
AATATGACCCTTCTCGACCAGCTACACACTGGTCTACACCAACAACCTGCAACACCTGGAA
ACATGTCTTCTACAAGTTGTGGGGGAGGGTGAGAGTGCTGGCGCCATATCAAGCCCTGCA
TTGACGCTCAGAAGGTATTTCCAGGGAATCAGAGTATACCTAAAAGAAAAAAGTATTCC
GATTGCGCCTGGGAGGTAGTGCGCATGGAAATCATGAAATCTTTGTTTCTCAGTACAAAC
ATGCAAGAGCGGTTAAGGTCCAAGGACAGAGATTTAGGCTCTTCA
```

#### Protein Sequence:

```
MALLFPLLAALVMTSYSPVGSILGCDLPQNHGLLSRNTLVLLHQMRRI SPFLCLKDRRDFR
FPQEMVKGSQQLQKAHVMSVLHEMLQQIFSLFHTERS SAAWNMTLLDQLHTGLHQQLQHLE
TCLLQVVGESESAGAISSPALTLRRYFQGIRVYLKEKKYSDCAWEVVRMEIMKSLFLSTN
MQERLRSKDRDLGSS
```



Negative CIS Elements	Negative repeat Elements
1	0

Indices based on non-uniform usage of synonymous codon				
Index	Description	Range	Value	Reference
RSCU	Relative Synonymous Codon Usage	0~6	0.96	<a href="#">[11]</a>

ENC	Effective Number of Codons	20~61	61	[2, 3]
RCBS	Relative Codon Bias Strength	$\geq 0$	0.13	[4]
DCBS	Directional Codon Bias Score	$\geq 1$	1.41	[5]
CDC	Codon Deviation Coefficient	0~1	0.07	[6]
MILC	Measure Independent of Length and Composition	-1~1	-0.7	[7]
ICDI	Intrinsic Codon Deviation Index	0~1	0.01	[8]
SCUO	Synonymous Codon Usage Order	0~1	0.01	[9, 10]
Ew	Weighted Sum of Relative Entropy	0~1	0.93	[11]
P	Codon Preference	$\geq 1$	1.02	[12]
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.02	[13]

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.6	[1]
CFD	Codon Frequency Distribution	0~1	0.09	[2]
FOP	Frequency of Optimal Codons	0~1	0.32	[3, 4]
COUSIN59	Codon Usage Similarity Index	$\infty$	0.04	[5]
COUSIN18			0.04	
CBI	Codon Bias Index	-1~1	0.01	[6]
Dmean	Mean Dissimilarity-based Index	0~2	0.47	[7]
RCA	Relative Codon Adaptation	$\geq 0$	1.05	[8]
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.16	[9]
B	Codon Usage Bias	0~2	0.28	[10]

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	0~1	0.43	[1]
gtAI	Genetic tRNA Adaptation Index	0~1	0.5	[2]
P2	P2 Index	0~1	0.5	[3]

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
GC3	GC Content at the Third Position of Synonymous Codons	0~1	0.52	[1]
GC	GC Content		0.48	
	GC Content at the First Position			

GC1	of Synonymous Codons		0.54	
GC2	GC Content at the Second Position of Synonymous Codons		0.37	
ENcp	Effective Number of Codon Pairs	20~61	23.11	<a href="#">[2]</a>
CPS	Codon Pair Score	-1~1	0.02	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	0.5~1	0.75	<a href="#">[5]</a>

**Gene Name:** GCSF

**Reference Source:** Codon Usage Database - Kazusa

**Expression Host Organism:** Pichia pastoris (budding yeasts)

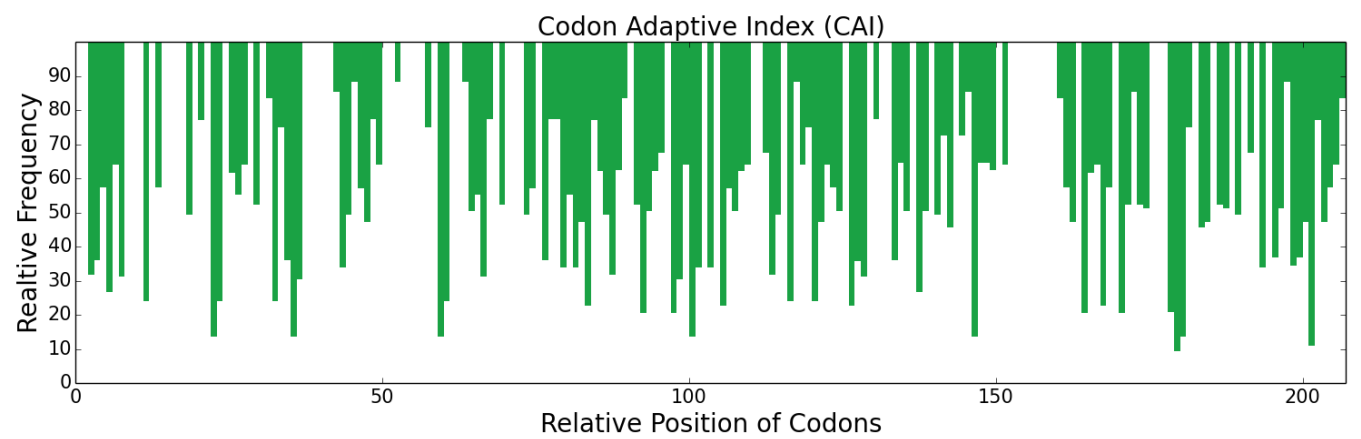
**DNA Sequence Length:** 621

**DNA Sequence:**

ATGGCTGGCCCCGCCACGCAGAGCCCAATGAAGCTCATGGCCTTGCAATTGTTGTTATGG  
CACTCTGCGCTCTGGACAGTCCAGGAAGCAACTCCTCTCGGACCCGCGTCGTCTTTGCCA  
CAATCTTTTCTATTAAAAATGCCTGGAGCAGGTTAGAAAAATTCAAGGTGATGGAGCTGCG  
CTCCAAGAAAAACTTGTTCAGCGAGTGTGCAACTTACAAGTTATGCCATCCCGAGGAGCTA  
GTCCTACTGGGGCACTCATTAGGCATCCCTTGGGCACCGCTTTCATCCTGTCCGTGCGAG  
GCGCTACAAC TAGCTGGGTGCCTTTCACAGTTGCATTCCGGCTTATTTCTCTATCAGGGA  
CTCCTGCAGGCCCTTGAAGGGATAAGCCCAGAGTTGGGTCCACCCCTTGATACGCTTCAA  
TTAGACGTGGCTGACTTCGCGACCACCATCTGGCAGCAAATGGAAGAATTGGGTATGGCT  
CCTGCCCTGCAACCGACACAGGGGGCCATGCCGGCATTTCGCAAGTGCTTTTCAACGACGG  
GCGGGAGGTGTGCTGGTTGCAAGTCATTTACAATCCTTTCTAGAAGTAAGTTATCGTGTA  
CTGCGCCACCTGGCCCAGCCT

**Protein Sequence:**

MAGPATQSPMKLMALQLLLWHSALWTVQEATPLGPASSLPQSFLKCLEQVRKIQGDGAA  
LQEKLVS ECATYKLC HPEELVLLGHSLGIPWAPLSSCPSQALQLAGCLSQLHSGFLYQG  
LLQALEGISPELGPTLDTLQLDVA DFATTIWQQMEELGMAPALQPTQGAMPAFASAFQRR  
AGGVLVASHLQSFLEVS YRVLRLHLAQP



Negative CIS Elements	Negative repeat Elements
0	0

Indices based on non-uniform usage of synonymous codon				
Index	Description	Range	Value	Reference



RSCU	Relative Synonymous Codon Usage	0~6	0.97	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	61	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.2	<a href="#">[4]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.58	<a href="#">[5]</a>
CDC	Codon Deviation Coefficient	0~1	0.11	<a href="#">[6]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.68	<a href="#">[7]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.02	<a href="#">[8]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.01	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.94	<a href="#">[11]</a>
P	Codon Preference	$\geq 1$	1.03	<a href="#">[12]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.02	<a href="#">[13]</a>

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.57	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.12	<a href="#">[2]</a>
FOP	Frequency of Optimal Codons	0~1	0.29	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	-0.11	<a href="#">[5]</a>
COUSIN18			-0.51	
CBI	Codon Bias Index	-1~1	-0.01	<a href="#">[6]</a>
Dmean	Mean Dissimilarity-based Index	0~2	1.1	<a href="#">[7]</a>
RCA	Relative Codon Adaptation	$\geq 0$	1.05	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.22	<a href="#">[9]</a>
B	Codon Usage Bias	0~2	0.33	<a href="#">[10]</a>

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	0~1	0.41	<a href="#">[11]</a>
gtAI	Genetic tRNA Adaptation Index	0~1	0.47	<a href="#">[2]</a>
P2	P2 Index	0~1	0.51	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
GC3	GC Content at the Third Position of Synonymous Codons	0~1	0.52	<a href="#">[11]</a>
GC	GC Content		0.54	

GC1	GC Content at the First Position of Synonymous Codons		0.64	
GC2	GC Content at the Second Position of Synonymous Codons		0.45	
ENcp	Effective Number of Codon Pairs	20~61	23.56	<a href="#">[2]</a>
CPS	Codon Pair Score	-1~1	0.02	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	0.5~1	0.73	<a href="#">[5]</a>

**Gene Name:** Tumor necrosis factor

**Reference Source:** Codon Usage Database - Kazusa

**Expression Host Organism:** Pichia pastoris (budding yeasts)

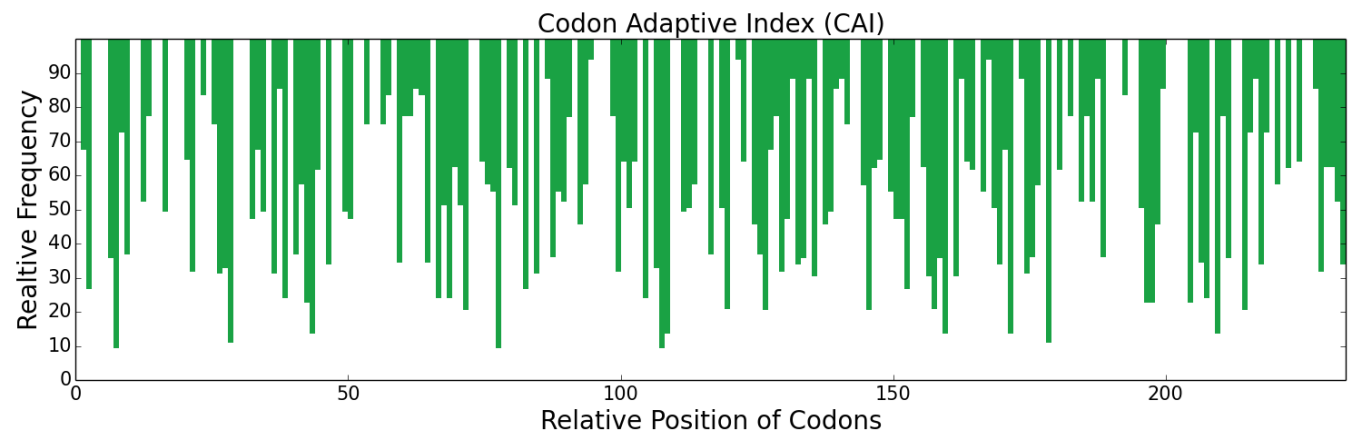
**DNA Sequence Length:** 699

**DNA Sequence:**

ATGTCCACGGAATCTATGATACGGGACGTAGAAATTGGCAGAGGAAGCTTTACCAAAGAAG  
ACCGGCGGTCTCAAGGAAGCAGGCGCTGTTTGTCTGTCCTTATTTAGCTTCCTCATT  
GTAGCCGGGGCGACAACCTCTATTTTGTCTTACTGCATTTTGGAGTTATTGGACCTCAACGT  
GAGGAGTTCCCTCGTGATCTCAGTCTCATCAGTCCGTTGGCTCAGGCCGTCCGGTCTTCA  
AGTAGAACGCCAAGCGATAAACCCGTCGCACACGTTGTGGCCAATCCACAAGCTGAGGGC  
CAGCTTCAGTGGCTCAACAGGCGGGCGAACGCTTTACTTGCCAACGGTGTAGAACTTCGA  
GATAATCAGTTGGTGGTACCGTCCGAGGGCCTGTATCTAATATATTCGCAAGTGTTATTC  
AAAGGACAAGGTTGCCCCGTCAACCCATGTCCTGCTGACGCACACTATCTCGCGAATAGCG  
GTTTCGTATCAGACAAAGGTCAATCTTCTATCCGCGATTAAAAGCCCCTGCCAACGCGAA  
ACACCAGAGGGTGCAGAGGCAAAACCCTGGTACGAACCTATTTACCTTGGGGGGGTGTTT  
CAATTGGAAGAGGGGGACCGTCTCTCTGCGGAGATAAACAGACCGGACTATCTAGACTTT  
GCCGAATCAGGTCAGGTTTACTTCGGCATCATCGCACTA

**Protein Sequence:**

MSTESMIRDVELAEELPKKTGGPQGSRRCLFLSLFSFLIVAGATTLFCLLHFGVIGPQR  
EEFPRDLISLISPLAQAVRSSSRTPSDKPVAVVNPQAEGLQWLNRRANALLANGVELR  
DNQLVVPSEGLYLIYSQVLFKQGQCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRE  
TPEGAEAKPWYEPIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGI IAL



Negative CIS Elements	Negative repeat Elements
0	0

Indices based on non-uniform usage of synonymous codon

Index	Description	Range	Value	Reference
RSCU	Relative Synonymous Codon Usage	0~6	0.99	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	61	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.08	<a href="#">[4]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.28	<a href="#">[5]</a>
CDC	Codon Deviation Coefficient	0~1	0.04	<a href="#">[6]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.67	<a href="#">[7]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.01	<a href="#">[8]</a>
SCUO	Synonymous Codon Usage Order	0~1	0	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.98	<a href="#">[11]</a>
P	Codon Preference	$\geq 1$	1.01	<a href="#">[12]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.01	<a href="#">[13]</a>

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.58	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.12	<a href="#">[2]</a>
FOP	Frequency of Optimal Codons	0~1	0.31	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.04	<a href="#">[5]</a>
COUSIN18			0.08	
CBI	Codon Bias Index	-1~1	-0.01	<a href="#">[6]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.94	<a href="#">[7]</a>
RCA	Relative Codon Adaptation	$\geq 0$	1.01	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.2	<a href="#">[9]</a>
B	Codon Usage Bias	0~2	0.33	<a href="#">[10]</a>

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	0~1	0.42	<a href="#">[11]</a>
gtAI	Genetic tRNA Adaptation Index	0~1	0.5	<a href="#">[2]</a>
P2	P2 Index	0~1	0.52	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
			0.5	

GC	GC Content	0~1	0.51	<a href="#">[1]</a>
GC1 GC3	GC Content at the First Position GC Content at the Third Position of Synonymous Codons		0.59	
GC2	GC Content at the Second Position of Synonymous Codons		0.43	
ENcp	Effective Number of Codon Pairs	20~61	21.18	<a href="#">[2]</a>
CPS	Codon Pair Score	-1~1	0.02	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	0.5~1	0.74	<a href="#">[5]</a>

**Gene Name:** Alpha-1-antitrypsin

**Reference Source:** Codon Usage Database - Kazusa

**Expression Host Organism:** *Pichia pastoris* (budding yeasts)

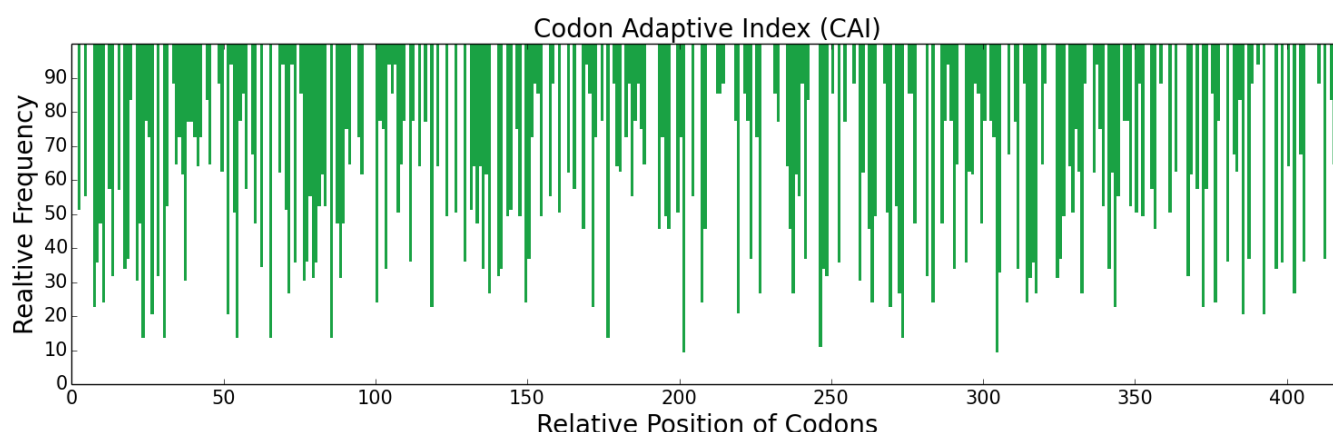
**DNA Sequence Length:** 1254

**DNA Sequence:**

```
ATGCCAAGTTCTGTCTCTTGGGGGATACTGCTCTTGGCCGGCTTGTGCTGTCTAGTACCT
GTTTCGCTGGCGGAGGACCCGCAAGGCGATGCGGCACAAAAAACCGACACATCGCACCAC
GACCAGGACCATCCTACCTTTAACAAAATCACTCCGAATCTTGCGGAGTTCGCCTTTTCC
CTGTACCGTCAATTGGCGCATCAATCAAATAGTACGAATATATTTTTCTCGCCCGTCAGC
ATAGCAACAGCATTTTGCATGCTGAGCCTGGGAACCAAGGCTGACACACATGATGAAATT
CTCGAGGGACTAAATTTCAATCTTACCGAGATTCCCGAGGCTCAGATTCACGAAGGGTTT
CAGGAATTGTTAAGAACTCTTAACCAACCCGATAGTCAGCTGCAGCTAACAACGGGTAAC
GGCCTATTTTTAAGTGAAGGATTAAAGCTCGTAGACAAATCTTAGAAGATGTCAAAAAG
CTTTACCATTGAGAAGCCTTTACTGTGAATTTGCGGGGACACTGAGGAAGCGAAGAAACAG
ATCAACGACTATGTCGAGAAAGGAACCCAAGGTAAGATTGTGGACTTAGTGAAGGAACCTT
GACCGGGATACTGTCTTTGCTCTCGTGAACCTACATTTTCTTCAAAGGTAAGTGGGAGCGA
CCATTCGAGGTAAAGGACACGGAAGAAGAAGATTTCCACGTTGATCAGGTGACGACAGTC
AAAGTACCTATGATGAAGCGCCTAGGCATGTTCAACATACAACACTGTAAGAAATTGTCG
TCATGGGTGCTCTTAATGAAGTATCTTGGGAACGCAACGGCGATTTTCTTCCTGCCAGAT
GAAGGCAAGCTCCAACATCTGGAGAATGAGCTAACCCATGATATAATCACAAAATTCCTG
GAGAACGAGGACCGGAGGTCTGCTTCCCTTGACCTACCAAACTCAGCATAACGGGTACC
TATGATTTGAAGAGCGTATTAGGTGAGCTTGGAATCACGAAAGTTTTTCAAATGGAGCA
GATCTATCAGGGGTCACTGAGGAGGCACCACTTAAATTATCTAAGGCCGTGCATAAAGCT
GTTCTTACTATCGATGAAAAGGGCACAGAAGCCGCTGGGGCCATGTTCTCGAGGCTATT
CCCATGTCCATCCCTCCGGAAGTAAATTTAATAAGCCGTTTGTTTTTCTAATGATAGAA
CAGAACACGAAGTCCCCCTTGTTTATGGGTAAAGTTGTAAACCCTACCCAAAAA
```

**Protein Sequence:**

```
MPSSVSWGILLLAGLCCCLVPVSLAEDPQGDAQKTDTSHHQDHPFNFNKITPNLAEFASF
LYRQLAHQSNSTNIFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTETPEAQIHEGF
QELLRTLNPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFVNFVDTEEAKKQ
INDYVEKGTQGKIVDLVKELDRDVFALVNYIFFKGKWERPFVEKDTTEEDFHVDQVTTV
KVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIIITKFL
ENEDRRSASLHLPKLSITGTYDLKSVLGLGITKVFSNGADLSGVTEEAPLKLSKAVHKA
VLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK
```



Negative CIS Elements	Negative repeat Elements
1	0

### Indices based on non-uniform usage of synonymous codon

Index	Description	Range	Value	Reference
RSCU	Relative Synonymous Codon Usage	0~6	0.97	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	61	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.11	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.38	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.08	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.6	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.01	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.97	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.01	<a href="#">[131]</a>

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.64	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.09	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.35	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.06	<a href="#">[51]</a>
COUSIN18			0.15	
CBI	Codon Bias Index	-1~1	0	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.72	<a href="#">[71]</a>

RCA	Relative Codon Adaptation	$\geq 0$	1.04	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.19	<a href="#">[9]</a>
B	Codon Usage Bias	$0 \sim 2$	0.26	<a href="#">[10]</a>

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	$0 \sim 1$	0.46	<a href="#">[11]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.54	<a href="#">[2]</a>
P2	P2 Index	$0 \sim 1$	0.51	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
GC3	GC Content at the Third Position of Synonymous Codons	$0 \sim 1$	0.51	<a href="#">[11]</a>
GC	GC Content		0.46	
GC1	GC Content at the First Position of Synonymous Codons		0.53	
GC2	GC Content at the Second Position of Synonymous Codons		0.33	
ENcp	Effective Number of Codon Pairs	$20 \sim 61$	61	<a href="#">[2]</a>
CPS	Codon Pair Score	$-1 \sim 1$	0.02	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	$0.5 \sim 1$	0.76	<a href="#">[5]</a>



**Gene Name:** Tissue-type plasminogen activator

**Reference Source:** Codon Usage Database - Kazusa

**Expression Host Organism:** *Pichia pastoris* (budding yeasts)

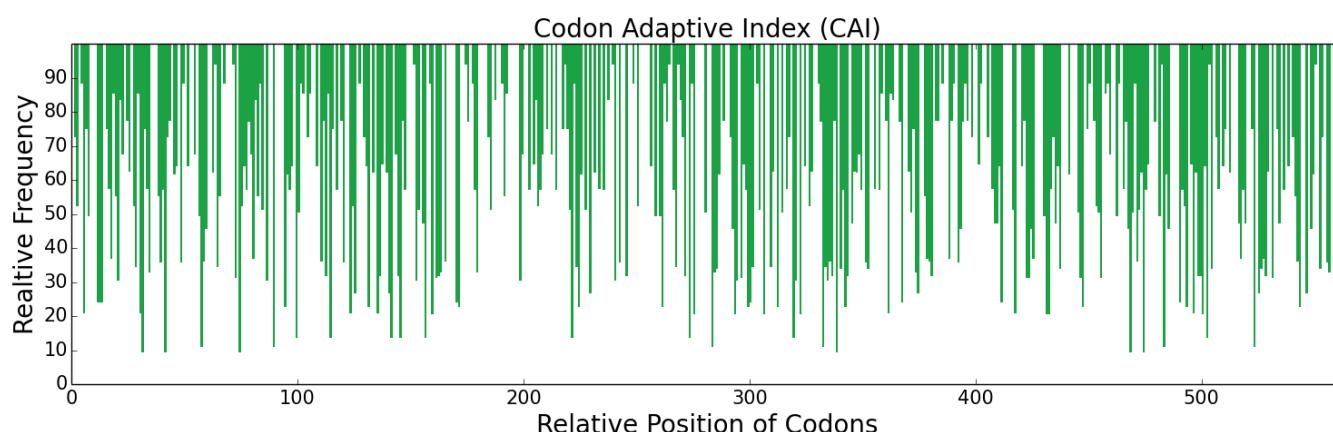
**DNA Sequence Length:** 1686

**DNA Sequence:**

```
ATGGACGCAATGAAACGAGGATTATGTTGTGTTCTCCTCCTCTGTGGAGCCGTATTTCGTC
TCGCCTTCCCAAGAGATCCATGCACGTTTCCGACGGGGAGCCAGGTCTTACCAAGTCATA
TGCCGGGACGAGAAGACACAGATGATATATCAACAGCATCAATCCTGGTTACGCCCCGTG
TTGAGATCAAATCGTGTGCAATATTGTTGGTGTAAATAGCGGTCGGGCACAGTGCCACTCC
GTACCTGTCAAAAAGTTGTTTCGGAACACGCTGTTTAAACGGTGGGACATGCCAGCAAGCG
CTTTATTTCTCTGACTTCGTTTGTCAAGTGTCCCGAGGGCTTCGCGGGAAAGTGCTGTGAG
ATAGATACTCGAGCAACGTGTTATGAAGACCAGGGGATTCATACCGAGGCACCTGGTCA
ACGGCGGAATCCGGCGCGGAGTGCATAACTGGAATTCGAGTGCTCTGGCGCAAAAACCG
TACAGCGGCAGGAGACCCGATGCTATTAGACTCGGGTTGGGTAATCACAATATTGCAGG
AACCCAGATAGAGACAGTAAGCCTTGGTGTATGTCTTCAAGGCTGGTAAGTACTCGTCC
GAATTTTGTCTTACCCCTGCATGCTCCGAAGGAAACTCCGATTGCTACTTTGGAAATGGA
AGTGCGTATCGTGGGACACATAGTTTGACGGAATCAGGTGCCTCTTGCTTGCCCTGGAAT
TCGATGATATTGATTGGCAAGGTTTATACTGCACAAAACCCATCTGCTCAGGCTTTAGGT
TTAGGGAAACACAATTACTGCCGTAATCCTGACGGCGATGCGAAACCGTGGTGTGATGTT
CTTAAGAACCGCAGGCTAACATGGGAGTACTGTGACGTGCCGTCGTGTAGCACCTGCGGG
CTCCGTCAATATAGTCAACCGCAATTTCTGTATCAAGGGGGGTCTTTTGGCCGACATTGCG
TCGCATCCGTGGCAGGCTGCAATCTTTGCTAAACACCGCCGTTTCGCCCCGCGAGCGGTTT
CTATGCGGGGGCATTCTGATCTCATCTGCTGGATACTATCTGCTGCCATTGCTTCCAA
GAGCGATTCCCTCCACATCACCTCACTGTTATCCTTGAAGGACGTACAGAGTCGTACCC
GGCGAAGAGGAGCAAAAATTTGAAGTAGAGAAATACATAGTGCACAAAGAGTTTGACGAT
GATACCTATGATAACGACATTGCCCTGCTGCAGCTCAAGTCTGATTCTAGTCGATGTGCT
CAGGAGAGCAGCGTGGTAAGAAGTGTGTTTACCGCCGGCCGACCTGCAGCTACCAGAT
TGGACAGAATGTGAAGTACGCGGTACGGAACATGAGGCACTTAGCCCATTTCTATTCC
GAAAGATTAAAAGAAGCCACGTGCGGCTTTATCCAGTTCACGGTGCACCTCTCAACAC
TTGTTAAATCGCACAGTGAAGTATGCTCTGCGCAGGGGATACCCGATCAGGCGGC
CCGAGGCGAATCTACATGACGCTGTGAGGAGATTGAGGTGGTCCACTGGTATGCCTG
AACGATGGACGCATGACGCTAGTAGGCATCATTAGCTGGGGACTGGGTTGCGGTGAGAAG
GACGTCCCCGGGGTTTACACGAAGGTGACAAATTACCTAGACTGGATAAGGGATAACATG
CGGCCT
```

**Protein Sequence:**

```
MDAMKRGLLCVLLLCGAVFVSPSQEIHARFRRGARSYQVICRDEKTQMIYQQHQSWLRPV
LRSNRVEYCWCNSGRAQCHSVPVKSCSEPRCFNGGTCQQALYFSDFCVQCPEGFAGKCCE
IDTRATCYEDQGISYRGTWSTAESGAECTNWNSSALAQKPYSGRRPDAILRLGLGNHNYCR
NPDRDSKPWCYVFKAGKYSSEFCSTPACSEGNSDCYFNGSAYRGTHSLTESGASCLPWN
SMILIGKVYTAQNPSAQALGLGKHNCRNPDGAPWCHVLKNRRLTWEYCDVPSCSTCG
LRQYSQPQFRIKGLFADIASHWPQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQ
ERFPPHHLTVILGRITYRVVPGEQKFEVEKYIVHKEFDDDTYDNDIALQLKSDSSRCA
QESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQH
LLNRTVTDNMLCAGDTRSGGPQANLHDACQGDGGPLVCLNDGRMTLVGIIISWGLGCGQK
DVPGVYTKVTNYLDWIRDNMRP
```



Negative CIS Elements	Negative repeat Elements
0	0

### Indices based on non-uniform usage of synonymous codon

Index	Description	Range	Value	Reference
RSCU	Relative Synonymous Codon Usage	0~6	0.97	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	61	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.08	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.22	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.04	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.57	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.96	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0	<a href="#">[131]</a>

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.6	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.11	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.33	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	-0	<a href="#">[51]</a>
COUSIN18			0.01	
CBI	Codon Bias Index	-1~1	-0	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.87	<a href="#">[71]</a>

RCA	Relative Codon Adaptation	$\geq 0$	0.99	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.19	<a href="#">[9]</a>
B	Codon Usage Bias	$0 \sim 2$	0.3	<a href="#">[10]</a>

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	$0 \sim 1$	0.43	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.5	<a href="#">[2]</a>
P2	P2 Index	$0 \sim 1$	0.5	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
GC3	GC Content at the Third Position of Synonymous Codons	$0 \sim 1$	0.51	<a href="#">[1]</a>
GC	GC Content		0.51	
GC1	GC Content at the First Position of Synonymous Codons		0.53	
GC2	GC Content at the Second Position of Synonymous Codons		0.49	
ENcp	Effective Number of Codon Pairs	$20 \sim 61$	35.81	<a href="#">[2]</a>
CPS	Codon Pair Score	$-1 \sim 1$	0.01	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	$0.5 \sim 1$	0.76	<a href="#">[5]</a>

Gene Name: Interleukin-2

Reference Source: Codon Usage Database - Kazusa

Expression Host Organism: Pichia pastoris (budding yeasts)

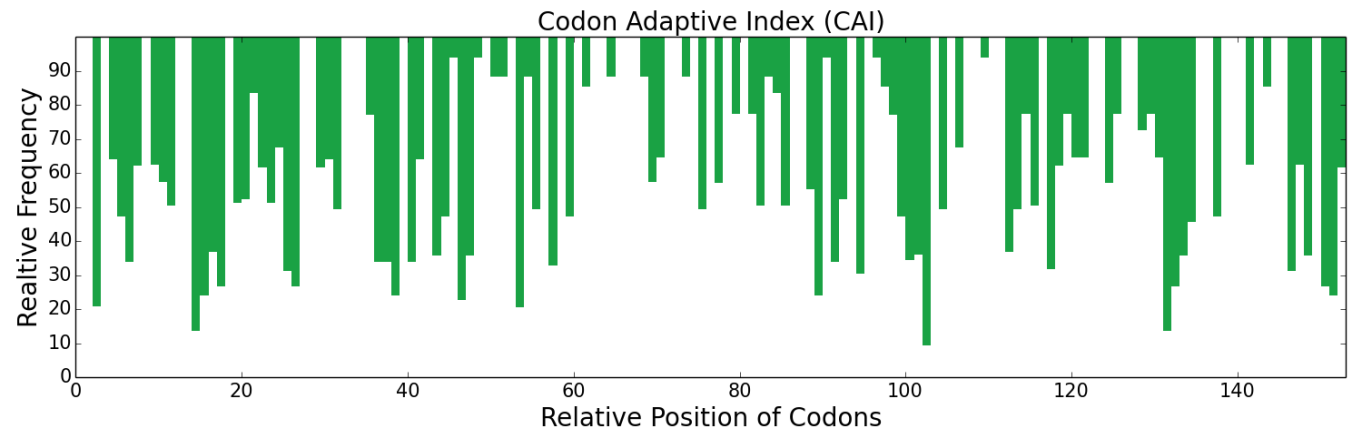
DNA Sequence Length: 459

DNA Sequence:

ATGTACCGAATGCAGCTGCTATCATGTATCGCCCTTTCTTTGGCGCTCGTAACGAACAGT  
GCACCTACAAGTTCCAGCACGAAGAAGACACAGTTACAATTGGAACACCTACTACTCGAT  
CTACAGATGATACTGAATGGGATAAAATAACTATAAAAAACCCGAAATTAAGTAGGATGCTG  
ACTTTCAAGTTTATATGCCAAAGAAAGCCACCGAATTGAAACATTTACAATGCTTGGAG  
GAAGAGCTTAAACCTCTTGAAGAAGTCCTCAATCTAGCACAATCGAAGAATTTCCACCTG  
CGTCCCCGGGATTTAATTTCCAACATTAATGTTATTGTATTAGAGCTTAAGGGCTCAGAG  
ACCACCTTTATGTGCGAGTACGCTGACGAGACCGCGACGATAGTGAATTTCTGAACAGA  
TGGATCACTTTCTGTCAAAGCATCATATCTACGCTCACA

Protein Sequence:

MYRMQLLSICIALSLALVTNSAPTSSSTKKTQLQLEHLLLDLQMLNGINNYKNPKLTRML  
TFKFYMPKKATELKHLLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSE  
TTFMCEYADETATIVEFLNRWITFCQSIISTLT



Negative CIS Elements	Negative repeat Elements
0	0

Indices based on non-uniform usage of synonymous codon				
Index	Description	Range	Value	Reference
RSCU	Relative Synonymous Codon Usage	0~6	1	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	61	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	≥0	0.15	<a href="#">[41]</a>

DCBS	Directional Codon Bias Score	$\geq 1$	1.45	<a href="#">[5]</a>
CDC	Codon Deviation Coefficient	0~1	0.09	<a href="#">[6]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.74	<a href="#">[7]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.04	<a href="#">[8]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.02	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.93	<a href="#">[11]</a>
P	Codon Preference	$\geq 1$	1.03	<a href="#">[12]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.03	<a href="#">[13]</a>

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.62	<a href="#">[1]</a>
CFD	Codon Frequency Distribution	0~1	0.09	<a href="#">[2]</a>
FOP	Frequency of Optimal Codons	0~1	0.32	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.05	<a href="#">[5]</a>
COUSIN18			-0.05	
CBI	Codon Bias Index	-1~1	-0.02	<a href="#">[6]</a>
Dmean	Mean Dissimilarity-based Index	0~2	1.02	<a href="#">[7]</a>
RCA	Relative Codon Adaptation	$\geq 0$	1.03	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.28	<a href="#">[9]</a>
B	Codon Usage Bias	0~2	0.3	<a href="#">[10]</a>

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	0~1	0.43	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	0~1	0.5	<a href="#">[2]</a>
P2	P2 Index	0~1	0.5	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
GC3	GC Content at the Third Position of Synonymous Codons	0~1	0.51	<a href="#">[1]</a>
GC	GC Content		0.42	
GC1	GC Content at the First Position of Synonymous Codons		0.42	
GC2	GC Content at the Second Position of Synonymous Codons		0.32	

ENcp	Effective Number of Codon Pairs	20~61	20	<a href="#">[2]</a>
CPS	Codon Pair Score	-1~1	0.05	<a href="#">[3, 4]</a>
Codon Volatility	Codon Volatility	0.5~1	0.76	<a href="#">[5]</a>

**Gene Name:** Hepatitis B large envelope protein

**Reference Source:** Codon Usage Database - Kazusa

**Expression Host Organism:** *Pichia pastoris* (budding yeasts)

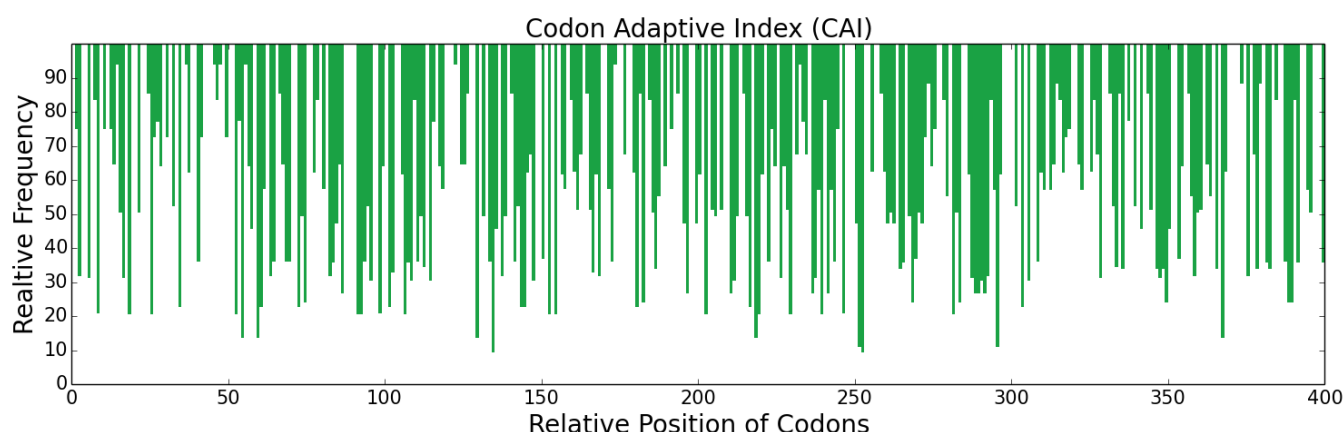
**DNA Sequence Length:** 1200

**DNA Sequence:**

```
ATGGGAGGCTGGTCTAGCAAGCCTCGACAAGGAATGGGAACCAATCTTAGCGTTCCGAAC
CCACTTGGTTTTTTTCCCGGACCACCAGTTGGACCCAGCATTTGGGGCTAATTCAAACAAC
CCCGACTGGGATTTTAATCCTAATAAGGACCATTGGCCGGAGGCGAATCAGGTGGGTGCG
GGGGCCTTTGGCCCCGGTTTACCCCCCCCCCATGGTGGGTACTCGGTTGGTCACCTCAA
GCCAAGGCATACTGACCACGTTGCCAGCTGCTCCGCCGCCCGCATCGACTAACCACAG
TCTGGGAGGCAACCAACACCGATATCGCCTCCCTTACGTGATTCGCACCCACAGGCCATG
CAATGGAATTCTACCACCTTCCATCAAGCGTTGTTAGATCCCCGGGTGAGAGGCTTATAC
TTCCCCGCAGGGGGGTTCATCTCGGGTACTGTAAACCCGGTTCCGACTACAGCCTCTCCT
ATCAGTTCCATTTTTCAGTAGGACAGGCGATCCAGCCCCCAATATGGAATCCACTACTTCA
GGGTTCCTCGGTCCTCTTCTAGTCTTGCAGGCTGGATTTTTCTTGCTGACGAGAATTCTG
ACAATTCCGCAAAGTTTAGATAGTTGGTGGACGTCGTTAAACTTCTTAGGGGGTGCGCCG
ACATGTCCCGGACAGAACAGCCAGAGTCCGACTTCCAATCACTCCCCAACGAGCTGCCCC
CCTACGTGCCCCGGATACCGATGGATGTGTCTGCGCCGGTTTATTATCTTTTTGTTTCATC
CTGCTTCTGTGTCTAATATTTTTTACTCGTACTTCTGGACTATCAGGGAAATGTTGCCTGTC
TGTCGCCCTTCTCCCAGGTACAAGCACGACGTCGACGGGCCCTTGCCGCACATGTACTATT
CCAGCACAAAGGGAATTTCGATGTTTTCCCTCATGCTGTTGCACCAAACCTTCAGACGAAAC
TGTACCTGCATTCCAATCCCTTCCAGCTGGGCTTTCGCACGTTTCCTATGGGAGTGGGCA
TCTGTGAGATTTCAGTTGGCTAAGCCTACTCGTGCCATTTGTACAGTGGTTCGTCGGCCTT
AGTCCAACCGTCTGGCTATCTGCGATCTGGATGATGTGGTATTGGGGCCCATCCCTATAT
AACATACTATCTCCTTTTTTGGCCCTCCTCCCTATATTTTTTTGCCTTTGGGTTTACATA
```

**Protein Sequence:**

```
MGGWSSKPRQGMGTNLSVNPPLGFFPDHQLDPAFGANSNNPDWDFNPNKDHWPENQVGA
GAFGPGFTPPHGGLLGWSPQAQGILTTLPAAPPPASTNRQSGRQPTPI SPPLRDSHPQAM
QWNSTTFHQALLDPRVRGLYFPAGGSSSGTVNPVPTTASPISSIFSRTGDPAPNMESTTS
GFLGPLLVLQAGFFLLTRILTIPQSLDSWWTSLNFLGGAPTCPGQNSQSPTSNHSPTSCP
PTCPGYRWMCLRRFIIIFLIFLLLLCLIFLLVLLDYQGMLPVCPLLPGTSTTSTGPCRTCTI
PAQGTSMFPPSCCCTKPSDGNCTCIPIPSSWAFARFLWEWASVRFSWLSLLVPFVQWFVGL
SPTVWLSAIWMMWYWGPSLYNILSPFLPLLPFIFFCLWVYI
```



Negative CIS Elements	Negative repeat Elements
3	0

### Indices based on non-uniform usage of synonymous codon

Index	Description	Range	Value	Reference
RSCU	Relative Synonymous Codon Usage	0~6	0.94	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	61	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.16	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.55	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.09	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.6	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.01	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.93	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1.01	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.01	<a href="#">[131]</a>

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.58	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.12	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.3	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.08	<a href="#">[51]</a>
COUSIN18			0.22	
CBI	Codon Bias Index	-1~1	0	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.87	<a href="#">[71]</a>



RCA	Relative Codon Adaptation	$\geq 0$	1.03	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.19	<a href="#">[9]</a>
B	Codon Usage Bias	$0 \sim 2$	0.33	<a href="#">[10]</a>

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	$0 \sim 1$	0.41	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.48	<a href="#">[2]</a>
P2	P2 Index	$0 \sim 1$	0.5	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
GC3	GC Content at the Third Position of Synonymous Codons	$0 \sim 1$	0.53	<a href="#">[1]</a>
GC	GC Content		0.53	
GC1	GC Content at the First Position of Synonymous Codons		0.49	
GC2	GC Content at the Second Position of Synonymous Codons		0.56	
ENcp	Effective Number of Codon Pairs	$20 \sim 61$	38.65	<a href="#">[2]</a>
CPS	Codon Pair Score	$-1 \sim 1$	0.03	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	$0.5 \sim 1$	0.73	<a href="#">[5]</a>

**Gene Name:** HPV major capsid protein L1

**Reference Source:** Codon Usage Database - Kazusa

**Expression Host Organism:** *Pichia pastoris* (budding yeasts)

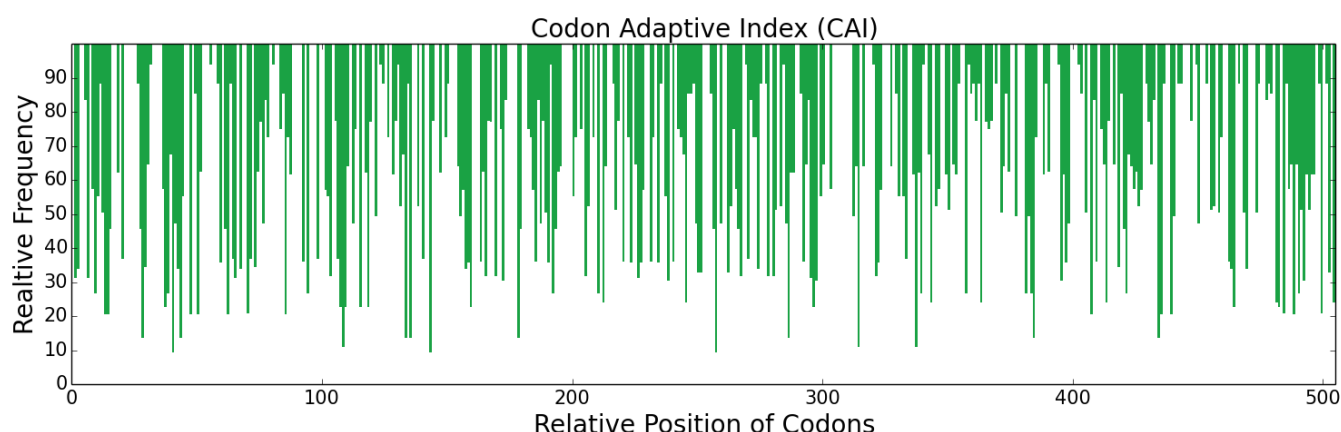
**DNA Sequence Length:** 1515

**DNA Sequence:**

```
ATGAGCCTATGGTTGCCTAGCGAAGCCACGGTCTATCTTCCGCCGGTGCCAGTTTCAAAG
GTAGTTTCTACTGATGAATATGTGGCGCGTACCAATATTTACTACCATGCCGGGACGTCC
CGGCTGCTAGCGGTCGGTCATCCGTACTTCCCGATCAAGAAGCCAAATAACAACAAAATA
TTGGTGCCGAAAGTAAGCGGTCTACAATACCGAGTATTTCTGATCCACCTGCCTGACCCA
AATAAGTTTGGATTCCCGGACACATCTTTTACAACCCCGATACGCAAAGATTGGTATGG
GCTTGGCTCGGCGTTGAGGTAGGGCGCGGGCAGCCACTGGGAGTTGGGATTTACAGGGCAC
CCATTATTGAATAAATTGGACGATACAGAGAATGCATCCGCGTATGCGGCTAACGCAGGT
GTAGATAACCGGGAGTGTATTTCAATGGACTATAAGCAAACCTCAGTTATGCCTAATAGGG
TGTAAGCCACCCATCGGCGAGCACTGGGGCAAGGGATCGCCTTGTAATAACGTTGCGGTG
AACCCAGGAGACTGCCCCCTCTGGAGCTTATAAATACGGTGATCCAGGATGGTGATATG
GTCGACACTGGATTTGGCGCAATGGACTTTACGACTCTCCAGGCTAACAAAAGTGAGGTT
CCCTTGACATATGTACCAGCATATGCAAGTACCCCGACTACATAAAAAATGGTCTCGGAA
CCCTACGGAGACTCCCTCTTCTTCTATCTGAGGAGGGAACAAATGTTCTGCGGCATCTG
TTTAACAGGGCAGGAGCCGTGGGCGAAAAATGTACCTGACGACCTATATATTAAAGGCTCT
GGCAGTACTGCAAATCTGGCGTCATCAAACTACTTCCCCACCCCTAGCGGGTCGATGGTC
ACCTCTGATGCCCAAATTTTTTAACAAGCCATACTGGTTACAGCGCGCTCAGGGTCATAAC
AATGGCATATGCTGGGGTAACCAAGTTGTTCTGTCAGTGTCTAGATACTACACGCTCAACG
AATATGTCCCTCTGTGCAGCCATTTCTACAAGTGAAACCACATATAAGAACACGAATTTT
AAAGAGTATCTCAGACACGGAGAGGAATATGATCTTCAGTTCATCTTTCAATTATGTAAG
ATTACGTTAACGGCGGACGTTATGACATATATCCATTCTATGAATTCGACAATACTGGAA
GATTGGAATTTCTGGTCTTCAACCGCCTCCCGGTGGAACCCTCGAGGATACCTACCGTTTC
GTGACGTCCAGGCCATCGCATGCCAAAAACACACCCCTCCAGCGCCGAAAGAAGATCCG
TTAAAGAAATATACTTTTTGGGAGGTTAATCTGAAGGAAAAATTTAGTGCAGATCTTGAC
CAATTTCCCCTAGGGAGAAAATTTCTTCTACAAGCTGGTCTTAAAGCTAAGCCTAAATTC
ACTCTCGGGAAGCGAAAAGCCACCCCGACCACGAGTTCGACAAGTACAACAGCTAAACGA
AAGAAAAGGAAGCTC
```

**Protein Sequence:**

```
MSLWLPSEATVYLPPVPVSKVSTDEYVARTNIYYHAGTSRLLAVGHPYFPIKKPNNNKI
LVPKVSGLQYRVFRIHLPDPNKFDPDTSFYNPDTQRLVWACVGVGVGRGQPLGVGISGH
PLLNKLDDETENASAYAANAGVDNRECISMDYKQTQLCLIGCKPPIGEHWGKGSPTNVAV
NPGDCPPELINTVIQDGMVDTFGFAMDFTTLQANKSEVPLDICTSICKYPDYIKMVSE
PYGDSLFFYLRRQMFVRHLFNAGAVGENVPDDLYIKGSGSTANLASSNYFPTPSGSMV
TSDAQIFNKPWYLQRAQGHNNIGICWGNQLFVTVVDTRSTNMSLCAAISTSETTYKNTNF
KEYLRHGEEDYDLQFIFQLCKITLTADVMTYIHSMNSTILEDWNFGLQPPPGGTLEDITYRF
VTSQAIACQKHTPPAPKEDPLKKYTFWEVNLKEKFSADLDQFPLGRKFLLQAGLKAKPKF
TLGKRKATPTTSSTSTAKRKKRKL
```



Negative CIS Elements	Negative repeat Elements
0	0

### Indices based on non-uniform usage of synonymous codon

Index	Description	Range	Value	Reference
RSCU	Relative Synonymous Codon Usage	0~6	0.97	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	61	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.08	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.29	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.05	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.58	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.97	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.01	<a href="#">[131]</a>

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.62	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.11	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.34	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	-0.02	<a href="#">[51]</a>
COUSIN18			-0.01	
CBI	Codon Bias Index	-1~1	-0	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.68	<a href="#">[71]</a>

RCA	Relative Codon Adaptation	$\geq 0$	1	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.19	<a href="#">[9]</a>
B	Codon Usage Bias	$0 \sim 2$	0.29	<a href="#">[10]</a>

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	$0 \sim 1$	0.45	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.53	<a href="#">[2]</a>
P2	P2 Index	$0 \sim 1$	0.5	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
GC3	GC Content at the Third Position of Synonymous Codons	$0 \sim 1$	0.51	<a href="#">[1]</a>
GC	GC Content		0.48	
GC1	GC Content at the First Position of Synonymous Codons		0.5	
GC2	GC Content at the Second Position of Synonymous Codons		0.42	
ENcp	Effective Number of Codon Pairs	$20 \sim 61$	32.6	<a href="#">[2]</a>
CPS	Codon Pair Score	$-1 \sim 1$	0.01	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	$0.5 \sim 1$	0.76	<a href="#">[5]</a>

**Gene Name:** Covid-19 spike protein

**Reference Source:** Codon Usage Database - Kazusa

**Expression Host Organism:** Pichia pastoris (budding yeasts)

**DNA Sequence Length:** 3819

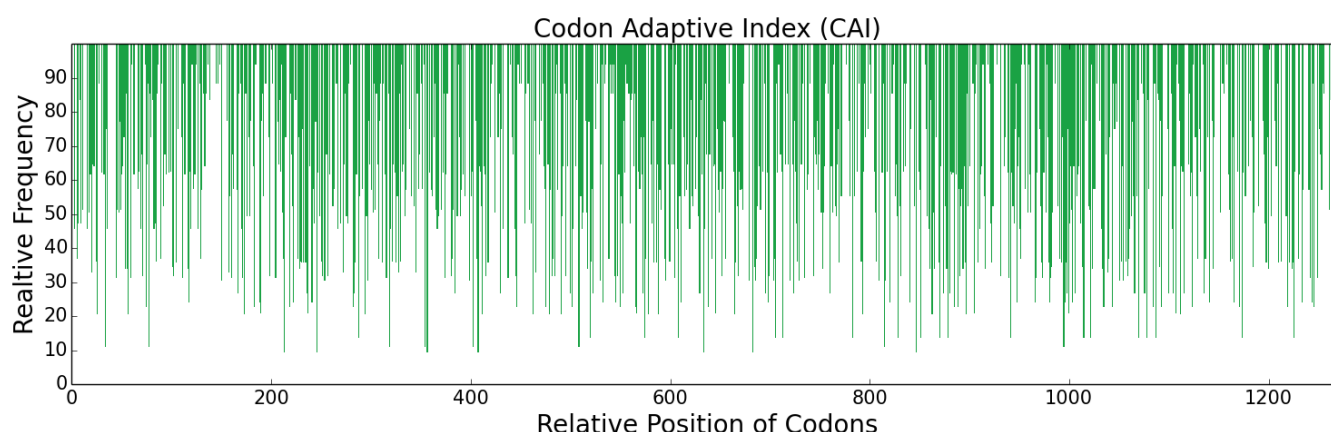
**DNA Sequence:**

```
ATGTTTGTGTTTTTGGTACTGTTGCCTCTGGTTAGTTCTCAATGTGTGAACCTTACAACA
AGGACCCAGTTGCCCCCGGCTTATACTAACTCATTTACACGCGGAGTGTAACCCAGAT
AAGGTTTTTTAGAACAGTGTTCTTCACAGTACACAGGACCTATTCCCTACCGTTTTTTAGC
AATGTTACATGGTTTTCATGCCATCCATGTGTCCGGCACTAATGGGACCAAACGCTTCGAC
AACCCTGTGCTGCCCTTCAATGATGGTGTATATTTTGCATCCACAGAAAAGTCAAACATC
ATTCGTGGCTGGATATTTGGAAGTACTTTGGACAGCAAAACACAATCTCTACTCATCGTG
AATAATGCCACAAATGTTGTGATTAAAGTATGCGAATTCCAGTTCTGTAATGATCCTTTT
TTGGGTGTTTACTATCATAAAAACAATAAGTCGTGGATGGAATCTGAGTTTAGGGTCTAC
AGCTCCGCCAACAACTGCACGTTTCAATATGTGAGCCAACCGTTCTTAATGGACTTAGAG
GGTAAGCAGGGGAATTTTAAAGAACCTCCGAGAGTTCGTCTTTAAAAACATTGACGGCTAC
TTTAAATTTTACAGCAAGCACACCCCTATCAATCTTGTACGGGACTTGCCACAAGGGTTC
TCCGCACTCGAACCTTTGGTAGACCTACCCATAGGAATAAACATAACGCGATTTTCAGACT
CTCCTCGCCCTGCACCGGTCACTTAACTCCCGGCGATTTCGTCTCGTCCGGCTGGACAGCT
GGTGCAGCAGCCTACTATGTGGGTACCTGCAACCAAGGACCTTCTTACTGAAATACAAT
GAAAACGGGACGATAACAGATGCGGTTCGATTGTGCCTTGGATCCGTTATCGGAGACCAAG
TGCACTCTTAAAGTTTTACCGTAGAGAAAGGTATATATCAAACAAGCAACTTCCGCGTG
CAACCCACCGAATCAATAGTCAGGTTCCCCAATATCACCAACTTATGCCATTTGGAGAA
GTCTTTAACGCAACTAGGTTTCGCTCCGTTTATGCCTGGAATCGCAAGCGGATTTCAAAC
TGCGTCGCTGACTATAGTGTGTTATACAACAGTGCTTCATTACGACATTCAGTGTTAC
GGCGTAAGTCCAACGAAGTTAAATGACTTATGCTTTACAAACGTCTACGCTGATTCGTTT
GTCATCCGCGGTGATGAGGTACGGCAGATCGCACCGGGTCAGACAGGCAAGATAGCTGAC
TATAATTACAAGCTTCCAGATGACTTCACGGGATGTGTGATTGCTTGGAACAGCAACAAT
TTGGACTCCAAGGTGGGCGGGAATTATAACTATTTGTACAGACTGTTTCAAAAAAGTAAC
CTGAAGCCGTTTGTAGAGGGATATTTCCACTGAGATTTATCAGGCCGGGTCTACCCCGTGC
AACGGCGTAGAAGGCTTCAATTGCTACTTCCCGTTACAGTCTTATGGCTTCCAGCCAACG
AACGGGGTGGGTACCAGCCTTACCGCGTCGTGCTGCTTTCTTTTGTAGCTTCTACACGCG
CCCGCCACGGTTTGTGGACCAAAAAAGTCGACCAATCTCGTTAAAAATAAGTGTGTAAAT
TTCAATTTCAATGGCCTCACTGGCACAGGGGTCTGACGGAGTCAAATAAAAAATTCCTG
CCTTTCCAACAGTTTCGGGCGAGATATCGCCGACACAACGGACGCGGTAAGAGATCCGCAA
ACCCTGGAGATATTGGATATAACCCCGTGCAGTTTGGTGGTGATCGGTTATTACCCCC
GGAACCAACACCAGCAATCAAGTGGCGGTCTCTACCAAGACGTCAACTGCACCGAAGTG
CCTGTCGCAATTATGCGGACCAATTAACGCCTACATGGCGGGTGATTTCCACTGGGTCC
AACGTATTTTCAACCCGAGCTGGATGCCTTATCGGCGCCGAGCACGTAAACAACCTCTTAT
GAATGTGACATCCCGATAGGTGCAGGCATCTGCGCCAGTTATCAAACCTCAAACCTAACTCG
CCAAGACGGGCTCGTTCCGGTAGCATCTCAGAGTATTATCGCTTATACGATGTCACTCGGC
GCTGAAAACCTCGGTAGCGTATTCAAATAATTCCATCGCGATTCCAACCAACTTCACCAT
TCGGTTACCACGGAGATCCTGCCCGTTTCGATGACCAAACTAGCGTTGATTGCACAATG
TATATTTGTGGCGACTCCACCGAGTGCTCCAACCTTCTACTTCAGTATGGTTCTTTCTGT
ACGCGCTTAATAGAGCATTAACCGGAATAGCTGTGCAACAAGATAAGAATACTCAAGAG
GTCTTTGCGCAAGTCAAGCAAACTTACAAAACCTCCCCGATCAAAGACTTTGGTGGATTT
AATTTCTCTCAAATCCTTCCCGATCCATCGAAGCCATCAAACGCTCGTTTATCGAAGAT
CTCTTGTTCAATAAGGTCACCTTAGCGGATGCAGGCTTTATCAAACAGTATGGTGATTGT
```

CTCGGAGATATTGCAGCTCGGGATTGATCTGCGCGCAAAAGTTTAATGGATTAACTGTG  
CTACCTCCGCTTCTAACTGACGAAATGATAGCGCAGTACACGTCTGCACTACTAGCGGGT  
ACGATCACATCAGGGTGGACATTTGGGGCCGGCGCAGCCCTACAGATACCGTTTCGCAATG  
CAGATGGCTTATCGATTCAATGGTATAGGTGTGACACAGAATGTCCTATACGAAAATCAA  
AACTGATAGCAAACCAATTTAATTCTGCTATTGGCAAGATTCAGGACTCTTTGTCAAGC  
ACTGCGTCAGCACTGGGAAAACCTCCAGGACGTGGTAAATCAAAATGCCCAAGCTCTTAAT  
ACACTTGTTAAGCAACTCAGCTCAAACTTTGGAGCAATAAGCTCAGTTCTTAATGACATA  
CTCAGCCGTCTTGATAAAGTTGAAGCAGAAGTACAAATAGACCGCCTCATAACGGGACGA  
CTGCAGAGTCTCCAGACGTACGTACACAGCAACTGATTCGTGCGGCTGAGATTAGAGCA  
AGTGCGAATCTAGCCGCCACTAAAATGTCTGAGTGTGTGCTAGGGCAATCCAAGAGGGTA  
GACTTTTGTGGGAAAGGATATCACTTGATGTCTGTTTTCCCCAGTCGGCTCCCCATGGCGTA  
GTGTTTTTACACGTCACGTACGTCCCTGCGCAAGAAAAAACTTCACGACTGCGCCTGCC  
ATTTGTCATGATGGGAAAGCGCATTTCCCTCGTGAGGGGGTCTTTGTTTCTAACGGAACG  
CATTGGTTTCGTGACGCAGCGAAATTTTATGAGCCGCAGATCATCACGACTGATAACACC  
TTCGTCTCAGGGAATTGTGACGTCGTAATTGGAATCGTTAACAATACGGTATACGACCCA  
CTCCAACCAGAGCTAGACTCTTTAAGGAAGAACTTGATAAATATTTCAAGAATCATACA  
AGTCCCGATGTAGACCTCGGTGATATCTCTGGGATTAACGCGTCAGTTGTCAACATTCAG  
AAGGAGATTGACCGTCTTAACGAAGTTGCAAAGAACTGAACGAGTCCCTGATAGACCTA  
CAAGAATTAGGTAAGTACGAGCAGTATATAAAGTGGCCCTGGTACATTTGGTTAGGGTTT  
ATAGCTGGTCTAATAGCGATCGTTATGGTAACAATTATGCTCTGCTGTATGACTTCTTGC  
TGCAGCTGTCTCAAAGGGTGTGTAGCTGTGGATCCTGCTGCAAAATTCGATGAAGATGAT  
AGTGAACCTGTTCTTAAGGGGGTTAAATTGCACTACACT

### Protein Sequence:

MFVFLVLLPLVSSQCVNLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFS  
NVTWFHAIHVSNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLLI  
NNATNVVIVKVEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLE  
GKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLDPQGFSALEPLVDLPIGINITRFQT  
LLALHRSYLTTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETK  
CTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISN  
CVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVQRQIAPGQTGKIAD  
YNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIIYQAGSTPC  
NGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVN  
FNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLILDITPCSFGGVSVITP  
GTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSY  
ECDIPIGAGICASYQTQNSPRRARSVASQSIIAYTMSLGAENSVAYSNNISIAIPTNFTI  
SVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKNTQE  
VFAQVKQIYKTPPIKDFGGFNFSQILPDPSPKPSKRSFIEDLLFNKVTLADAGFIKQYGDC  
LGDIAARDLICAQKFNGLTVLPLLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAM  
QMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSTASALGKLQDVVNQNAQALN  
TLVKQLSSNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRA  
SANLAATKMSECVLGQSKRVDFCGKGYHLSFPQSAPHGVVFLHVTYVPAQEKNFTTAPA  
ICHGDKAHFPREGVVFVSNGTHWFTVQRNFYEPQIITDNTFVSGNCDVIGIVNNTVYDP  
LQPELDSFKEELDKYFKNHTSPDVLGDISGINASVNNIQKEIDRLNEVAKNLNESLIDL  
QELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCMTSCCSCLKGCCSCGSCCKFDEDD  
SEPVLLKGVKLHYT



Negative CIS Elements	Negative repeat Elements
3	0

### Indices based on non-uniform usage of synonymous codon

Index	Description	Range	Value	Reference
RSCU	Relative Synonymous Codon Usage	0~6	0.98	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	61	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.08	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.27	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.04	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.53	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.98	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0	<a href="#">[131]</a>

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.63	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.09	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.34	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.01	<a href="#">[51]</a>
COUSIN18			0.06	
CBI	Codon Bias Index	-1~1	0	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.75	<a href="#">[71]</a>

RCA	Relative Codon Adaptation	$\geq 0$	1	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.19	<a href="#">[9]</a>
B	Codon Usage Bias	$0 \sim 2$	0.28	<a href="#">[10]</a>

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	$0 \sim 1$	0.44	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.53	<a href="#">[2]</a>
P2	P2 Index	$0 \sim 1$	0.49	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
GC3	GC Content at the Third Position of Synonymous Codons	$0 \sim 1$	0.5	<a href="#">[1]</a>
GC	GC Content		0.46	
GC1	GC Content at the First Position of Synonymous Codons		0.48	
GC2	GC Content at the Second Position of Synonymous Codons		0.4	
ENcp	Effective Number of Codon Pairs	$20 \sim 61$	44.69	<a href="#">[2]</a>
CPS	Codon Pair Score	$-1 \sim 1$	0.03	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	$0.5 \sim 1$	0.76	<a href="#">[5]</a>



**Gene Name:** C-Reactive Protein

**Reference Source:** Codon Usage Database - Kazusa

**Expression Host Organism:** Pichia pastoris (budding yeasts)

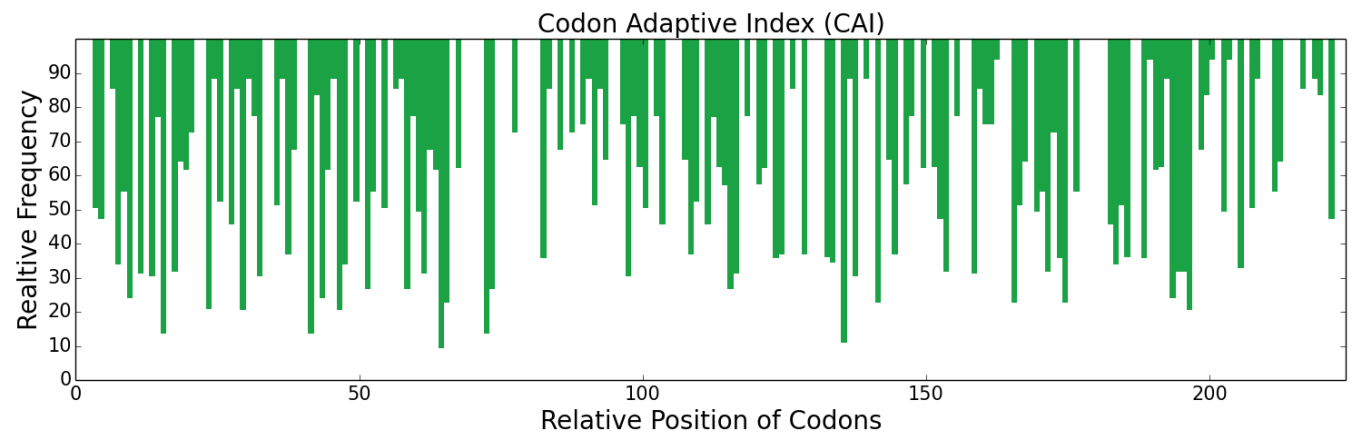
**DNA Sequence Length:** 672

**DNA Sequence:**

ATGGAAGCTTCTGTGTTTCTAGTCCTCACTAGCTTGTCGCACGCGTTTGGCCAGACA  
GACATGTCTCGAAAAGCATTGTGTGTTCCCGAAAAGAGTCGGATACTAGTTATGTATCCTTG  
AAGGCGCTCTCACAAAACCGCTAAAGGCATTTACGGTCTGTCTTCATTTCTATACGGAG  
TTAAGCTCCACACGGGGGTACTCAATTTTTTCTTACGCGACGAAGAGACAAGACAACGAA  
ATTTTGATATTCTGGTCCAAGGACATTGGATATAGTTTCACCGTTGGTGGATCGGAGATC  
CTTTTGTAGGTGCCAGAAGTTACCGTAGCACCAGTGCACATCTGCACGAGCTGGGAGTCT  
GCCTCAGGTATAGTAGAATTCTGGGTAGATGGTAAGCCCCGTGTCGCAAATCGTTGAAA  
AAGGGGTACACCGTAGGTGCCGAGGCTTCAATTATCCTGGGCCAAGAGCAAGATAGCTTC  
GGAGGAAATTTGAAGGGAGTCAGTCTTTAGTCGGCGACATAGGGAACGTCAACATGTGG  
GATTTTGTGCTAAGTCCCGATGAAATAAATACAATCTATCTCGGCGGCCCGTTTTCCCCT  
AATGTTTTAAATTGGAGGGCTCTTAAATACGAAGTCCAGGGTGAAGTTTTCACTAAACCT  
CAACTGTGGCCA

**Protein Sequence:**

MEKLLCFLVLTSLSHAFGQTDMSRKAFVFPKESDTSYVSLKAPLTKPLKAFTVCLHFYTE  
LSSTRGYSIFSATKRQDNEILIFWSKDIGYSFTVGGSEILFEVPEVTVAPVHICTSWES  
ASGIVEFWVDGKPRVRKSLKKGTVGAEASII LGQEQDSFGGNFEGSQSLVGDIGNVNMW  
DFVLSPDEINTIYLGGPFSPNVLNWRALKYEVQGEVFTKPQLWP



Negative CIS Elements	Negative repeat Elements
1	0

Indices based on non-uniform usage of synonymous codon

Index	Description	Range	Value	Reference
RSCU	Relative Synonymous Codon Usage	0~6	0.97	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	61	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.13	<a href="#">[4]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.41	<a href="#">[5]</a>
CDC	Codon Deviation Coefficient	0~1	0.08	<a href="#">[6]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.68	<a href="#">[7]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.02	<a href="#">[8]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.01	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.95	<a href="#">[11]</a>
P	Codon Preference	$\geq 1$	1.01	<a href="#">[12]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.01	<a href="#">[13]</a>

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.62	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.09	<a href="#">[2]</a>
FOP	Frequency of Optimal Codons	0~1	0.34	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	-0.07	<a href="#">[5]</a>
COUSIN18			-0.23	
CBI	Codon Bias Index	-1~1	0.01	<a href="#">[6]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.98	<a href="#">[7]</a>
RCA	Relative Codon Adaptation	$\geq 0$	1.04	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.19	<a href="#">[9]</a>
B	Codon Usage Bias	0~2	0.28	<a href="#">[10]</a>

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	0~1	0.45	<a href="#">[11]</a>
gtAI	Genetic tRNA Adaptation Index	0~1	0.54	<a href="#">[2]</a>
P2	P2 Index	0~1	0.5	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
			0.5	

GC	GC Content	0~1	0.46	<a href="#">[1]</a>
GC1 GC3	GC Content at the First Position GC Content at the Third Position of Synonymous Codons		0.49	
GC2	GC Content at the Second Position of Synonymous Codons		0.41	
ENcp	Effective Number of Codon Pairs	20~61	20	<a href="#">[2]</a>
CPS	Codon Pair Score	-1~1	0.04	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	0.5~1	0.76	<a href="#">[5]</a>

**Gene Name:** Lysosomal acid glucosylceramidase

**Reference Source:** Codon Usage Database - Kazusa

**Expression Host Organism:** *Pichia pastoris* (budding yeasts)

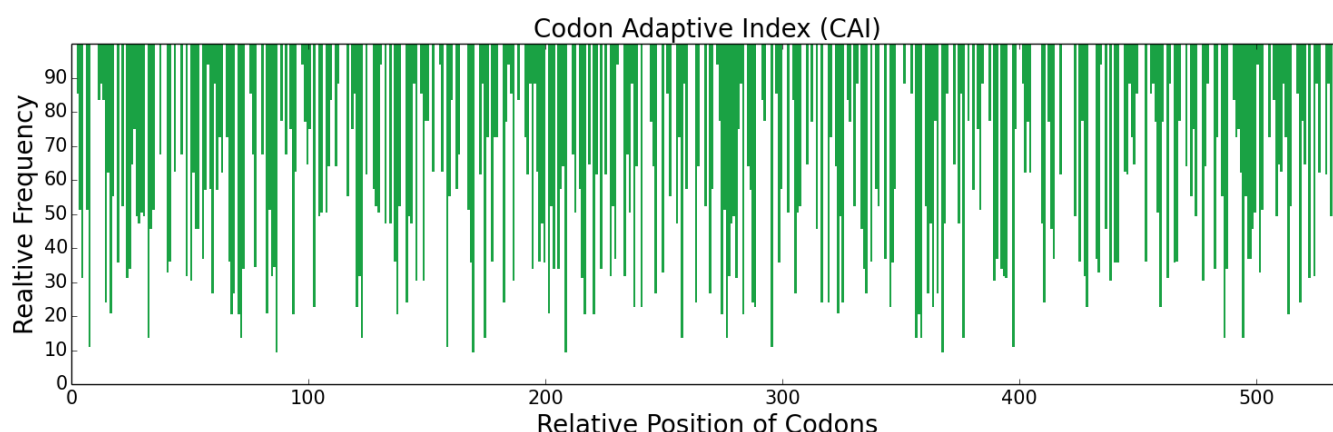
**DNA Sequence Length:** 1608

**DNA Sequence:**

```
ATGGAATTTCAGTAGCCCCAAGTCGCGAAGAATGTCCTAAACCTCTCTCAGAGTCTCTATA
ATGGCAGGTAGCCTAACCGGATTACTGCTTTTACAAGCGGTGAGTTGGGCTTCCGGTGCT
AGGCCCTGTATCCCAAAGTCCTTTGGCTACTCGTCAGTGGTGTGTGTATGCAATGCCACG
TATTGCGACTCATTTGACCCCCCGACGTTTCCGGCGCTAGGTACTTTCTCCCGTTACGAA
TCCACTCGAAGTGGCCGTCGGATGGAGTTGTCCATGGGACCGATCCAAGCTAATCACACC
GGAAGTGGGTTGTTACTTACTCTTCAGCCTGAACAGAAATTTCAAAGGTCAAGGGATTC
GGGGGCGCGATGACAGATGCTGCCGCACTTAATATTCTGGCTCTGTCTCCCCCGGCACAA
AACCTCTTACTGAAATCGTACTTCTCGGAGGAGGGTATCGGTTACAATATCATTTCGCGTC
CCTATGGCCTCCTGTGATTTTAGTATACGGACTTACACATATGCGGACACTCCCGACGAC
TTTCAACTCCACAATTTCTCGTTGCCTGAAGAAGACACAAAACCTAAAAATCCCCCTGATA
CATCGAGCACTACAAGTAGCCAGCGGCCAGTTTCCCTTTTGGCCAGCCCGTGGACCTCT
CCGACATGGCTAAAGACAAACGGCGCAGTAAATGGTAAGGGCTCCCTTAAAGGGCAGCCA
GGGGATATTTACCACCAGACGTGGGCTAGGTACTTCGTCAAGTTTCTGGACGCGTATGCC
GAACATAAGCTCCAGTTTGGGCGAGTTACGGCCGAAAATGAGCCGAGTGCGGGCCTGTTA
AGCGGATATCCGTTTCAGTGCCTCGGGTTTACTCCTGAGCATCAACGCGATTTTCATAGCC
AGAGATCTTGGTCCTACGCTTGCAAACCTCTACCCATCACAAACGTGAGACTCTTGATGCTC
GACGATCAGCGATTACTCTTGCCCTACTGGGCAAAAGTTGTGCTAACGGATCCCGAAGCC
GCAAAGTACGTACATGGGATAGCCGTTCAATTGGTATTTGGATTTCTTGGCGCCGCGAAG
GCAACGCTGGGGGAGACGCATCGGCTGTTCCCAAACACCATGCTGTTTCGCGTCTGAGGCT
TGCCTTGAAGTAAATTTTGGGAGCAATCGGTAAGACTAGGCAGCTGGGATCGCGGAATG
CAATATTCACACTCAATTATTACTAACCTGCTCTACCACGTGGTAGGTTGGACAGATTGG
AACTTGGCTTTAAACCCCGAGGGCGGGCCAAACTGGGTAAGGAATTTTGTGGATTTCGCCA
ATAATAGTTGATATCACAAAAGACACCTTCTACAAGCAACCCATGTTCTATCACCTTGGG
CACTTTAGCAAATTTATACCCGAGGGTTCTCAGAGAGTCGGATTAGTTGCTTCGCAGAAA
AACGATCTAGACGCTGTGCGGCTAATGCATCCTGACGGATCAGCGGTCGTAGTAGTGCTT
AATAGGAGTTCTAAGGACGTTCCCTTAACCATCAAAGACCCGGCAGTTGGTTTCCTCGAG
ACCATTAGCCCAGGCTATTCAATTCATACATATTTATGGCGTCGTCAG
```

**Protein Sequence:**

```
MEFSSPSREECPKPLSRVSIAGSLTGLLLLQAVSWASGARPCIPKSFYSSVVCVNCAT
YCDFDPPTFPALGTFSTRYESTRSGRRMELSMGPIQANHTGTGLLLTLQPEQKFQKVKGF
GGAMTDAAALNILALSPPAQNLLLSYFSEEGIGYNIIRVPMASCDFSIRTYTYADTPDD
FQLHNFSLPEEDTKLKIPLIHRALQLAQRPVSLASPWTSPTWLKTNGAVNGKSLKGQP
GDIYHQTWARYFVKFLDAYAEHKLQFWAVTAENEPSAGLLSGYPFQCLGFTPEHQRFIA
RDLGPTLANSTHHNVRLMLDDQRLLLPHWAKVVLTDPEAAKYVHGIHVHWYLDLFLAPAK
ATLGETHRLFPNTMLFASEACVGSKFWEQSVRLGSDRGMQYSHSIITNLLYHVVGWTDW
NLALNPEGPNWVRNFVDSPIIVDITKDTFYKQPMFYHLGHFSKFIPEGSQRVGLVASQK
NDLDAVALMHPDGSAAVVVVLNRSSKDVPLTIKDPVGVFLETISPGYSIHTYLWRRQ
```



Negative CIS Elements	Negative repeat Elements
0	0

### Indices based on non-uniform usage of synonymous codon

Index	Description	Range	Value	Reference
RSCU	Relative Synonymous Codon Usage	0~6	0.96	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	61	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.07	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.23	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.03	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.58	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.95	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0	<a href="#">[131]</a>

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.59	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.11	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.32	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.05	<a href="#">[51]</a>
COUSIN18			0.09	
CBI	Codon Bias Index	-1~1	-0	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	1.04	<a href="#">[71]</a>

RCA	Relative Codon Adaptation	$\geq 0$	1.01	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.19	<a href="#">[9]</a>
B	Codon Usage Bias	$0 \sim 2$	0.3	<a href="#">[10]</a>

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	$0 \sim 1$	0.43	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.51	<a href="#">[2]</a>
P2	P2 Index	$0 \sim 1$	0.51	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
GC3	GC Content at the Third Position of Synonymous Codons	$0 \sim 1$	0.51	<a href="#">[1]</a>
GC	GC Content		0.5	
GC1	GC Content at the First Position of Synonymous Codons		0.54	
GC2	GC Content at the Second Position of Synonymous Codons		0.44	
ENcp	Effective Number of Codon Pairs	$20 \sim 61$	29.17	<a href="#">[2]</a>
CPS	Codon Pair Score	$-1 \sim 1$	0.01	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	$0.5 \sim 1$	0.75	<a href="#">[5]</a>

**Gene Name:** Coagulation factor IX

**Reference Source:** Codon Usage Database - Kazusa

**Expression Host Organism:** *Pichia pastoris* (budding yeasts)

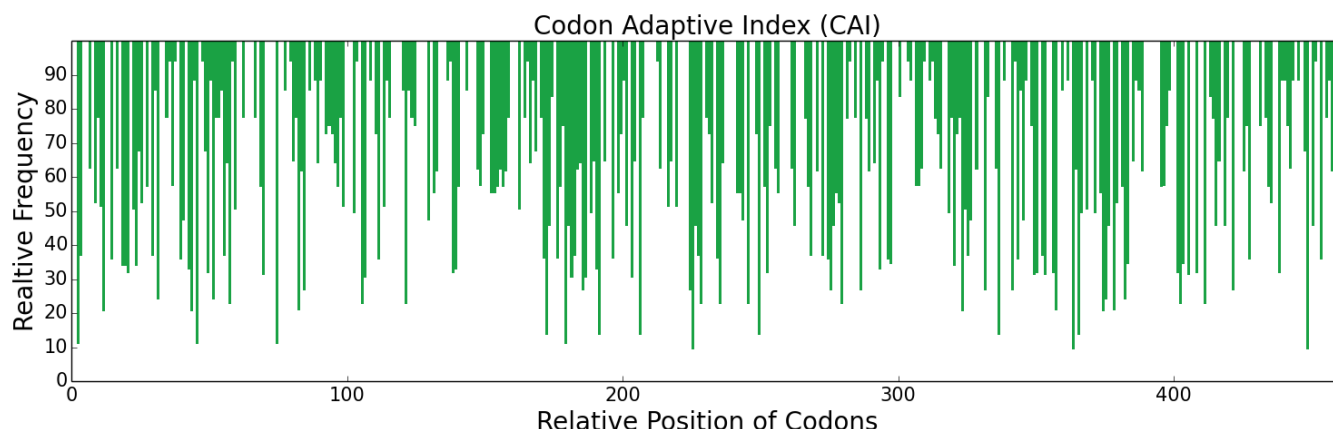
**DNA Sequence Length:** 1383

**DNA Sequence:**

```
ATGCAACGCGTAAACATGATCATGGCAGAGAGTCCGGGTTTGATAACTATCTGTCTACTA
GGCTACCTTCTATCCGCAGAATGCACTGTATTCCCTCGATCATGAGAATGCCAATAAGATA
CTGAACAGGCCGAAACGCTACAATTCCGGCAAACCTCGAGGAGTTCTGACAGGGGAATCTT
GAAAGAGAGTGTATGGAAGAGAAGTGCAGCTTTGAAGAAGCTCGCGAAGTTTTCGAAAAT
ACCGAGCGAACAACGGAATTCTGGAACAGTATGTTGACGGAGACCAGTGCGAGAGTAAC
CCATGTTTAAATGGTGGGTCGTGTAAAGATGACATAAACAGTTATGAGTGTGGTGTCCA
TTCGGGTTTCGAGGGAAAGAACTGTGAACTGGATGTCACATGTAAACATTAATAATGGCAGG
TGCGAACAATTCTGTAAAGAACTCAGCCGACAACAAGGTCGTCTGCTCATGCACAGAGGGT
TACAGACTTGCTGAGAATCAGAAATCCTGTGAGCCCGGGTGCCTTTTCCCTGCGGACGC
GTGTCCGTATCACAGACGTCGAAGTTAACCAGGGCGGAAACCGTTTTTCCCGATGTCGAC
TATGTGAACCTCGACCGAAGCGGAGACTATTTTGGATAATATCACTCAAAGTACCCAAAGT
TTTAACGATTTTACGCGGGTGGTAGGGGGTGAGGACGCAAAGCCCGGGCAGTTTCCATGG
CAAGTCGTCCTGAACGGGAAGGTTGACGCGTTTTTGCGGCGGATCTATCGTCAACGAAAAG
TGGATCGTGACTGCTGCTCACTGCGTAGAAAACAGGTGTAAAGATAACGGTGGTCGCAGGG
GAACACAATATTGAGGAAACGGAACACACAGAACAGAAAAGGAATGTTATACGTATTATT
CCTCATCATAATTATAACGCCGCCATCAATAAGTATAATCACGACATCGCTTTGTTAGAG
CTAGACGAGCCGCTTGTACTGAACTCATACGTTACGCCTATTTGTATCGCGGATAAAGAA
TACACGAATATATTCTGAAATTTGGAAGCGCTACGTAAGCGGTTGGGGCCGAGTTTTTC
CATAAAGGTCGGTCAGCGTTAGTTCTTCAATATTTAAGAGTCCCGCTCGTGGATCGAGCA
ACTTGCCCTCCGTTCTACCAAATTCACAATTTACAACAACATGTTTTGCGCCGGATTCCAT
GAAGGCGGGCGTGATAGCTGTCAAGGCGATTCTGGGGGTCTCACGTGACCGAAGTGGAG
GGTACGTCTTTTTTACAGGAATAATTTCTTGGGGAGAAGAGTGCGCAATGAAGGGCAA
TATGGAATCTATACTAAAGTTTCCCGGTACGTGAATTGGATAAAGGAGAAAACAAAGCTC
ACT
```

**Protein Sequence:**

```
MQRVNMIMAESPLITICLLGYLLSAECTVFLDHENANKILNRPKRYNSGKLEEFVQGNL
ERECMEEKCSFEEAREVFENTERTEFWKQYVDGDQCESNPCLNGGSKDDINSYECWCP
FGFEGKNCELDVTCNIKNRCEQFCKNSADNKVVCSCTEGYRLAENQKSCEPAVPFPCGR
VSVSQTSKLTRAETVFPDQVYVNSTEAETILDNITQSTQSFNDFTRVVGGEDAKPGQFPW
QVVLNGKVDAFCGGSIVNEKWIVTAAHCVETGVKITVAGEHNIEETEHETEQKRNVIIRI
PHHNYNAAINKYNHDIALLELDEPLVLNSYVTPICIAADKEYTNIFLKFGSGYVSGWGRVF
HKGRSALVLQYLRVPLVDRATCLRSTKFTIYNMFCAGFHEGGRDSCQGDSSGPHVTEVE
GTSFLTGIISWGEECAMKGKYGIYTKVSRYVNWIKETKLT
```



Negative CIS Elements	Negative repeat Elements
1	0

### Indices based on non-uniform usage of synonymous codon

Index	Description	Range	Value	Reference
RSCU	Relative Synonymous Codon Usage	0~6	0.98	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	61	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.1	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.34	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.06	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.59	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.97	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1.01	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.01	<a href="#">[131]</a>

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.64	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.09	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.35	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	-0.01	<a href="#">[51]</a>
COUSIN18			-0.02	
CBI	Codon Bias Index	-1~1	-0.01	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.88	<a href="#">[71]</a>



RCA	Relative Codon Adaptation	$\geq 0$	1	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.19	<a href="#">[9]</a>
B	Codon Usage Bias	$0 \sim 2$	0.28	<a href="#">[10]</a>

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	$0 \sim 1$	0.46	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.54	<a href="#">[2]</a>
P2	P2 Index	$0 \sim 1$	0.5	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
GC3	GC Content at the Third Position of Synonymous Codons	$0 \sim 1$	0.51	<a href="#">[1]</a>
GC	GC Content		0.46	
GC1	GC Content at the First Position of Synonymous Codons		0.49	
GC2	GC Content at the Second Position of Synonymous Codons		0.39	
ENcp	Effective Number of Codon Pairs	$20 \sim 61$	61	<a href="#">[2]</a>
CPS	Codon Pair Score	$-1 \sim 1$	-0	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	$0.5 \sim 1$	0.77	<a href="#">[5]</a>

**Gene Name:** Adalimumab light chain

**Reference Source:** Codon Usage Database - Kazusa

**Expression Host Organism:** Pichia pastoris (budding yeasts)

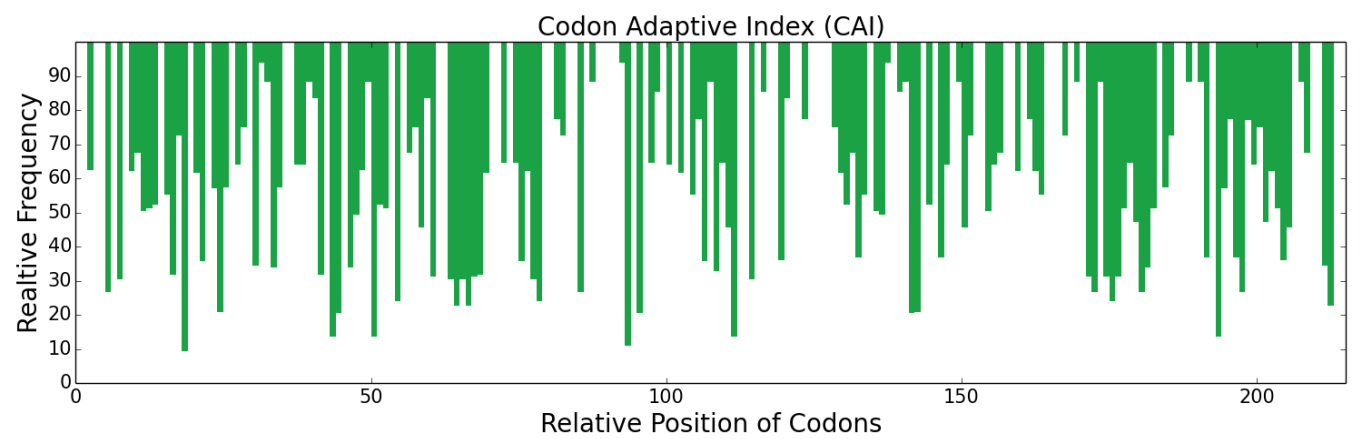
**DNA Sequence Length:** 645

**DNA Sequence:**

ATGGATATCCAAATGACGCAATCGCCATCATCCCTTAGTGCATCTGTCGGCGACCGGGTT  
ACAATAACTTGCCGAGCCTCTCAGGGAATTTCGTAATTATCTAGCCTGGTACCAGCAGAAA  
CCTGGCAAGGCGCCGAAGCTATTAATCTATGCGGCAAGTACTCTCCAATCCGGAGTGCCT  
AGCAGATTTTCGGGGTCGGGGAGCGGCACAGATTTTACCTTGACCATATCATCGCTCCAA  
CCAGAGGACGTTGCTACGTACTATTGTCAAAGATAACAATCGCGCTCCGTACACCTTCGGT  
CAGGGTACAAAGGTCGAGATAAAAAGGACCGTGGCGGCTCCATCGGTTTTCATTTTTCCC  
CCTTCTGATGAGCAATTGAAGTCTGGAACAGCATCCGTAGTCTGTCTTTTAAATAACTTC  
TATCCGCGAGAAGCAAAGGTACAGTGGAAAGTGGACAACGCTCTTCAGTCCGGTAACTCA  
CAAGAGTCAGTCACTGAACAAGACTCTAAAGATAGCACGTATAGCCTCAGCAGTACCCTG  
ACGCTAAGTAAGGCCGACTACGAAAAACATAAAGTATACGCGTGCGAGGTAACGCACCAG  
GGACTGTCAAGTCCCGTGACTAAATCCTTTAACCGTGGGGAATGT

**Protein Sequence:**

MDIQMTQSPSSLSASVGDRTITCRASQGIRNYLAWYQQKPGKAPKLLIYAASTLQSGVP  
SRFSGSGSGTDFTLTISSLQPEDVATYYCQRYNRAPYTFGQGTKVEIKRTVAAPSVFIFP  
PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTL  
TLISKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC



Negative CIS Elements	Negative repeat Elements
0	0

Indices based on non-uniform usage of synonymous codon				
Index	Description	Range	Value	Reference

RSCU	Relative Synonymous Codon Usage	0~6	1	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	61	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.12	<a href="#">[4]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.39	<a href="#">[5]</a>
CDC	Codon Deviation Coefficient	0~1	0.08	<a href="#">[6]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.68	<a href="#">[7]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.01	<a href="#">[8]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.01	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.97	<a href="#">[11]</a>
P	Codon Preference	$\geq 1$	1.01	<a href="#">[12]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.02	<a href="#">[13]</a>

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.61	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.1	<a href="#">[2]</a>
FOP	Frequency of Optimal Codons	0~1	0.32	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.14	<a href="#">[5]</a>
COUSIN18			0.3	
CBI	Codon Bias Index	-1~1	-0	<a href="#">[6]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.87	<a href="#">[7]</a>
RCA	Relative Codon Adaptation	$\geq 0$	1.01	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.19	<a href="#">[9]</a>
B	Codon Usage Bias	0~2	0.32	<a href="#">[10]</a>

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	0~1	0.43	<a href="#">[11]</a>
gtAI	Genetic tRNA Adaptation Index	0~1	0.51	<a href="#">[2]</a>
P2	P2 Index	0~1	0.54	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
GC3	GC Content at the Third Position of Synonymous Codons	0~1	0.49	<a href="#">[11]</a>
GC	GC Content		0.49	

GC1	GC Content at the First Position of Synonymous Codons		0.49	
GC2	GC Content at the Second Position of Synonymous Codons		0.48	
ENcp	Effective Number of Codon Pairs	20~61	30.27	<a href="#">[21]</a>
CPS	Codon Pair Score	-1~1	-0.01	<a href="#">[3, 4]</a>
Codon Volatility	Codon Volatility	0.5~1	0.75	<a href="#">[51]</a>

**Gene Name:** Adalimumab heavy chain

**Reference Source:** Codon Usage Database - Kazusa

**Expression Host Organism:** *Pichia pastoris* (budding yeasts)

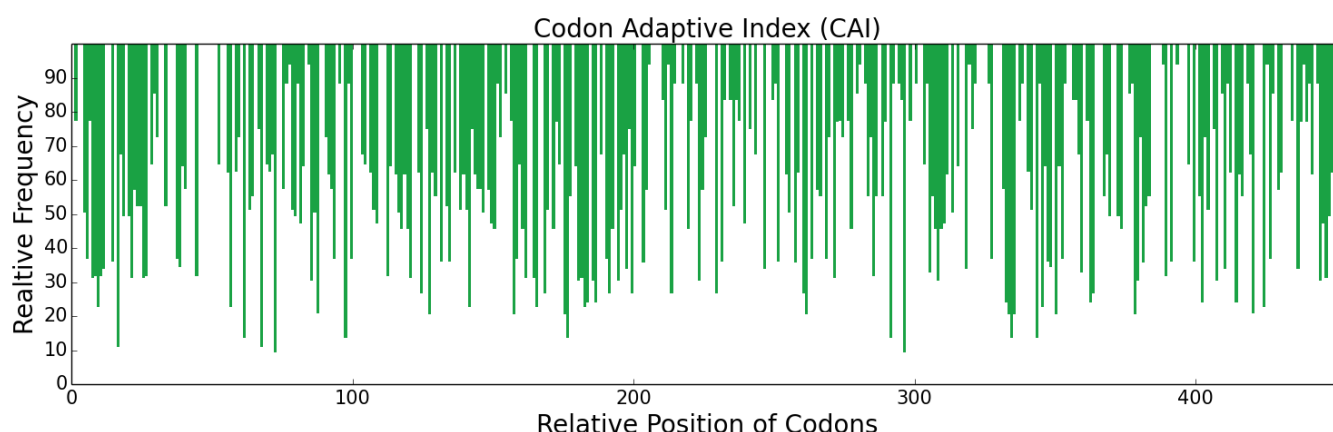
**DNA Sequence Length:** 1356

**DNA Sequence:**

```
ATGGAGGTTCAACTTGTAGAGAGCGGCGGGGGCCTAGTTCAACCCGGTCGCTCCTTAAGA
TTAAGCTGCGCAGCAAGCGGCTTTACCTTCGACGATTACGCAATGCATTGGGTACGTCAG
GCCCCAGGTAAGGGCTTGGAAATGGGTTTCTGCTATTACCTGGAACTCAGGGCATATCGAC
TACGCGGATAGTGTGCAAGGACGCTTTACCATCTCCCGGGATAACGCCAAAAATAGTTTA
TATCTGCAGATGAATTCGCTTCGAGCTGAAGACACAGCCGTATACTATTGTGCGAAAGTA
TCTTACTTGTCCACCGCTTCAAGTCTGGATTACTGGGGCCAGGGTACACTTGTGACAGTG
AGCTCTGCTTCAACGAAGGGACCGTCAGTCTTCCCTTGGCACCCCTCTTCAAAGAGTACA
AGTGGGGGAACAGCCGCCCTTGGTTGCCTGGTGAAAGACTACTTCCCAGAGCCGGTAACC
GTGAGCTGGAACAGCGGGGCTTTGACGAGTGGTGTGCACACCTTCCGGCGGTCTTGCA
TCGAGCGGGCTCTACTCGCTCTCTTCCGTTGTAACGGTGCCATCGAGTTCCTAGGAACG
CAGACTTACATATGCAATGTAAACCATAAGCCTAGTAATACGAAAGTTGATAAAAAGGTG
GAGCCAAAATCGTGCGACAAGACTCATACGTGTCCCCCTTGTCTGCACCTGAGTTGCTG
GGTGGACCATCCGTTTTTCTATTTCCACCTAAACCCAAGGATACACTTATGATATCAAGA
ACGCCGGAAGTAACCTTGCGTCGTTGTAGACGTTAGCCACGAGGACCCAGAGGTGAAGTTC
AATTGGTATGTGCGACGGCGTCGAAGTCCACAACGCGAAAACTAAACCTCGGGAAGAGCAA
TATAACTCTACCTATAGGGTCGTGTGCGGTGCTGACAGTTCTTCATCAGGATTGGCTAAAT
GGAAAAGAATACAAGTGTAAGTATCTAACAAGGCCCTCCCGGCGCCGATTGAGAAAAC
ATCAGTAAGGCGAAAGGGCAGCCCCGTGAACCGCAGGTATATACTTTGCCTCCTTCCAGG
GATGAGCTCACGAAGAACCAAGTCTCCTTAACCTGTTTAGTGAAGGGTTTCTATCCGTCG
GACATAGCAGTCGAATGGGAATCTAATGGCCAACCCGAAAATAACTACAAGACCACTCCC
CCAGTCCTCGACAGTGATGGATCGTTTTTCTATATTCAAAGCTCACAGTCGATAAATCC
CGATGGCAACAAGGAATGTATTCTTGTCTCAGTTATGCATGAGGCTCTACACAATCAC
TATACACAAAAATCGCTGAGCTTATCACCCGGTAAG
```

**Protein Sequence:**

```
MEVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSAITWNSGHID
YADSVETRFTISRDNKNSLYLQMNSLRAEDTAVYYCAKVSYLSTASSLDYWGQGLVTV
SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCPCPAPPELL
GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVVFSCSVMEALHNHYTQKSLSLSPGK
```



Negative CIS Elements	Negative repeat Elements
0	0

### Indices based on non-uniform usage of synonymous codon

Index	Description	Range	Value	Reference
RSCU	Relative Synonymous Codon Usage	0~6	0.97	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	61	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.11	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.35	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.07	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.59	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.97	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0	<a href="#">[131]</a>

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.62	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.09	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.33	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.04	<a href="#">[51]</a>
COUSIN18			0.04	
CBI	Codon Bias Index	-1~1	0	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	1	<a href="#">[71]</a>

RCA	Relative Codon Adaptation	$\geq 0$	1.01	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.19	<a href="#">[9]</a>
B	Codon Usage Bias	$0 \sim 2$	0.28	<a href="#">[10]</a>

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	$0 \sim 1$	0.44	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.52	<a href="#">[2]</a>
P2	P2 Index	$0 \sim 1$	0.5	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
GC3	GC Content at the Third Position of Synonymous Codons	$0 \sim 1$	0.51	<a href="#">[1]</a>
GC	GC Content		0.49	
GC1	GC Content at the First Position of Synonymous Codons		0.51	
GC2	GC Content at the Second Position of Synonymous Codons		0.46	
ENcp	Effective Number of Codon Pairs	$20 \sim 61$	41.38	<a href="#">[2]</a>
CPS	Codon Pair Score	$-1 \sim 1$	0.01	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	$0.5 \sim 1$	0.75	<a href="#">[5]</a>

**Gene Name:** Rituximab light chain

**Reference Source:** Codon Usage Database - Kazusa

**Expression Host Organism:** Pichia pastoris (budding yeasts)

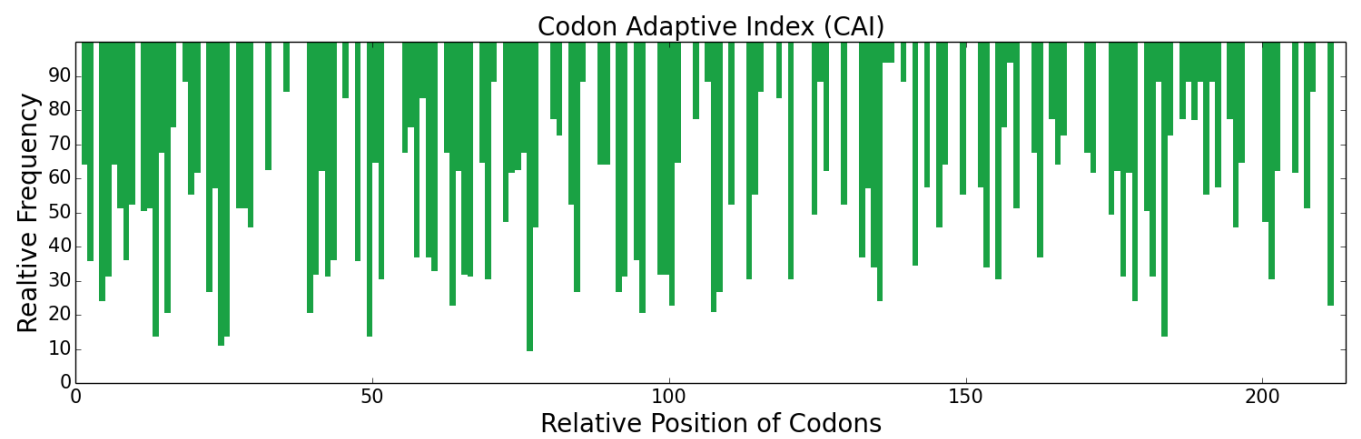
**DNA Sequence Length:** 642

**DNA Sequence:**

ATGCAGATAGTTCTCAGCCAGAGTCCCGCAATTCTTAGTGCGTCCCCGGGAGAAAAAGTC  
ACAATGACGTGCCGCGCGTCTAGTAGTGTGTCTTACATCCATTGGTTCCAACAAAAGCCG  
GGCTCAAGCCCCAAGCCTTGGATATACGCGACCTCGAACTTGGCTTCCGGAGTACCTGTA  
AGGTTTTCCGGGTCAGGCAGCGGTACCTCGTATTCTCTGACAATCTCCCGGTGGAAGCT  
GAGGACGCTGCAACGTATTACTGTCAGCAGTGGACGAGCAACCCCCGACTTTTGGCGGC  
GGGACCAAGTTGGAGATTAAACGAACGGTTGCAGCTCCATCGGTCTTCATTTTTCCTCCA  
TCGGATGAACAATTAAAATCAGGTACTGCATCTGTTGTATGCCTACTCAATAATTTTAT  
CCACGTGAAGCCAAGGTGCAGTGAAGGTCGATAACGCCCTACAATCGGGAAATAGTCAA  
GAATCCGTAAGTGAAGGTCAGTGAAGGTCGATAACGCCCTACAATCGGGAAATAGTCAA  
CTTAGCAAAGCGGACTACGAGAAACACAAAGTCTATGCCTGTGAGGTGACCCATCAAGGT  
CTGTGCTCACCAGTTACAAAGAGTTTCAACAGAGGGGAATGT

**Protein Sequence:**

MQIVLSQSPAILSASPGEKVTMTCRASSSVSYIHWFQQKPGSSPKPWIYATSNLASGVPV  
RFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFGGGKLEIKRTVAAPSVFIFPP  
SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLT  
LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC



Negative CIS Elements	Negative repeat Elements
0	0

Indices based on non-uniform usage of synonymous codon				
Index	Description	Range	Value	Reference



RSCU	Relative Synonymous Codon Usage	0~6	0.98	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	61	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.13	<a href="#">[4]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.42	<a href="#">[5]</a>
CDC	Codon Deviation Coefficient	0~1	0.09	<a href="#">[6]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.69	<a href="#">[7]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.01	<a href="#">[8]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.01	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.97	<a href="#">[11]</a>
P	Codon Preference	$\geq 1$	1.01	<a href="#">[12]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.01	<a href="#">[13]</a>

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.61	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.09	<a href="#">[2]</a>
FOP	Frequency of Optimal Codons	0~1	0.34	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.46	<a href="#">[5]</a>
COUSIN18			0.77	
CBI	Codon Bias Index	-1~1	0.03	<a href="#">[6]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.93	<a href="#">[7]</a>
RCA	Relative Codon Adaptation	$\geq 0$	1.02	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.18	<a href="#">[9]</a>
B	Codon Usage Bias	0~2	0.29	<a href="#">[10]</a>

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	0~1	0.43	<a href="#">[11]</a>
gtAI	Genetic tRNA Adaptation Index	0~1	0.51	<a href="#">[2]</a>
P2	P2 Index	0~1	0.5	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
GC3	GC Content at the Third Position of Synonymous Codons	0~1	0.5	<a href="#">[11]</a>
GC	GC Content		0.5	

GC1	GC Content at the First Position of Synonymous Codons		0.48	
GC2	GC Content at the Second Position of Synonymous Codons		0.5	
ENcp	Effective Number of Codon Pairs	20~61	28.37	<a href="#">[2]</a>
CPS	Codon Pair Score	-1~1	0.03	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	0.5~1	0.75	<a href="#">[5]</a>

**Gene Name:** Rituximab heavy chain

**Reference Source:** Codon Usage Database - Kazusa

**Expression Host Organism:** Pichia pastoris (budding yeasts)

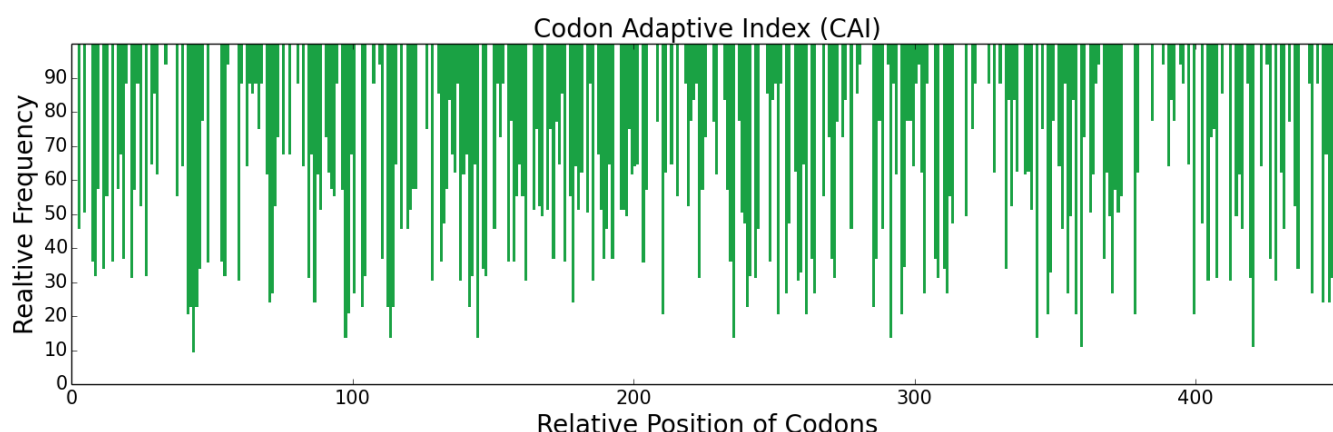
**DNA Sequence Length:** 1356

**DNA Sequence:**

```
ATGCAAGTGCAACTTCAACAACCCGGCGCCGAACTAGTCAAGCCCGGTGCCTCCGTAAAA
ATGAGCTGCAAAGCATCTGGCTACACCTTCACATCTTACAATATGCATTGGGTCAAGCAG
ACTCCGGGGCGGGGGCTAGAGTGGATAGGTGCTATTTACCCCGGCAATGGTGATACTTCG
TATAACCAGAAATTCAAAGGAAAAGCTACACTCACGGCAGACAAGTCCTCTTCCACTGCT
TATATGCAGTTGAGCTCCCTCACAAGTGAAGACTCAGCCGTCTATTACTGCGCGCGATCC
ACGTACTACGGGGGCGATTGGTATTTTAATGTATGGGGGGCGGGGACCACTGTGACTGTG
AGTGCCGCCTCTACTAAGGGACCATCGGTTTTCCCCCTGGCCCCCTTCCTCAAAATCGACA
TCCGGGGGCACCGCGGCTCTAGGCTGTTTGGTGAAAGACTATTTTCCCGAGCCCGTCACC
GTCTCGTGGAACAGTGGAGCATTAACTAGTGGAGTACACACCTTCCCCGCTGTCCTCCAG
AGTTCAGGTCTTTATTTCGTTGTCCAGTGTAGTGACCGTACCATCTAGTAGTTTAGGAACA
CAGACCTACATATGCAACGTTAACCACAAGCCGTCAAAACACCAAGGTCGATAAGAAAGCA
GAGCCTAAAAGCTGCGACAAGACTCACACATGTCCACCTTGCCCCGCGCCAGAGCTTCTG
GGGGGCCCAAGCGTGTTTTTGTTCCCCCCTAAACCGAAAAGATACGCTGATGATCTCGAGG
ACCCCGGAAGTAACGTGTGTTGTTCGTTGACGTAAGCCACGAAGACCCTGAAGTGAAGTTC
AATTGGTACGTTGATGGGGTAGAGGTGCATAATGCGAAAACAAAGCCGCGTGAGGAGCAG
TATAATTCAACGTATAGAGTTGTAAGCGTTCTAACGGTCCTGCATCAAGATTGGTTAAAC
GGAAAAGAATACAAGTGTAAGTTTTCAAACAAAGCTCTACCTGCACCTATCGAAAAGACA
ATCAGTAAGGCGAAGGGACAACCGAGGGAGCCACAGGTGTATACGTTACCTCCGTCTCGC
GACGAACCTACAAAAAATCAAGTATCATTAACTGCCTTGTCAAGGGTTTTTACCCGTCA
GATATTGCTGTTGAGTGGGAATCTAATGGTCAGCCTGAGAACAATTATAAGACCACTCCG
CCAGTTCTGGATTTCGGACGGAAGCTTTTTCTTGTAAGTGAAGTTAACAGTGGATAAAAGC
CGCTGGCAACAGGGTAATGTATTTTCGTGTTTCAGTGATGCACGAAGCACTACATAACCAT
TATACGCAAAAATCTCTCTCCCTCAGCCCAGGCAAG
```

**Protein Sequence:**

```
MQVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPNGDTS
YNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTTV
SAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
SSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELL
GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSVMSHEALHNHYTQKSLSLSPGK
```



Negative CIS Elements	Negative repeat Elements
0	0

### Indices based on non-uniform usage of synonymous codon

Index	Description	Range	Value	Reference
RSCU	Relative Synonymous Codon Usage	0~6	0.97	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	61	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.13	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.4	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.09	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.59	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.96	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.01	<a href="#">[131]</a>

### Indices based on codon frequency in a reference set of genes

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.62	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.09	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.32	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	-0.12	<a href="#">[51]</a>
COUSIN18			-0.17	
CBI	Codon Bias Index	-1~1	-0.02	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.86	<a href="#">[71]</a>

RCA	Relative Codon Adaptation	$\geq 0$	1.01	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.2	<a href="#">[9]</a>
B	Codon Usage Bias	$0 \sim 2$	0.3	<a href="#">[10]</a>

### Indices based on adaptation to the tRNA levels and their supply

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	$0 \sim 1$	0.44	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.52	<a href="#">[2]</a>
P2	P2 Index	$0 \sim 1$	0.5	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
GC3	GC Content at the Third Position of Synonymous Codons	$0 \sim 1$	0.52	<a href="#">[1]</a>
GC	GC Content		0.49	
GC1	GC Content at the First Position of Synonymous Codons		0.5	
GC2	GC Content at the Second Position of Synonymous Codons		0.46	
ENcp	Effective Number of Codon Pairs	$20 \sim 61$	36.91	<a href="#">[2]</a>
CPS	Codon Pair Score	$-1 \sim 1$	0.02	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	$0.5 \sim 1$	0.75	<a href="#">[5]</a>