

# GenRCA Rare Codon Analysis Report

**Gene Name:** Herceptin light chain

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

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

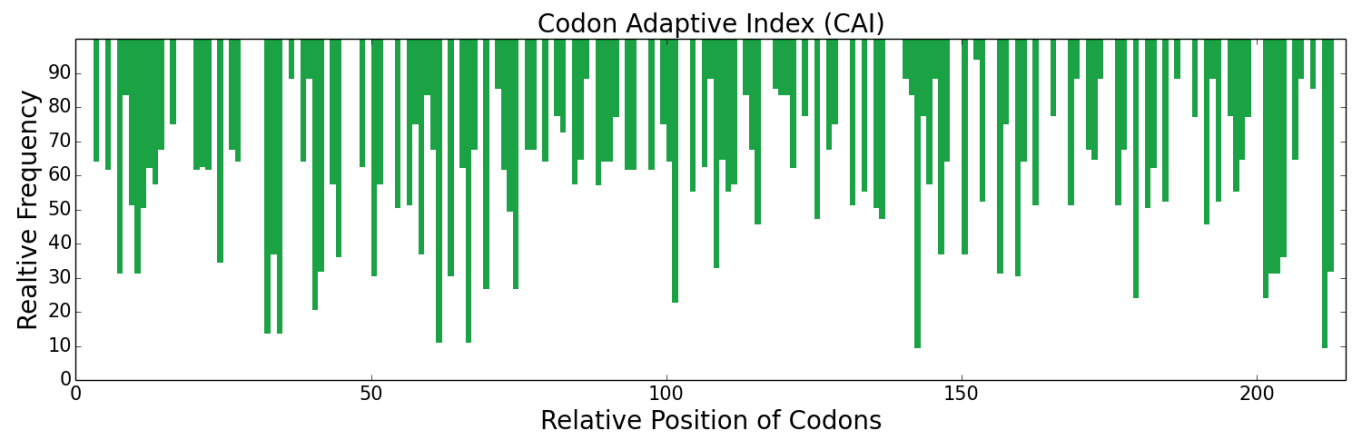
**DNA Sequence Length:** 645

**DNA Sequence:**

```
ATGGATATTTCAGATGACACAAAGCCCTAGTAGCCTTTTCAGCCTCCGTTGGAGATAGAGTT
ACAATCACATGTCGTGCTTCCCAGGATGTTAACTGCGGTAGCGTGGTATCAACAGAAA
CCGGGCAAGGCCCCCAAGTTGTTGATCTACTCGGCCTCTTTTCTTTACAGTGGAGTACCT
TCCCGCTTTTTCGGGTTTCACGCTCCGGTACGGATTTTCACATTAACGATTTCTCTCCTTGCAG
CCAGAGGACTTTGCCACCTATTACTGCCAGCAGCACTACACAACACCACCAACATTTGGA
CAGGGGACTAAGGTCGAAATCAAAAGGACCGTCGCCGCTCCTTCCGTGTTTATTTTCCCT
CCTTCAGATGAGCAACTGAAGTCCGGAAGTGTAGTGTGTCTGTCTTCTGAACAACTTT
TATCCTCGGGAGGCCAAAGTACAGTGGAAGGTAGATAATGCATTGCAAAGCGGAACTCG
CAGGAAAGTGTTACTGAGCAAGATAGTAAAGATTCCACCTATTCTTTGAGTTCCACTCTC
ACTCTTTCAAAGGCAGATTATGAAAAGCACAAGGTGTATGCATGTGAGGTCACCCACCAA
GGTCTCAGCAGCCCCGTTACCAAATCTTTCAACCGGGGCGAATGT
```

**Protein Sequence:**

```
MDIQMTQSPSSLASVGDVRTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSVGP
SRFSGSRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFP
PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTL
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	1.22	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	58.3	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.26	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.65	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.16	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.56	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.2	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.12	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.86	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1.13	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.26	<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	0.67	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.06	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.37	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	1.25	<a href="#">[51]</a>
COUSIN18			1.64	
CBI	Codon Bias Index	-1~1	0.07	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.6	<a href="#">[71]</a>
RCA	Relative Codon Adaptation	$\geq 0$	1.07	<a href="#">[81]</a>
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.3	<a href="#">[91]</a>
B	Codon Usage Bias	0~2	0.39	<a href="#">[101]</a>

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

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	0~1	0.46	<a href="#">[11]</a>
gtAI	Genetic tRNA Adaptation Index	0~1	0.55	<a href="#">[21]</a>
P2	P2 Index	0~1	0.5	<a href="#">[31]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
	GC Content at the Third Position			

GC3	of Synonymous Codons	0~1	0.49	<a href="#">[1]</a>
GC	GC Content		0.48	
GC1	GC Content at the First Position of Synonymous Codons		0.48	
GC2	GC Content at the Second Position of Synonymous Codons		0.47	
ENcp	Effective Number of Codon Pairs	20~61	24.15	<a href="#">[2]</a>
CPS	Codon Pair Score	-1~1	0.02	<a href="#">[3, 4]</a>
Codon Volatility	Codon Volatility	0.5~1	0.76	<a href="#">[5]</a>

**Gene Name:** Herceptin heavy chain

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

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

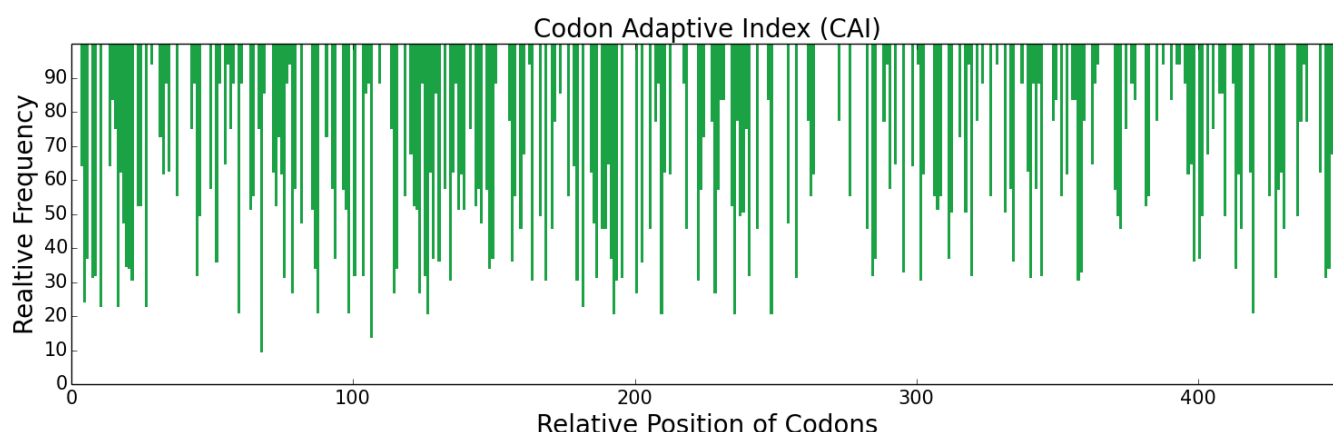
**DNA Sequence Length:** 1353

**DNA Sequence:**

```
ATGGAAGTTCAGCTCGTAGAAAGCGGCGGTGGGTTGGTTCAGCCTGGAGGGTCACTGCGT
CTATCGTGTGCAGCATCTGGGTTTAATATTAAGGACACATATATCCATTGGGTTCAGACAA
GCTCCAGGAAAAGGCTTAGAATGGGTTGCCAGAATATATCCAACCAATGGATATACTCGA
TATGCTGATAGTGTCAAGGGACGGTTCCTACTATTTTCAGCAGACACAAGCAAAAATACGGCC
TACCTGCAAATGAACAGTCTACGAGCTGAAGACACTGCCGTATACTACTGCAGTCGATGG
GGCGGTGATGGCTTCTATGCGATGGATTATTGGGGTCAAGGAACGCTAGTTACTGTCTCT
TCCGCAAGTACGAAAGGCCCCGTCAGTATTCCCCTTGGCCCCATCGTCAAAAAGTACAAGT
GGTGGAACTGCAGCCCTGGGTTGCCTAGTAAAAGATTACTTTCCAGAGCCCGTCACTGTG
TCCTGGAATTCGGGTGCTTTAACTTCGGGTGTGCACACTTTCCAGCTGTCTTGCAGTCG
TCTGGGTTGTACTCACTGAGCTCTGTGGTGACCGTACCGTCGTCTAGCTTGGGTACTCAA
ACGTACATATGTAACTGAACCAACCAACCGTCAAAACACAAAGGTTGATAAGAAAGTGGAA
CCAAAGTCGTGCGACAAGACTCACACGTGCCCTCCTTGTCCAGCACCGGAGTTACTTGGA
GGCCCATCTGTGTTTTTGTTCCTCCGAAGCCAAAAGGATACTCTGATGATTAGCAGAACT
CCAGAGGTCACATGTGTTGTTGTTGATGTTTCTCATGAGGATCCAGAAGTCAAGTTTAAC
TGGTACGTGGATGGCGTAGAAGTTTACAATGCCAAGACCAAGCCAAGGGAAGAACAGTAC
AATTCGACATACAGAGTTGTCACTGTCTTGACTGTACTTCATCAAGACTGGCTTAATGGC
AAGGAGTACAAATGTAAGGTCTCTAATAAGGCTCTTCCAGCCCCCATGAAAAAACTATC
AGCAAAGCCAAAGGCCAACCAAGAGAGCCTCAAGTCTACACATTGCCTCCTTCGAGGGAG
GAAATGACCAAAAATCAAGTTTCTTTGACTTGCTTAGTGAAGGGATTTTATCCTTCTGAT
ATTGCAGTCGAATGGGAGTCTAATGGTCAACCTGAAAATAATTACAAAACAACCCCCCA
GTATTAGATTCCGATGGATCTTTCTTCTTATACTCTAACTAACAGTGGATAAGTCACGA
TGGCAACAAGGTAACGTCTTTAGCTGCTCAGTGATGCATGAAGCTTTACACAATCACTAC
ACTCAAAGTCATTGAGCCTATCCCCAGGTAAA
```

**Protein Sequence:**

```
MEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTR
YADSVKGRFTISADTSKNTAYLQMNSLR AEDTAVYYCSRWGGDGFYAMDYWGQGLTVTS
SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSVSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTHTCPPCPAPELLG
GPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE
EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSR
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
```



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	1.12	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	56.52	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.18	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.53	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.11	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.51	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.08	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.07	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.9	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1.06	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.22	<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	0.69	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.05	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.43	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.49	<a href="#">[51]</a>
COUSIN18			0.4	
CBI	Codon Bias Index	-1~1	0.15	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.31	<a href="#">[71]</a>

RCA	Relative Codon Adaptation	$\geq 0$	1.07	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.16	<a href="#">[9]</a>
B	Codon Usage Bias	$0 \sim 2$	0.25	<a href="#">[10]</a>

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

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	$0 \sim 1$	0.47	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.55	<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	$0 \sim 1$	0.43	<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		0.46	
ENcp	Effective Number of Codon Pairs	$20 \sim 61$	36.16	<a href="#">[2]</a>
CPS	Codon Pair Score	$-1 \sim 1$	0.04	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	$0.5 \sim 1$	0.75	<a href="#">[5]</a>

**Gene Name:** Pegfilgrastim

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

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

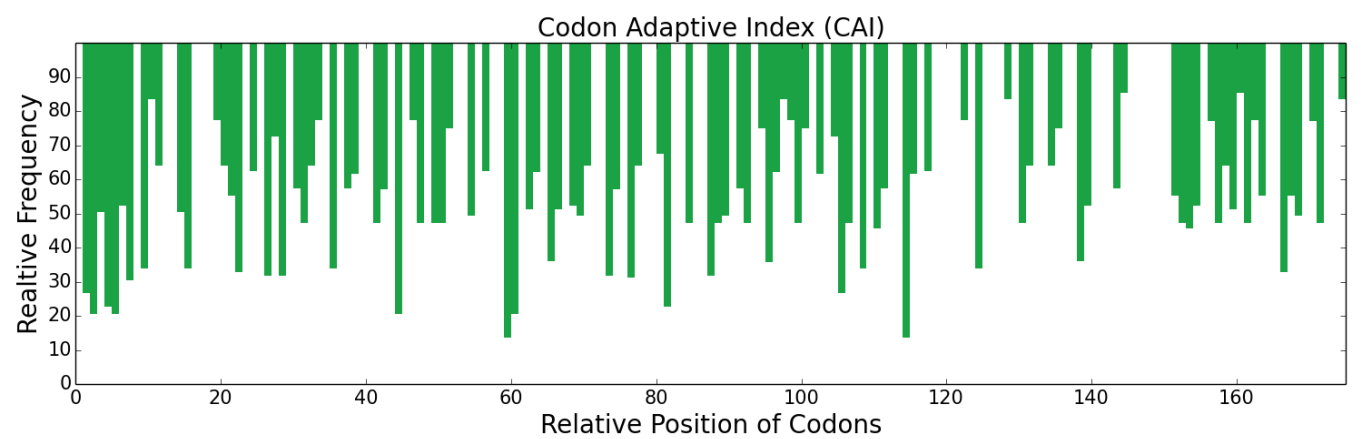
**DNA Sequence Length:** 525

**DNA Sequence:**

ATGACGCCGCTTGGGCCGGCATCGTCTCTACCTCAGTCTTTTCTTCTAAAGTGTTTGGAG  
CAGGTCAGGAAGATCCAAGGCGACGGCGCTGCCCTGCAGGAGAAGCTATGTGCCACATAC  
AAGCTGTGCCATCCGGAAGAGCTGGTTCTGCTGGGACATTCTTTAGGTATCCCATGGGCG  
CCGTTGAGTTCATGTCCAGTCAAGCATTACAGTTGGCTGGCTGCTTGAGCCAGTTGCAT  
TCCGGGTTGTTTCTGTACCAAGGCCTGTTACAAGCCCTGGAAGGAATATCACCTGAGCTG  
GGACCAACATTGGACACGCTGCAACTAGATGTGGCCGATTTTGCACAACTATCTGGCAA  
CAAATGGAGGAAGTAGGTATGGCTCCTGCTCTGCAGCCAACTCAGGGAGCTATGCCCACA  
TTTGCTTCTGCCTTCCAAAGAAGAGCTGGTGGTGTCTGGTGGCATCTCACCTGCAGAGT  
TTCCTGGAGGTCTCTTACAGGGTCTTAAGACACCTGGCTCAACCT

**Protein Sequence:**

MTPLGPASSLPQSFLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWA  
PLSSCPSQALQLAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQ  
QMEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRLHLAQP



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	1.37	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	50.01	<a href="#">[2, 3]</a>

RCBS	Relative Codon Bias Strength	$\geq 0$	0.45	<a href="#">[4]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.83	<a href="#">[5]</a>
CDC	Codon Deviation Coefficient	0~1	0.21	<a href="#">[6]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.51	<a href="#">[7]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.22	<a href="#">[8]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.16	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.8	<a href="#">[11]</a>
P	Codon Preference	$\geq 1$	1.25	<a href="#">[12]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.45	<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	0.65	<a href="#">[1]</a>
CFD	Codon Frequency Distribution	0~1	0.06	<a href="#">[2]</a>
FOP	Frequency of Optimal Codons	0~1	0.38	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	1.1	<a href="#">[5]</a>
COUSIN18			2.37	
CBI	Codon Bias Index	-1~1	0.11	<a href="#">[6]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.63	<a href="#">[7]</a>
RCA	Relative Codon Adaptation	$\geq 0$	1.13	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.37	<a href="#">[9]</a>
B	Codon Usage Bias	0~2	0.44	<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	0.46	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	0~1	0.52	<a href="#">[2]</a>
P2	P2 Index	0~1	0.62	<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	0.53	<a href="#">[1]</a>
GC	GC Content		0.54	
GC1	GC Content at the First Position of Synonymous Codons		0.63	



GC2	GC Content at the Second Position of Synonymous Codons		0.45	
ENcp	Effective Number of Codon Pairs	20~61	25.22	<a href="#">[2]</a>
CPS	Codon Pair Score	-1~1	0.02	<a href="#">[3, 4]</a>
Codon Volatility	Codon Volatility	0.5~1	0.73	<a href="#">[5]</a>

**Gene Name:** Beta-glucuronidase

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

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

**DNA Sequence Length:** 1953

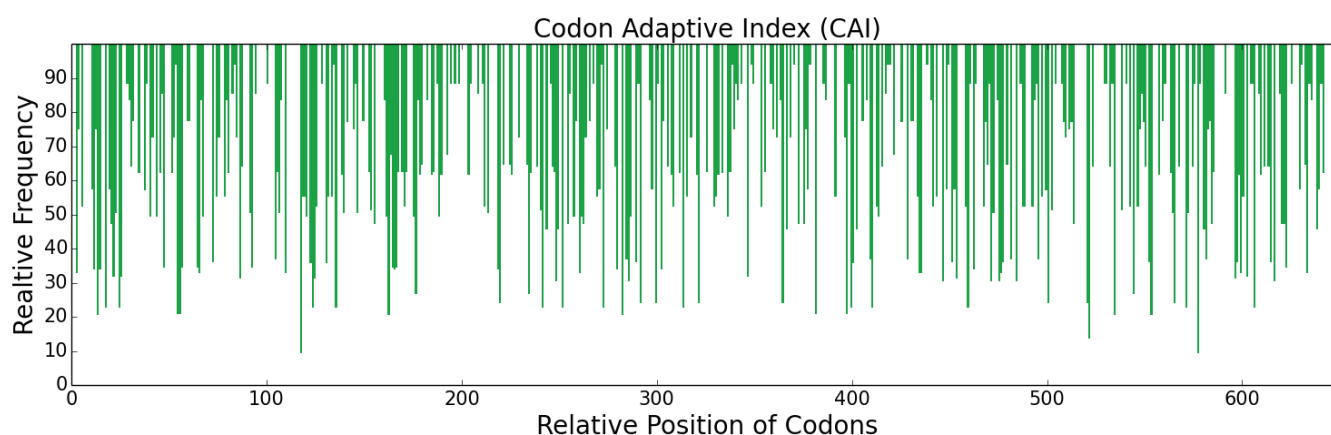
**DNA Sequence:**

```
ATGGCTAGGGGATCTGCAGTTGCTTGGGCTGCCCTAGGACCGCTATTGTGGGGGTGTGCC
CTGGGCCTTCAAGGGGGCATGTTGTATCCTCAGGAGTCTCCATCAAGAGAATGCAAAGAA
TTAGACGGTTTATGGTCATTCCGTGCTGATTTTTTCAGACAATCGACGACGTGGTTTTGAG
GAGCAATGGTACCGTAGGCCTTTATGGGAATCTGGTCCCACTGTGACATGCCAGTCCCT
TCATCTTTCAATGACATTAGCCAGGATTGGAGACTTCGTCAATTCGTTGGTTGGGTTTGG
TATGAAAGAGAAGTAATCCTTCCTGAAAGGTGGACTCAAGATTTGAGAACTCGGGTCGTC
TTAAGAATAGGGAGCGCACATTCTTATGCTATAGTCTGGGTCAATGGGGTTGATACACTT
GAACACGAAGGTGGATATCTTCCATTTGAGGCTGATATCAGTAACCTGGTTCAAGTTGGT
CCTTTACCGTCCCGTCTACGTATCACTATCGCAATCAACAACACTTTAACGCCTACAACC
TTGCCACCTGGTACAATCCAATATTTAACAGATACTTCCAAGTATCCAAAAGGTTATTTT
GTTCAAAACACATATTTTGATTTTTTCAACTATGCAGGTCTTCAAAGATCTGTTCTACTC
TACACCACTCCAACCACATACATTGATGACATTACTGTTACCACGTCAGTTGAACAGGAT
AGTGGGTTGGTGAACATCAGATCTCGGTGAAGGGGTCTAACCTGTTCAAGTTAGAGGTT
AGGTTACTGGACGCTGAGAACAAAGTTGTCGCCAATGGGACTGGAACCTCAAGGTCAGCTA
AAGGTTCCGGGTGTATCGTTATGGTGGCCCTATCTCATGCATGAAAGACCTGCCTACCTC
TATTCTCTAGAGGTTTCAGTTGACAGCACAAACTTCATTGGGGCCAGTCTCTGACTTTTAC
ACACTCCAGTTGGTATCAGAACTGTTGCAGTCACAAAGTCACAAATTTTAATCAATGGA
AAACCTTTTTTATTTTCATGGCGTTAATAAACATGAAGATGCAGATATCAGAGGTAAAGGA
TTTGACTGGCCTCTCTTGGTGAAGGACTTTAATTTGCTGAGATGGCTGGGAGCCAATGCT
TTTCGAACCTTCTCATTATCCTTACGCTGAAGAAGTCATGCAAATGTGTGACCGATATGGG
ATAGTTGTGATTGATGAGTGTCTGGTGTAGGGTTGGCATTACCACAGTTTTTCAATAAT
GTTTCCTTGATCATCATGCAAGTAATGGAGGAGGTTGTCAGGAGGGATAAGAATCAT
CCTGCAGTTGTGATGTGGTTCGGTTGCCAATGAACCCGCCAGCCATTTGGAATCTGCAGGG
TATTACCTAAAAATGGTTATTGCACACACCAAATCGCTTGATCCTTCGAGGCCCGTTACC
TTTGTATCTAACTCGAACTATGCAGCAGATAAGGGTGACCTTATGTAGATGTCATTTGC
CTCAACAGTTACTATTCTTGGTATCACGACTACGGACACCTGGAATTGATTCAATTGCAA
CTCGCGACTCAGTTTGAAAACCTGGTACAAAAAATACCAGAAACCGATTATTCAAAGTGAA
TATGGTGCAGAAACGATTGCAGGATTCCACCAGGATCCCCCGTTGATGTTTACAGAAGAG
TATCAAAAGTCACTTCTCGAACAGTACCATTTTGGGGCTTGATCAGAAAAGACGGAAATAC
GTGGTAGGAGAGCTGATCTGGAACCTTTGCTGATTTTCATGACTGAACAAAGCCCCACAAGG
GTCTTGGGCAACAAAAAAGGGATTTTCAAGACAGAGACAGCCCAAGTCGGCTGCTTTC
CTGCTGCGTGAAAGATATTGGAAGATTGCCAATGAAACCAGGTATCCTCATTCTGTGGCC
AAATCACAAATGTTTGGAAAACAGTCTGTTCACG
```

**Protein Sequence:**

```
MARGSAVAWAALGPLLWGCALGLQGMLYPQESPSRECKELDGLWSFRADFSDNRRRGFE
EQWYRRPLWESGPTVDMVPVPSSFNDISQDWRLRHFGVWVWYEREVILPERWTQDLRTRVV
LRIGSAHSYAIVWVNGVDLTLEHEGGYLPFEADISNLVQVGPLPSRLRITIAINNTLTPTT
LPPGTIQYLTDTSKYPKGYFVQNTYFDFFNAGLQRSVLLYTTPTTYIDDIIVTTSVEQD
SGLVNYQISVKGSNLFKLEVRLLDAENKVVANGTGTQGQLKVPVSLWWPYLMHERPAYL
YSLEVQLTAQTS LGPVSDFYTLFVGIRTVAVTKSQFLINGKPFYFHGVNKHEDADIRGKG
FDWPLLVKDFNLLRWLGANAFRTSHYPYAEVMMQCDRYGIVVIDECPGVGLALPQFFNN
```

VSLHHMQVMEEVVRRDKNHPAVVMWSVANEPASHLESAGYYLKMVIAHTKSLDPSRPVT  
 FVSNSNYAADKGAPYVDVICLNSYYSWYHDYGHLELIQLQLATQFENWYKKYQKPIIQSE  
 YGAETIAGFHDPPPLMFTEEYQKSLLEQYHLGLDQKRRKYVVGELIWNFADFMTEQSPTR  
 VLGKKGIFTRQRPKSA AFLLRERYWKIANETRYPHSVAKSQCLENSLFT



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	1.13	<a href="#">[1]</a>
ENC	Effective Number of Codons	20~61	53.99	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.16	<a href="#">[4]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.47	<a href="#">[5]</a>
CDC	Codon Deviation Coefficient	0~1	0.08	<a href="#">[6]</a>
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ICDI	Intrinsic Codon Deviation Index	0~1	0.07	<a href="#">[8]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.07	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.88	<a href="#">[11]</a>
P	Codon Preference	$\geq 1$	1.06	<a href="#">[12]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.29	<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	0.7	<a href="#">[1]</a>
CFD	Codon Frequency Distribution	0~1	0.06	<a href="#">[2]</a>
FOP	Frequency of Optimal Codons	0~1	0.43	<a href="#">[3, 4]</a>

COUSIN59	Codon Usage Similarity Index	$\infty$	0.65	<a href="#">[5]</a>
COUSIN18			0.76	
CBI	Codon Bias Index	-1~1	0.15	<a href="#">[6]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.21	<a href="#">[7]</a>
RCA	Relative Codon Adaptation	$\geq 0$	1.08	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.14	<a href="#">[9]</a>
B	Codon Usage Bias	0~2	0.22	<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	0.48	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	0~1	0.56	<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	0.41	<a href="#">[1]</a>
GC	GC Content		0.44	
GC1	GC Content at the First Position of Synonymous Codons		0.51	
GC2	GC Content at the Second Position of Synonymous Codons		0.4	
ENcp	Effective Number of Codon Pairs	20~61	61	<a href="#">[2]</a>
CPS	Codon Pair Score	-1~1	0.05	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	0.5~1	0.76	<a href="#">[5]</a>

**Gene Name:** Prothrombin

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

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

**DNA Sequence Length:** 1866

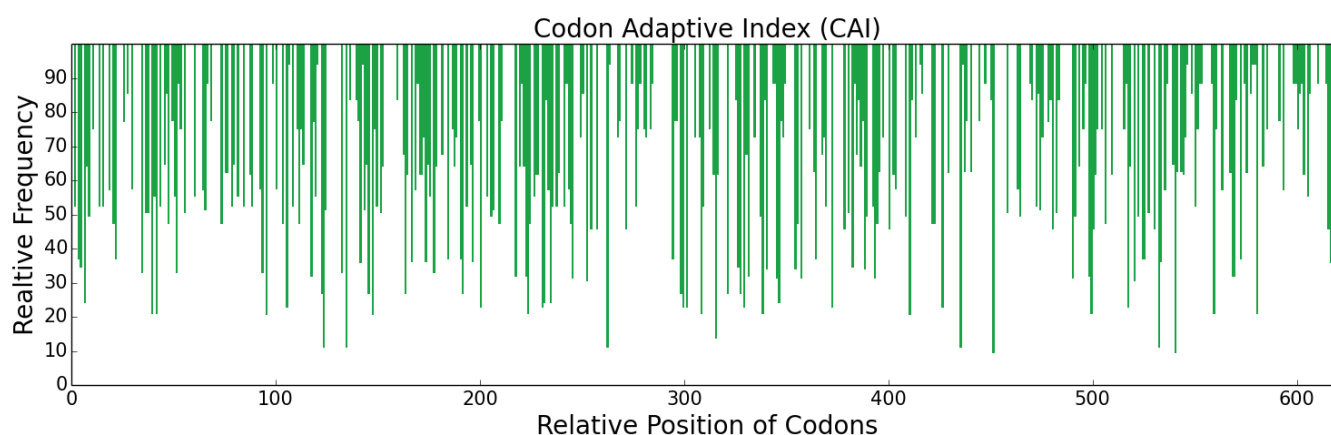
**DNA Sequence:**

```
ATGGCACATGTACGTGGTCTCCAGTTACCAGGATGTTTGGCATTGGCAGCTTTGTGCTCT
CTGGTACATTCTCAACACGTTTTCTTGGCCCCACAACAAGCTAGGTCTCTTCTTCAACGA
GTCCGAAGAGCAAAACACCTTCCTGGAAGAGGTCAGGAAAAGGAAACCTTGAAAGAGAATGT
GTCGAAGAAACTTGCAGTTATGAAGAGGCTTTTGAAGCTCTGGAATCATCAACTGCAACC
GATGTCTTTTGGGCAAAGTACACAGCATGTGAACTGCCAGGACTCCGAGAGATAAATTG
GCCGCTTGTCTGGAAGGGAATTGTGCAGAAGGACTGGGAACCAACTACAGAGGCCACGTC
AATATTACGCGCAGTGGTATTGAATGTCAATTGTGGAGGTCTCGCTACCCTCATAAGCCT
GAGATAAATAGTACCACGCATCCGGGAGCAGATCTTCAGGAAAACCTTTGTAGAAAACCT
GATTCTTCCACGACAGGTCCCTGGTGTCTATACAACAGACCCACCGTCAGAAGGCAGGAA
TGTTCCATTCCAGTATGTGGACAGGACCAAGTAACGGTTGCAATGACCCCCAGATCTGAG
GGGTCTTCTGTCAACTTAAGTCCACCACTGGAGCAATGTGTTCCAGATAGAGGCCAACAG
TATCAGGGCCGACTGGCTGTCACAACACATGGGCTCCCTTGCCCTCGCATGGGCATCAGCT
CAAGCAAAAAGCCCTGAGCAAGCATCAAGACTTCAACTCGGCTGTGCAATTGGTGGAAAAC
TTTTGTGCGCAATCCAGATGGTGACGAGGAAGGTGTGTGGTGTATGTTGCAGGAAAACCA
GGAGACTTTGGATATTGTGATTTGAACTACTGTGAAGAAGCTGTAGAGGAGGAAAACGGGG
GATGGGTTGGATGAAGACTCTGACCGAGCAATTGAAGGAAGAACAGCGACATCTGAATAC
CAAACGTTTTTTTAACCTTCGTACGTTTGGGTCCGGCGAAGCTGACTGTGGTTTACGACCT
CTATTTGAAAAAAAAGCCTCGAGGACAAAACCTGAAAGAGAACTACTGGAAAGCTACATT
GATGGAAGAATCGTAGAAGGTTCCGACGCAGAAATTGGGATGTCTCCATGGCAAGTGATG
CTTTTTTCGTAAATCCCTCAGGAGCTATTATGTGGTGCAAGCCTGATCTCTGACAGATGG
GTGTTGACAGCCGCTCATTGTTTGTATACCCGCTTGGGACAAGAATTTCACTGAAAAC
GATCTGCTGGTTAGAATTGGGAAGCATTCAAGAACTAGATACGAACGCAATATCGAGAAG
ATCTCTATGTTGGAGAAGATTTATATTCATCCTCGGTACAACCTGGAGAGAAAACCTTGAT
AGAGATATTGCCTTAATGAAGTTGAAGAAACCTGTTGCATTCAGTGACTACATTCACCCT
GTGTGTCTTCTGATAGAGAACTGCTGCTAGCTTATTGCAGGCTGGATATAAGGGCCGA
GTGACAGGATGGGGAAAACCTGAAGGAAAACATGGACTGCTAACGTTGGAAAAGGGCAGCCA
TCGGTTTTTACAAGTAGTAAACCTTCCAATTGTGGAACGCCCCGTTTGCAAAGATTCTACC
CGGATCAGAATCAGACAAATATGTTCTGTGCAGGATATAAAACCAGATGAAGGTAAACGA
GGAGATGCTTGCGAAGGTGATTACAGGCGGCCCTTTTGTAAATGAAATCACCATTCAATAAT
CGATGGTACCAGATGGGAATTGTTTCTTGGGGTGAGGGTTGCGATAGAGATGGTAAATAT
GGATTCTATACACATGTCTTCAGATTGAAGAAATGGATTCAAAAAGTGATAGACCAGTTT
GGGGAA
```

**Protein Sequence:**

```
MAHVRGLQLPGCLALAAALCSLVHSQHVFAPQQARSLQLQVRRANTFLEEVKGNLEREC
VEETCSYEEAFEALSSSTATDVFWAKYTACETARTPRDKLAACLEGNCAEGLGTNYRGHV
NITRSGIECQLWRSRYPHKPEINSTTHPGADLQENFCRNPDSSTGPWCYTDDPTVRRQE
CSIPVCGQDQVTVAMTPRSEGSSVNLSPPLEQCVPDRGQQYQGR LAVTTHGLPCLAWASA
QAKALSKHQDFNSAVQLVENFCRNPDGDEEGVWCYVAGKPGDFGYCDLNYCEEAVEEETG
DGLDESDRAIEGRTATSEYQTFNPRFTGSGEADCLRPLFEKKSLEDKTERELLESYI
DGRIVEGSDAEIGMSPWQVMLFRKSPQELLCGASLISDRWVLTAAHCLLYPPWDKNFTEN
DLLVRIGKHSRTRYERNIEKISMLEKIYIHPRYNWRENLDRIALMKLKKPVAFSDYIHP
```

VCLPDRETAASLLQAGYKGRVTGWGNLKETWTANVGKGQPSVLQVVNLPIVERPVCKDST  
 RIRITDNMFCAGYKPDEGKRGDACEGDSGGPFVMMKSPFNRRWYQMGIVSWGEGCDRDGKY  
 GFYTHVFLKKWIKVIDQFGE



Negative CIS Elements	Negative repeat Elements
2	0

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

Index	Description	Range	Value	Reference
RSCU	Relative Synonymous Codon Usage	0~6	1.19	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	51.89	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.17	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.5	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.1	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.46	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.1	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.09	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.87	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1.08	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.37	<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	0.71	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.06	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.47	<a href="#">[3, 4]</a>
			1.32	

COUSIN18	Codon Usage Similarity Index	$\infty$	1.54	<a href="#">[5]</a>
COUBI59	Codon Bias Index	-1~1	0.19	<a href="#">[6]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.24	<a href="#">[7]</a>
RCA	Relative Codon Adaptation	$\geq 0$	1.1	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.15	<a href="#">[9]</a>
B	Codon Usage Bias	0~2	0.24	<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	0.48	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	0~1	0.55	<a href="#">[2]</a>
P2	P2 Index	0~1	0.56	<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	0.39	<a href="#">[1]</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		0.45	
ENcp	Effective Number of Codon Pairs	20~61	33.37	<a href="#">[2]</a>
CPS	Codon Pair Score	-1~1	0.05	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	0.5~1	0.76	<a href="#">[5]</a>

**Gene Name:** Xylanase

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

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

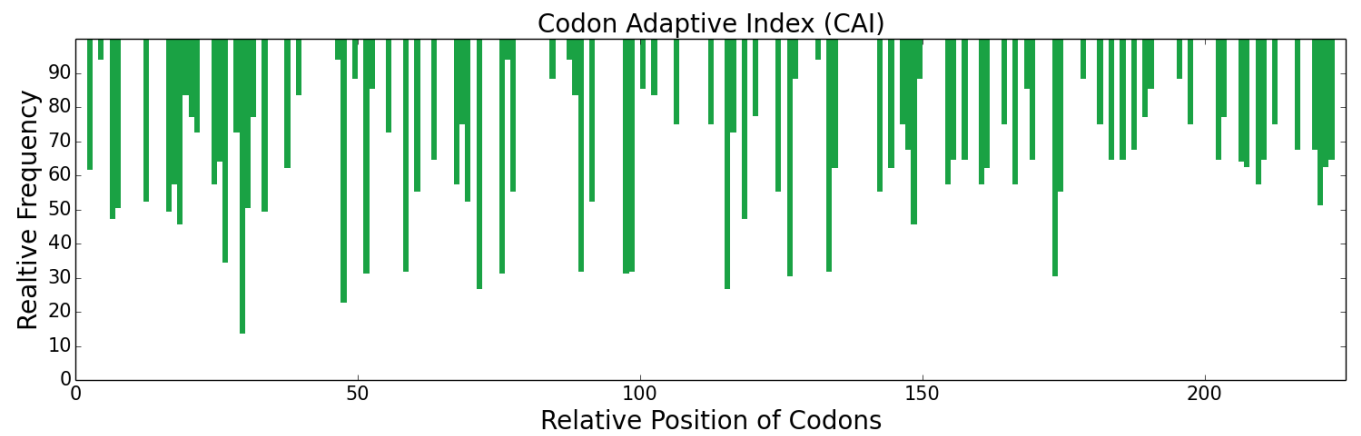
**DNA Sequence Length:** 675

**DNA Sequence:**

ATGTTGACAAAGAATTTGCTGCTTTGTTTTGCTGCTGCAAAGGCTGCTTTAGCCGTGCCT  
CACGACTCTGTTGCCAGCGTTCTGACGCGCTTCACATGTTATCTGAAAGATCAACTCCT  
TCTTCTACTGGTGAAAACAATGGGTTTTATTACAGCTTCTGGACTGACGGTGGTGGCGAT  
GTCACTTACACCAACGGTGATGCCGGAGCATAACACGGTTGAATGGAGCAATGTCGGTAAC  
TTTGTGGTGGTAAAGGTTGGAATCCTGGCTCTGCACAAGATATTACTTACAGCGGCACT  
TTCACCTCCTTCTGGTAACGGATACTTGTCTGTTTACGGATGGACTACGGACCCACTGATT  
GAGTACTACATTGTGAATCGTATGGTGATTACAATCCAGGCTCAGGTGGTACTTACAAG  
GGTACTGTCACTTCAGATGGATCCGTGTATGATATTTACACTGCCACCAGAACCAACGCT  
GCCTCAATTCAAGGAAGTCCACTTTACCCAATACTGGTCGGTCAGACAAAACAAAAGA  
GTTGGAGGTACCGTTACCACTTCCAACCACTTCAACGCTTGGGCTAAATTGGGAATGAAC  
TTGGGTACCCACAACCTACCAGATCGTTGCCACCGAAGGATACCAATCTTCCGGTTCTTCC  
AGTATCACCGTTCAA

**Protein Sequence:**

MLTKNLLLCFAAAKAALAVPHDSVAQSRDALHMLSERSTPSSTGENNGFYYSFWDGGGD  
VITYNGDAGAYTVEWSNVGNFVGKGWNPQSAQDITYSGTFTPSGNGYLSVYGWTTDPLI  
EYYIYESYGDYNPGSGGTYKGTVTSDSVYDIYTATRTNAASIQGTATFTQYWSVRQNR  
VGGTVTTSNHFNAWAKLGMNLGTHNYQIVATEGYQSSGSSSITVQ



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	1.5	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	40.63	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.4	<a href="#">[4]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.96	<a href="#">[5]</a>
CDC	Codon Deviation Coefficient	0~1	0.21	<a href="#">[6]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.39	<a href="#">[7]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.32	<a href="#">[8]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.24	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.72	<a href="#">[11]</a>
P	Codon Preference	$\geq 1$	1.21	<a href="#">[12]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.64	<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	0.79	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.02	<a href="#">[2]</a>
FOP	Frequency of Optimal Codons	0~1	0.56	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	2.59	<a href="#">[5]</a>
COUSIN18			2.18	
CBI	Codon Bias Index	-1~1	0.34	<a href="#">[6]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.19	<a href="#">[7]</a>
RCA	Relative Codon Adaptation	$\geq 0$	1.13	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.33	<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	0.56	<a href="#">[11]</a>
gtAI	Genetic tRNA Adaptation Index	0~1	0.63	<a href="#">[2]</a>
P2	P2 Index	0~1	0.68	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
			0.44	

GC	GC Content	0~1	0.47	<a href="#">[1]</a>
GC1 GC3	GC Content at the First Position GC Content at the Third Position of Synonymous Codons		0.45	
GC2	GC Content at the Second Position of Synonymous Codons		0.52	
ENcp	Effective Number of Codon Pairs	20~61	21.32	<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:** Chymosin

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

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

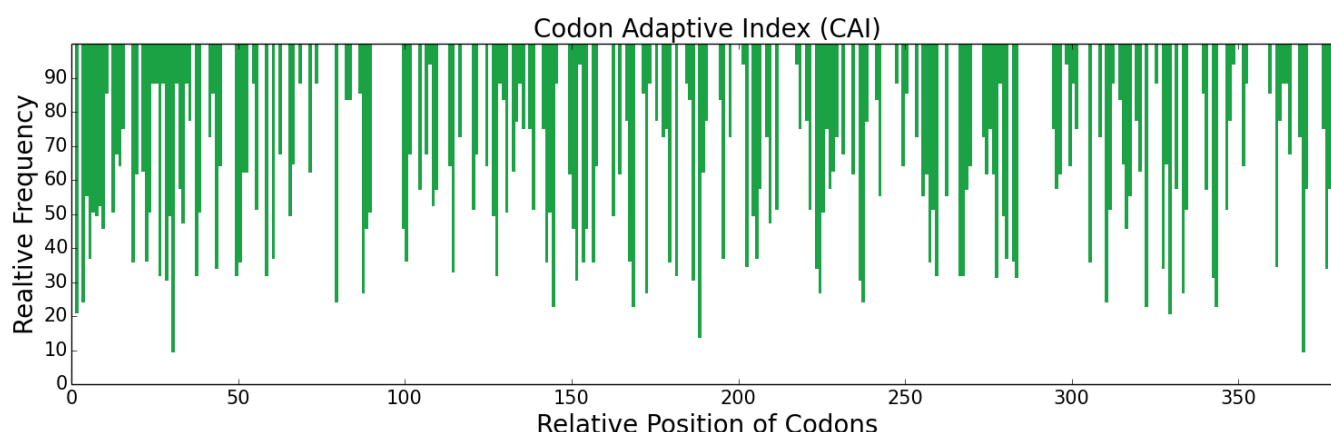
**DNA Sequence Length:** 1143

**DNA Sequence:**

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AGAATCCCCCTTTATAAAGGCAAATCGTTACGGAAAGCCCTGAAAGAGCATGGCCTTTTG
GAAGACTTCCTACAGAAGCAACAATACGGCATATCATCAAAGTATAGTGGTTTTGGCGAA
GTAGCTTCCGTTCCATTAAACCAACTATTTGGATTACACAATATTTTGGTAAGATTTACCTC
GGTACTCCTCCTCAAGAATTCACGGTGCTTTTTGATACTGGTTCCTCTGATTTTTGGGTG
CCCTCCATTTACTGCAAGTCCAATGCATGCAAGAACCATCAGAGGTTTGACCCAAGAAAG
AGTTCCACTTTTCAGAACTTAGGCAAACCTCTTCTATCCACTATGGAAGTGAAGTATG
CAAGGAATACTTGGGTATGATACTGTTACAGTGTGCAATATAGTGGATATACAGCAAAC
GTTGGTTTATCTACACAAGAGCCCGGGGATGTTTTCACGTATGCTGAGTTTGACGGAATA
TTGGGCATGGCTTATCCTTCGTTGGCGTCAGAGTACTCTATTCCTGTATTTGACAACATG
ATGAATCGTCATTTAGTAGCCCAAGACCTGTTTAGTGTTTACATGGATAGAAATGGACAA
GAGAGTATGCTAACGCTTGGAGCCATCGACCCATCCTACTACACAGGTTTCGCTCCACTGG
GTTCTGTCACTGTTCAACAATATTGGCAGTTCACTGTTGACTCTGTCAACAATAAGTGGC
GTTGTTGTGCGCTTGTGAAGGCGGCTGCCAGGCTATTTTGGACACAGGAACAAGCAAATTA
GTAGGTCCCAGCTCTGATATTTTGAACATTCAACAAGCTATTGGAGCCACACAAAATCAG
TATGGAGAATTTGATATAGATTGTGACAACCTCAGTTATATGCCTACCGTGGTCTTTGAG
ATCAACGGGAAGATGTATCCACTAACCCCGTCTGCCTACACGAGTCAAGATCAAGGTTTC
TGCACTAGCGGGTTTCAAAGTGAGAATCATTCTCAGAAATGGATTTTGGGTGATGTTTTC
ATTCGTGAGTATTATTCCGTTTTTGACCGGGCCAACAACCTGGTTGGACTAGCCAAGGCC
ATA
```

**Protein Sequence:**

```
MRCLVLLAVFALSQGAETRIPLYKGKSLRKALKEHGLLEDFLQKQQYGISSKYSGFGE
VASVPLTNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPK
SSTFQNLGKPLSIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDVFTYAEDGI
LGMAYPSLASEYSIPVFDNMMNRHLVAQDLFSVYMDRNGQESMLTLGAIDPSYYTGSLSHW
VPVTVQQYWQFTVDSVTISGVVVACEGGCQAILDTGTSLKLVGPSSDILNIQQAIGATQNQ
YGEFDIDCDNLSYMP TVVFEINGKMYPLTPSAYTSQDQGFCTSGFQSENHSQKWILGDVF
IREYYSVFDRANNLVGLAKAI
```



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	1.1	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	60.05	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.16	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.5	<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	-0.53	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.06	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.06	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.91	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1.05	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.19	<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	0.69	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.04	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.41	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.72	<a href="#">[51]</a>
COUSIN18			0.86	
CBI	Codon Bias Index	-1~1	0.11	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.34	<a href="#">[71]</a>

RCA	Relative Codon Adaptation	$\geq 0$	1.07	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.17	<a href="#">[9]</a>
B	Codon Usage Bias	$0 \sim 2$	0.25	<a href="#">[10]</a>

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

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	$0 \sim 1$	0.47	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.56	<a href="#">[2]</a>
P2	P2 Index	$0 \sim 1$	0.46	<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	$0 \sim 1$	0.41	<a href="#">[1]</a>
GC	GC Content		0.43	
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	$20 \sim 61$	29.77	<a href="#">[2]</a>
CPS	Codon Pair Score	$-1 \sim 1$	0.05	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	$0.5 \sim 1$	0.76	<a href="#">[5]</a>

**Gene Name:** Alpha-amylase

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

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

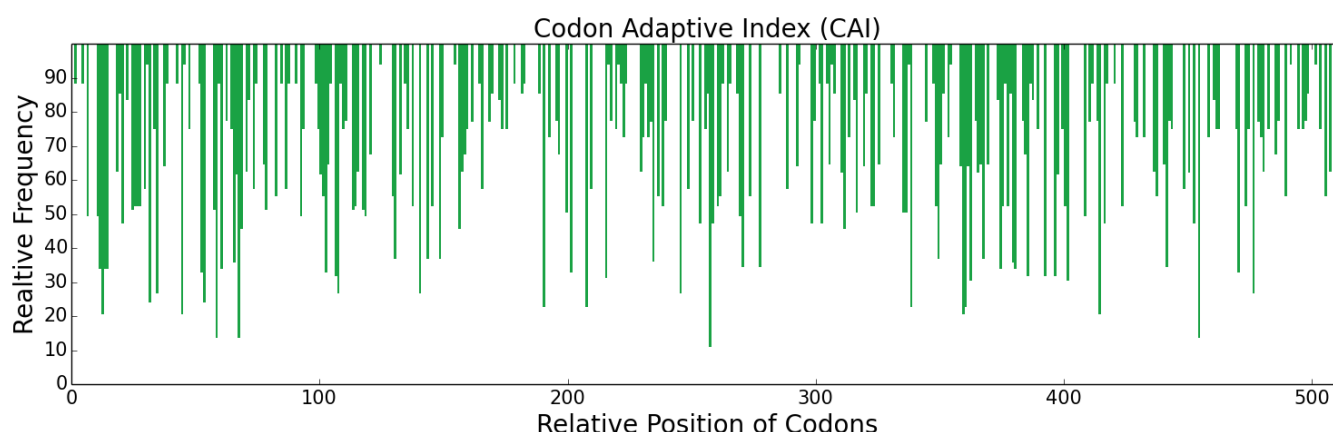
**DNA Sequence Length:** 1536

**DNA Sequence:**

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CTGTTGCCTCATAGTGCAGCAGCAGCTGCCAATCTCAAGGGAACGTTGATGCAGTATTTT
GAATGGTATATGCCGAATGATGGACAACATTGGAAAAAGGCTCCAAAACGATAGTGCAT
CTAGCTGAGCATGGAATAACAGCGGTGTGGATCCCTCCAGCCTATAAGGGTACCAGTCAA
GCTGATGTTCGGTTATGGTGCCTATGATTTGTATGATTTAGGAGAATTCATCAAAAAGGA
ACAGTCAGGACCAAATACGGCACGAAAGGAGAGTTGCAAAGTGCAATCAAGAGTTTACAT
TCCAGAGATATTAATGTTTACGGTGATGTCGTAATTACAAACAAAGGAGGTGCAGATGCT
ACGGAAGATGTAAGTGCAGTTGAAGTAGACCCAGCTGATAGAAATAGAGTGATCTCCGGA
GAACACAGAATTAAAGCCTGGACTCACTTCCATTTTCCTGGAAGAGGATCTACTTATTCT
GATTTCAAATGGCATTGGTACCATTTTCGATGGGACTGACTGGGATGAGTCCAGAAAGCTT
AACAGGATTTACAAGTTTCAAGGGAAGGCCTGGGATTGGGAAGTTAGCAATGAGAACGGA
AATTATGACTATTTGATGTACGCTGATATCGACTATGACCACCCCGATGTCGCTGCAGAG
ATTAAGAGATGGGGTACGTGGTACGCCAACGAGTTGCAACTGGATGGATTCCGCCTGGAT
GCAGTCAAACATATCAAATTTTCTTTCTTACGTGATTGGGTCAACCATGTTCTGTGAAAAG
ACTGGTAAGGAAATGTTCACTGTTGCCGAATACTGGCAGAATGATTTGGGTGCTCTGGAG
AACTATCTGAACAAAACCAATTTCAACCATTTCAGTGTTTGACGTTCTCTTATTACCAG
TTCCATGCAGCATCTACCCAAGGTGGTGGTTATGACATGGGTAAGCTTCTTAATGGGACT
GTTGTTTCTAAGCACCCATTGAAAGCAGTAACCTTCGTTGACAATCATGATACTCAGCCG
GGGCAGTCGTTGGAGTCAACCGTACAAACCTGGTTTAAGCCTCTAGCATATGCATTCATA
CTAACTAGAGAGTCCGGCTATCCTTCTGGATTTTACGGCGATATGTACGGCACAAAGGGA
GCATCGCAAAGAGAAATTCCAGCTTTAAAGCACAAAATTGAGCCGATTCTGAAAGCTAGA
AAACAATACGCATACGGTGCTCAACACGACTACTTTGACCATCATGATATCGTCGGTTGG
ACCCGTGAGGGAGATTCTTCTGTTGCCAACTCAGGTCTGGCTGCGTTGATTACTGACGGT
CCTGGAGGAGCTAAGAGAATGTACGTTGGAAGGCAAAACGCAGGAGAAACGTGGCACGAC
ATCACTGGAAACAGATCCGAGCCAGTTGTCATTAATTCTGAAGGATGGGGAGAGTTCCAT
GTTAATGGTGGATCTGTCTCTATCTACGTCCAACGG
```

**Protein Sequence:**

```
MKQQKRLYARLLPLLFLALIFLLPHSAAAAANLKGTLMQYFEWYMPNDGQHWKRLQND SAY
LAEHGITAVWIPPAYKGT SQADVGYGAYDLYDLGEFHQKGT VRTKYGTKGELQSAIKSLH
SRDINVYGDVVI TNKGGADATEDVTAVEVDPADRNRVISGEHRIKAWTHFHFPGRGSTYS
DFKWHWHYHFDGTDWDESRLNRIYKFQ GKAWDWEVSNENGN YDILMYADIDYDHPDVAAE
IKRWGTWYANELQLDGFRLDAVKHIKFSFLRDWVNHVREKTGKEMFTVAEYWQNDLGALE
NYLNKTNFNHVSFVDVPLHYQFHAAS TQGGGYDMGKLLNGTVVSKHPLKAVTFVDNHDTQP
GQSLESTVQTWFKPLAYAFIL TRESGYPSGFYGD MYGTKGASQREIPALKHKIEPILKAR
KQYAYGAQHDFDHHDIVGWTREGDSSVANSGLAALITDGP GAKRMVGRQNAGETWHD
ITGNRSEPVVINSEGWGEFHVNGGSVSIYVQR
```



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	1.2	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	50.12	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.23	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.63	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.12	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.45	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.09	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.09	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.86	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1.09	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.38	<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	0.75	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.04	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.47	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.87	<a href="#">[51]</a>
COUSIN18			0.91	
CBI	Codon Bias Index	-1~1	0.19	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.22	<a href="#">[71]</a>

RCA	Relative Codon Adaptation	$\geq 0$	1.1	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.14	<a href="#">[9]</a>
B	Codon Usage Bias	$0 \sim 2$	0.21	<a href="#">[10]</a>

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

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	$0 \sim 1$	0.51	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.6	<a href="#">[2]</a>
P2	P2 Index	$0 \sim 1$	0.6	<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	$0 \sim 1$	0.41	<a href="#">[1]</a>
GC	GC Content		0.44	
GC1	GC Content at the First Position of Synonymous Codons		0.52	
GC2	GC Content at the Second Position of Synonymous Codons		0.39	
ENcp	Effective Number of Codon Pairs	$20 \sim 61$	28.01	<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	$0.5 \sim 1$	0.77	<a href="#">[5]</a>



**Gene Name:** Cellulase

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

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

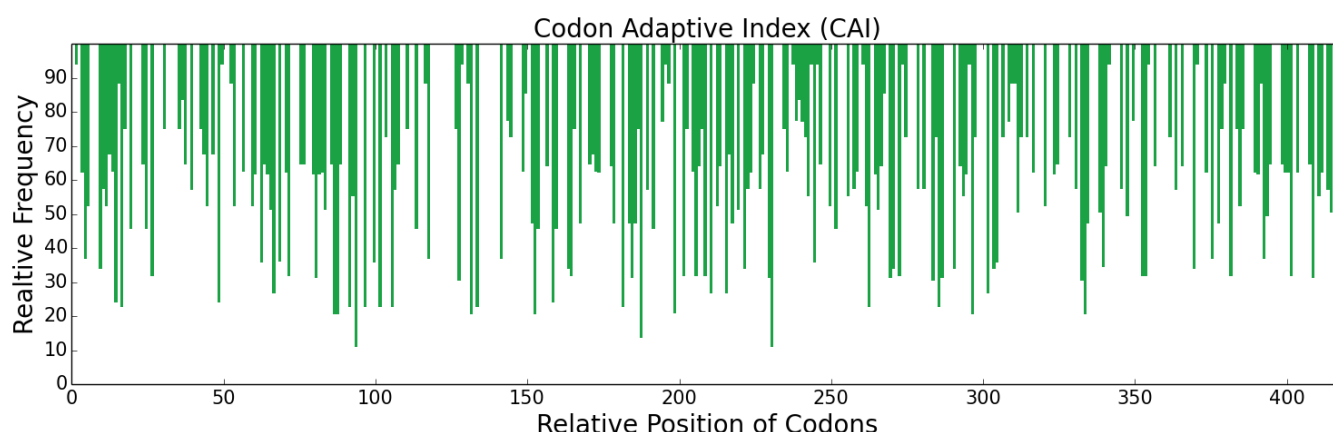
**DNA Sequence Length:** 1254

**DNA Sequence:**

```
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GCTCAACAAACCGTGTGGGGCCAATGTGGTGGAATTGGTTGGTCTGGACCTACCAACTGC
GCTCCAGGATCCGCATGTTCCACTCTCAATCCATACTATGCACAAATGTATCCCAGGTGCA
ACAACATAAACCACAAGTACGAGACCCCCATCAGGCCCACTACTACCACCAGAGCTACA
AGCACATCAAGTTCTACCCCGCCGACCTCTTCTGGGGTCCGCTTTGCTGGGGTTAACATA
GCTGGGTTTGACTTTGGGTGCACCACTGATGGAACCTGTGTGACTTCTAAAGTATACCCA
CCATTGAAGAACTTTACTGGATCGAATAACTATCCGGATGGGATTGGTCAAATGCAACAT
TTTGTAACGAGGACGGTATGACTATCTTCAGACTGCCGGTGGGTGGCAGTACCTCGTG
AACAACAACCTAGGCGGAAACCTGGATTCTACCTCCATCTCAAAGTACGATCAGCTGGTT
CAAGGGTGTCTGAGCCTGGGAGCGTACTGCATTGTGGATATTCACAATTATGCTCGATGG
AACGGCGGAATTATCGGCCAGGGAGGCCCAACGAACGCACAGTTTACGTCCCTGTGGAGT
CAACTAGCCTCAAAATACGCCTCCCAAAGCCGCGTTTGGTTTGGGAATCATGAATGAGCCT
CACGACGTCAATATAAAATACCTGGGCTGCAACTGTGCAAGAAGTTGTCACTGCCATCAGA
AATGCAGGGGCTACAAGTCAGTTCATTAGCCTACCAGGCAATGACTGGCAATCTGCCGGT
GCCTTTATTTTCGGACGGGAGCGCTGCTGCTCTATCTCAGGTCACAAATCCGGACGGTTCT
ACTACGAACCTAATATTTGACGTTTACAAATATCTTGACTCTGACAACTCAGGTACTCAT
GCAGAATGTACAACCAACAACATTGACGGTGCCTTTTCGCCGCTGGCTACTTGGCTTCGT
CAGAATAACAGACAAGCCATTTTAACTGAGACTGGTGGCGGCAATGTTCACTCTTGTATT
CAAGACATGTGCCAACAGATTCAATACCTAAATCAAACTCAGATGTATACCTGGGATAT
GTTGGCTGGGGAGCAGGATCTTTTGATTCAACATATGTATTAACCGAACTCCAACCTCA
TCAGGCAACTCATGGACTGATACCAGCTTGGTCTCATCTTGCTTAGAAAAG
```

**Protein Sequence:**

```
MNKSVAPLLAAASILYGGAVAQQTVWGQCGGIGWSGPTNCAPGSACSTLNPYYAQCIPGA
TTITTSTRPPSGPTTTTTRATSTSSSTPPTSSGVRFAGVNIAGFDGCTTDGTCVTSKVYP
PLKNFTGSNNYPDGIGQMQLHFVNEDGMTIFRLPVGWQYLVNNNLGGNLDSTSISKYDQLV
QGCLSLGAYCIVDIHNYARWNGGIIGQGGPTNAQFTSLWSQLASKYASQSRVWFGIMNEP
HDVNINTWAATVQEVVTAIRNAGATSQFISLPGNDWQSAGAFISDGSAAALSQVTNPDGS
TTNLI F DVH KYLDSDNSGTHAECTTNIDGAFSPLATWLRQNNRQAILTETGGGNVQSCI
QDMCQQIQYLNQNSDVYLG YVGW GAGSFDSTYVLTETPTSSGNSWTDTSLVSSCLARK
```



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	1.16	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	53.03	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.25	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.72	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.13	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.5	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.09	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.08	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.88	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1.09	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.28	<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	0.68	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.06	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.43	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	1.2	<a href="#">[51]</a>
COUSIN18			1.28	
CBI	Codon Bias Index	-1~1	0.16	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.33	<a href="#">[71]</a>

RCA	Relative Codon Adaptation	$\geq 0$	1.06	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.2	<a href="#">[9]</a>
B	Codon Usage Bias	$0 \sim 2$	0.26	<a href="#">[10]</a>

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

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	$0 \sim 1$	0.48	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.57	<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	$0 \sim 1$	0.44	<a href="#">[1]</a>
GC	GC Content		0.48	
GC1	GC Content at the First Position of Synonymous Codons		0.48	
GC2	GC Content at the Second Position of Synonymous Codons		0.52	
ENcp	Effective Number of Codon Pairs	$20 \sim 61$	61	<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	$0.5 \sim 1$	0.74	<a href="#">[5]</a>

**Gene Name:** Lipase

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

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

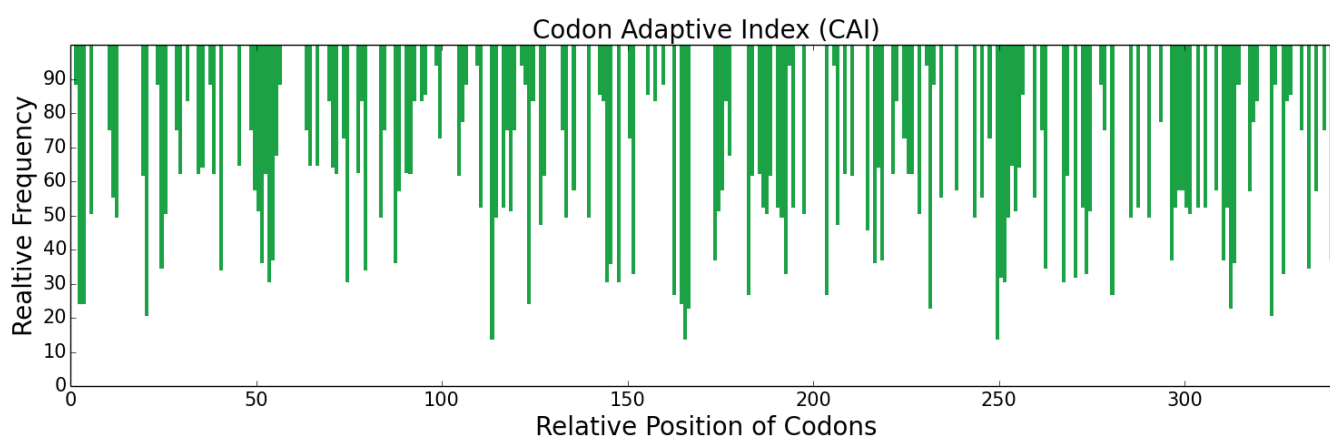
**DNA Sequence Length:** 1026

#### DNA Sequence:

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CCGTTGGTTAAACGTCTTCCATCTGGATCAGATCCTGCTTTTTTCACAGCCAAAATCAGTT
CTAGATGCTGGTTTGACCTGTCAAGGAGCCAGTCCCTCATCGGTATCCAAACCAATTTTG
TTGGTTCCAGGAACCGGTACCACTGGTCCCTCAGTCATTTGACTCGAACTGGATCCCTCTA
TCTACTCAATTAGGATACACTCCCTGCTGGATCTCACCTCCACCTTTCATGTTGAATGAC
ACTCAAGTTAACACAGAGTATATGGTTAATGCAATTACTGCGTTATACGCAGGAAGTGGA
AACAATAAACTCCCTGTTCTGACATGGTCTCAAGGTGGATTAGTTGCCCAATGGGGTTTA
ACTTTTTTCCCTTCGATAAGATCGAAGGTTGACAGGTTGATGGCTTTCGCTCCTGATTAT
AAGGTTACGGTTCGCGGGGGCCATTGGATGCTTTGGCTGTAAGTGCCCTTCCGTTTGG
CAACAAACGACAGGTTTCAGCACTTACAACATGCATTAAGGAATGCAGGTGGTCTTACTCAA
ATTGTTCCAACGACTAATCTGTACTCAGCTACAGATGAAATTGTGCAACCCAGGTATCT
AACTCACCTTTGGACTCATCATACCTTTTTTAATGGGAAAAACGTCCAAGCTCAAGCCGTT
TGTGGTCCATTATTTGTCATTGACCATGCGGGCTCGTTAACCAGTCAGTTCTCTTACGTC
GTTGGACGTTCTGCTTTGAGATCGACAACATGGCCAAGCAAGGAGTGCTGATTATGGAATT
ACGGAATTGTAACCCATTACCAGCAAACGATTTAACTCCAGAGCAAAAGGTAGCAGCCGCC
GCACTTTTGGCACCAGCAGCTGCTGCCATTGTAGCAGGGCCCAACAAAACACTGCGAGCCT
GATTTGATGCCGTATGCTAGGCCCTTTCGCTGTTGGAAAGCGTACTTGCTCTGGAATTGTA
ACTCCC
```

#### Protein Sequence:

```
MKLLSLTGAVGLATCVAATPLVKRLPSGSDPAFSQPKSVLDAGLTCQGASPSVSKPIL
LVPGTGTTGPQSFDSNWIPLSTQLGYTPCWISPPPFMLNDTQVNT EYMVNAITALYAGSG
NNKLPVLTWSQGGLVAQWGLTFFPSIRSKVDRLMAFAPDYKGTVLAGPLDALVSAPSVW
QQTGSA LTALRNAGGLTQIVPTTNLYSATDEIVQPQVSN SPLDSSYLFNGKNVQAQAV
CGPLFVIDHAGSLTSQFSYVVGRSALRSTTGQARSADYGITDCNPLPANDLTPEQKVAAA
ALLAPAAAAIVAGPKQNCEPDLMPYARPFVAVGKRTCSGIVTP
```



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	1.33	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	49.92	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.24	<a href="#">[4]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.66	<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	-0.43	<a href="#">[7]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.18	<a href="#">[8]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.14	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.83	<a href="#">[11]</a>
P	Codon Preference	$\geq 1$	1.11	<a href="#">[12]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.51	<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	0.71	<a href="#">[1]</a>
CFD	Codon Frequency Distribution	0~1	0.05	<a href="#">[2]</a>
FOP	Frequency of Optimal Codons	0~1	0.46	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	1.09	<a href="#">[5]</a>
COUSIN18			1.17	
CBI	Codon Bias Index	-1~1	0.23	<a href="#">[6]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.28	<a href="#">[7]</a>
RCA	Relative Codon Adaptation	$\geq 0$	1.09	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.25	<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	0.47	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	0~1	0.54	<a href="#">[2]</a>
P2	P2 Index	0~1	0.63	<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	0.33	<a href="#">[1]</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		0.53	
ENcp	Effective Number of Codon Pairs	20~61	24.6	<a href="#">[2]</a>
CPS	Codon Pair Score	-1~1	0.02	<a href="#">[3, 4]</a>
Codon Volatility	Codon Volatility	0.5~1	0.73	<a href="#">[5]</a>

**Gene Name:** Phytase

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

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

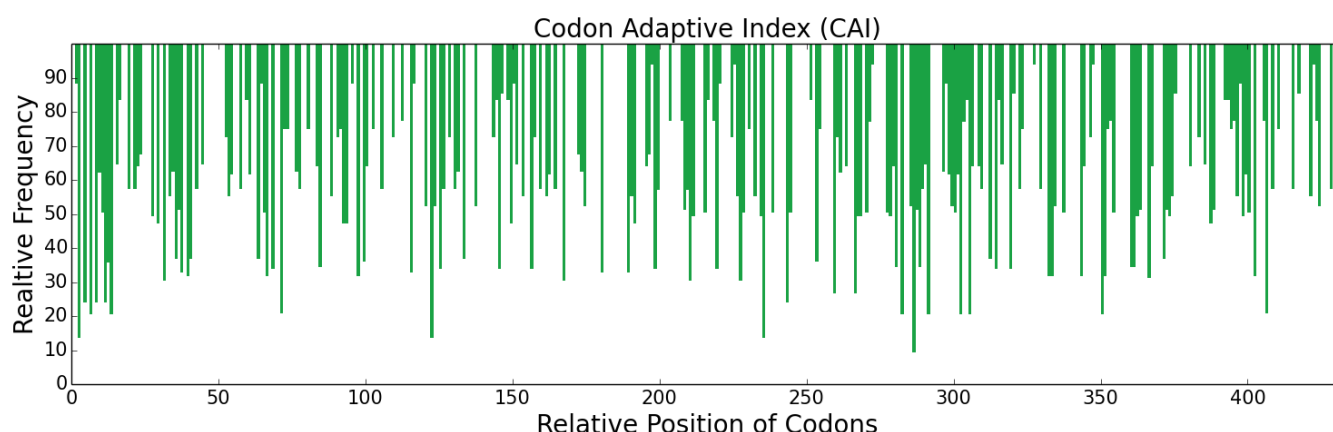
**DNA Sequence Length:** 1296

**DNA Sequence:**

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ACATGGCCAGTAAAACTTGGCTGGCTAACTCCACGAGGAGGAGAATTGATCGCCTACTTG
GGACATTACCAGCGTCAAAGATTGGTCGCTGACGACTGCTGGCTAAAAAGGGCTGTCCC
CAGTCTGGACAAGTTGCCATTATTGCTGACGTTGATGAGAGAACTAGGAAAAGTGGTAA
GCATTTGCGGCAGGTCTAGCCCCAGACTGTGCCATCACTGTACATACTCAAGCAGATACT
TCTTCTCCAGACCCTCTATTCAACCCTCTGAAAACCGGTGTCTGTCAACTAGACAACGCC
AACGTCACAGATGCCATTTTGTGAGAGCTGGTGGTTCATCGCAGATTTTACTGGTCAT
AGGCAAAGTCTTTTAGAGAATTGGAAAGGGTCTGAACTTTCCACAGTCCAATCTATGC
TTGAAGAGAGAGAAGCAAGATGAGAGTTGCTCGTTAACTCAAGCTCTTCCTTCTGAGCTA
AAAGTTTCTGCTGACAATGTCTCGCTTACTGGAGCTGTCTCTTTAGCGTCTATGCTTACT
GAAATTTTTCTCCTTCAACAAGCTCAAGGTATGCCTGAACCCGGATGGGGTAGAATTACG
GACTCACATCAGTGGAACACGTTATTATCTCTTCACAATGCTCAATTTTACCTTTTACAG
CGTACTCCGGAAGTTGCACGGAGTCGTGCCACCCCGTTGTTGGATTTGATCAAAACAGCA
CTTACACCGCACCTCCGCAGAAGCAGGCCTACGGTGTAACCTACCTACCTCTGTTCTA
TTCATTGCCGGACATGATACTAATTTGGCCAACCTGGGCGGCGCATTGGAAGTTAACTGG
ACTTTGCCAGGCCAGCCAGACAATACTCCACCGGGCGGAGAGCTTGTTTTTGAAAGATGG
CGTCGTTTAAAGTGATAACAGCCAGTGGATTCAAGTAAGTTTAGTCTTCCAACTTTGCAA
CAGATGAGAGACAAGACCCCACTGAGTTTGAACACTCCTCCTGGAGAGGTCAAATTAACA
CTTGCTGGCTGTGAAGAGCGAAACGCCCAAGGAATGTGTTCTTTGGCCGGTTTCACTCAA
ATTGTCAATGAGGCAAGAATTCCAGCCTGTTCTCTA
```

**Protein Sequence:**

```
MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
TWPVKLGWLTTPRGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE
AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH
RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT
EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIKTA
LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
IVNEARIPACSL
```



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	1.27	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	48.07	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.27	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.69	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.14	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.43	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.17	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.13	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.84	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1.16	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.45	<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	0.7	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.04	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.47	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	1.5	<a href="#">[51]</a>
COUSIN18			2.56	
CBI	Codon Bias Index	-1~1	0.23	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.26	<a href="#">[71]</a>



RCA	Relative Codon Adaptation	$\geq 0$	1.11	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.23	<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	$0 \sim 1$	0.49	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.56	<a href="#">[2]</a>
P2	P2 Index	$0 \sim 1$	0.53	<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	$0 \sim 1$	0.4	<a href="#">[1]</a>
GC	GC Content		0.48	
GC1	GC Content at the First Position of Synonymous Codons		0.56	
GC2	GC Content at the Second Position of Synonymous Codons		0.47	
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	$0.5 \sim 1$	0.74	<a href="#">[5]</a>

**Gene Name:** Superoxide Dismutase

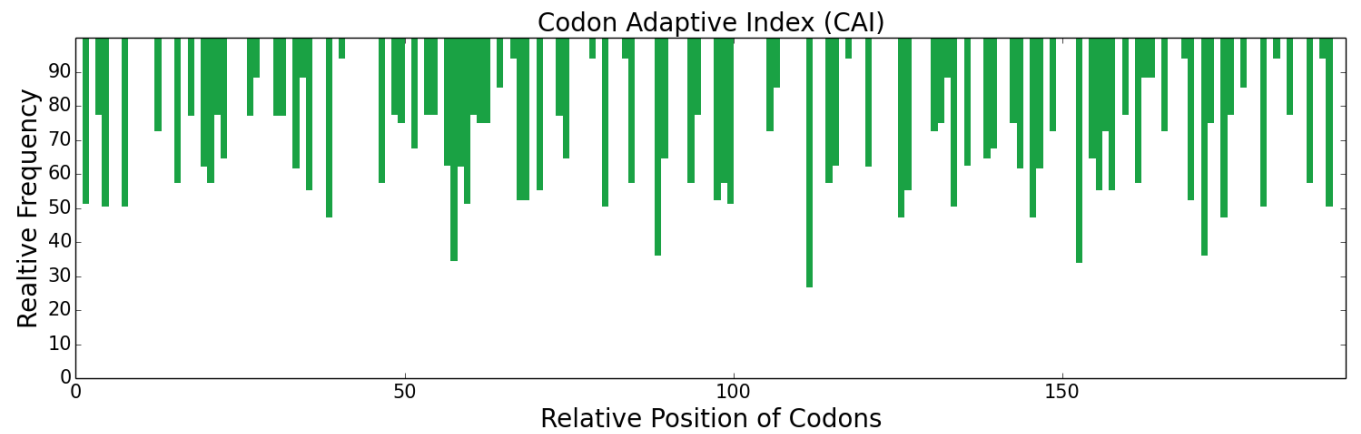
**Reference Source:** Codon Usage Database - Kazusa

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

**DNA Sequence Length:** 579

**DNA Sequence:**  
ATGAGTTTTGAGCTTCCAGCTCTTCCATACGCTAAGGACGCTTTGGCCCCACACATTTCA  
GCCGAGACCATTGAATACCACTATGGTAAGCACCACCAAAACATATGTCACCTAACCTGAAC  
AATTTGATTAAGGGTACTGCCTTTGAGGGAAAGTCCTTGGAGGAGATTATCCGTTCAAGT  
GAGGGAGGAGTTTTCAACAATGCAGCACAAAGTCTGGAACCACACCTTTTACTGGAATTGT  
CTTGCTCCAAATGCCGGTGGTGAACCCACCGGTAAGGTTGCCGAGGCTATTGCAGCCAGT  
TTTGGTTCTTTTGCTGACTTCAAGGCTCAATTTACGGATGCTGCCATCAAGAATTTTGGT  
TCAGGTTGGACTTGGCTGGTCAAGAACTCTGACGGAACAACTTGCTATCGTTTCTACCTCC  
AACGCTGGAACACCACTGACAACTGACGCTACTCCACTATTGACCGTCGACGCTCTGGGAG  
CATGCCTATTATATTGACTACAGAAATGCAAGACCCGGATACCTGGAGCATTCTCTGGGCT  
CTTGTTAATTGGGAGTTTGTGTTGCCAAGAATCTTGCTGCT

**Protein Sequence:**  
MSFELPALPYAKDALAPHISAETIEYHYGKHHQTYVTNLNNLIKGTAFEGKSLEEIIRSS  
EGGVFNNAQVWNHTFYWNCLAPNAGGEPTGKVAEAIASFGSFADFKAQFTDAAIKNFG  
SGWTWLVKNSDGKLAIVSTSNAGTPLTTDATPLLTVDVWEHAYYIDYRNARPGYLEHFWA  
LVNWEFVAKNLAA



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	1.53	<a href="#">[11]</a>

ENC	Effective Number of Codons	20~61	41.25	[2, 3]
RCBS	Relative Codon Bias Strength	$\geq 0$	0.57	[4]
DCBS	Directional Codon Bias Score	$\geq 1$	2.06	[5]
CDC	Codon Deviation Coefficient	0~1	0.23	[6]
MILC	Measure Independent of Length and Composition	-1~1	-0.35	[7]
ICDI	Intrinsic Codon Deviation Index	0~1	0.36	[8]
SCUO	Synonymous Codon Usage Order	0~1	0.3	[9, 10]
Ew	Weighted Sum of Relative Entropy	0~1	0.66	[11]
P	Codon Preference	$\geq 1$	1.35	[12]
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.62	[13]

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

Index	Description	Range	Value	Reference
CAI	Codon Adaptation Index	0~1	0.8	[1]
CFD	Codon Frequency Distribution	0~1	0.01	[2]
FOP	Frequency of Optimal Codons	0~1	0.49	[3, 4]
COUSIN59	Codon Usage Similarity Index	$\infty$	1.06	[5]
COUSIN18			1.36	
CBI	Codon Bias Index	-1~1	0.22	[6]
Dmean	Mean Dissimilarity-based Index	0~2	0.31	[7]
RCA	Relative Codon Adaptation	$\geq 0$	1.14	[8]
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.39	[9]
B	Codon Usage Bias	0~2	0.46	[10]

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

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	0~1	0.57	[1]
gtAI	Genetic tRNA Adaptation Index	0~1	0.66	[2]
P2	P2 Index	0~1	0.52	[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	0.45	[1]
GC	GC Content		0.47	
	GC Content at the First Position			

GC1	of Synonymous Codons		0.52	
GC2	GC Content at the Second Position of Synonymous Codons		0.44	
ENcp	Effective Number of Codon Pairs	20~61	23.87	<a href="#">[2]</a>
CPS	Codon Pair Score	-1~1	-0.05	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	0.5~1	0.76	<a href="#">[5]</a>

**Gene Name:** Alcohol Dehydrogenase

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

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

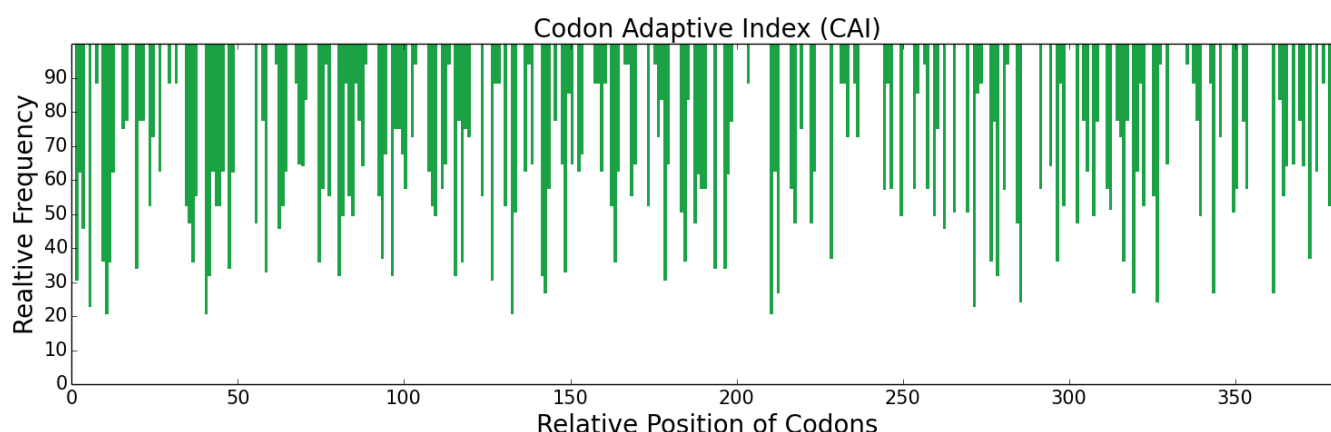
**DNA Sequence Length:** 1146

**DNA Sequence:**

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GAGGAGACTGCAGACTACATCAAGAACAAAGATTATAAGAAGGCACTGATAGTCACTGAT
CCGGGCATCGCAGCAATCGGTCTATCAGGTAGAGTTCAAAAAGATGCTGGAAGAGAGGGAT
TTGAATGTGGCAATCTACGATAAAACCCAGCCTAACCCTAAACATAGCCAATGTCAGTGCT
GGCTTAAAGTCTTAAAGAGCAGAATTCTGAAATTGTCGTATCCATTGGCGGAGGATCC
GCCCATGACAATGCTAAGGCTATCGCATTATTGGCCACCAATGGTGGCGAGATAGGAGAC
TACGAAGGTGTCAACCAATCGAAAAAGCTGCATTGCCGCTTTTGTCTATCAATACCACT
GCTGGCACGGCCTCTGAGATGACCAGGTTACCATTATCTCCAACGAAGAAAAAAAATC
AAAATGGCAATAATCGATAATAATGTCACCCAGCTGTTGCAGTTAATGACCCTTCGACC
ATGTTTGGTCTTCCCCCTGCTCTGACAGCCGCACTGGTCTAGATGCTCTAACACACTGT
ATTGAAGCTTATGTTTCTACTGCTTCTAACCCGATCACGGATGCTTGTGCCCTGAAGGGA
ATTGATCTGATCAACGAATCTTTGGTAGCTGCTTATAAAGACGGTAAAGACAAGAAGGCT
AGAAGTATGATGTGCTATGCCGAATACTTAGCTGGTATGGCCTTCAACAATGCCTCTTTA
GGATACGTGCATGCTCTTGCTCATCAACTTGGTGGGTTCTATCATTTGCCCCACGGCGTT
TGCAATGCTGTTCTGCTCCACATGTTCAAGAAGCCAACATGCAGTGTCCTCAAAGCAAAG
AAGAGACTGGGTGAGATCGCTTTTACACTTTGGTGCCAGTCAAGAGGACCCCGAGGAAACG
ATCAAAGCATTGCATGTCTCAATAGAACCATGAACATTCCAAGAAATTTGAAAGAGTTA
GGTGTTAAAACGGAAGACTTTGAAATCTTGCCGAACACGCCATGCATGATGCTTGTGTCAT
TTGACGAACCTGTCCAGTTTACCAAGGAGCAGGTTGTAGCTATCATTAAGGCATAC
GAATAC
```

**Protein Sequence:**

```
MSSVTGFYIPPIISFFGEGALEETADYIKNKDYKKALIVTDPGIAAIGLSGRVQKMLEERD
LNVAIYDKTQPNPNIANVTAGLKVLEQNSEIVVSIGGSAHDNAKAIALLATNGGEIGD
YEGVNQSKKAALPLFAINTTAGTASEMTRFTIISNEEKKIKMAIDNNVTPAVAVNDPST
MFGLPPALTAATGLDALTHCIEAYVSTASNPITDACALKGIDLINESLVAAYKDGDKKA
RTDMCYAEYLAGMAFNNASLGYVHALAHQLGGFYHLPHGVCNAVLLPHVQEANMQCPKAK
KRLGEIALHFGASQEDPEETIKALHVLNRTMNI PRNLKELGVKTEDFEILAEHAMHDACH
LTNPVQFTKEQVVAIIKKAYEY
```



Negative CIS Elements	Negative repeat Elements
2	0

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

Index	Description	Range	Value	Reference
RSCU	Relative Synonymous Codon Usage	0~6	1.19	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	51.04	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.19	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.53	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.13	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.48	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.09	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.09	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.88	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1.09	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.29	<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	0.73	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.03	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.44	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.52	<a href="#">[51]</a>
COUSIN18			0.82	
CBI	Codon Bias Index	-1~1	0.15	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.25	<a href="#">[71]</a>

RCA	Relative Codon Adaptation	$\geq 0$	1.07	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.2	<a href="#">[9]</a>
B	Codon Usage Bias	$0 \sim 2$	0.23	<a href="#">[10]</a>

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

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	$0 \sim 1$	0.52	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.61	<a href="#">[2]</a>
P2	P2 Index	$0 \sim 1$	0.55	<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	$0 \sim 1$	0.44	<a href="#">[1]</a>
GC	GC Content		0.45	
GC1	GC Content at the First Position of Synonymous Codons		0.52	
GC2	GC Content at the Second Position of Synonymous Codons		0.38	
ENcp	Effective Number of Codon Pairs	$20 \sim 61$	31.72	<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:** Nattokinase

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

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

**DNA Sequence Length:** 1143

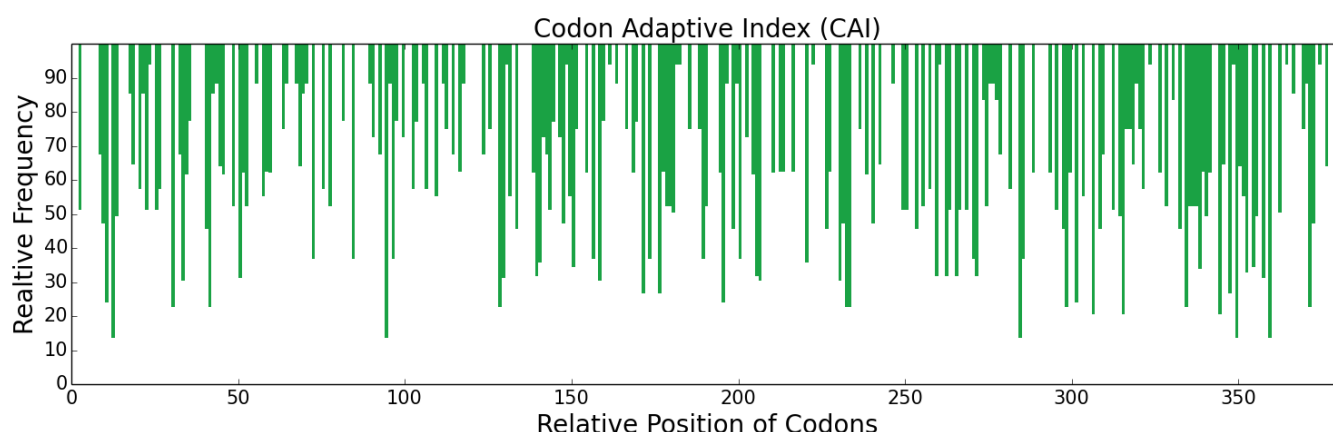
**DNA Sequence:**

```
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GCCTTCAGTAATATGAGTGCCCAAGCTGCTGGGAAGTCCCTCGACAGAGAAGAAGTACATT
GTGGGGTTCAAACAGACAATGTCTGCAATGAGCTCAGCAAAGAAGAAAGATGTCATCTCA
GAAAAGGGTGGAAAAGTTCAAAAACAGTTCAAATACGTAAACGCTGCCGCTGCAACTTTG
GATGAGAAGGCTGTAAAGGAATTGAAGAAAGACCCATCCGTTGCGTATGTAGAGGAAGAC
CATATTGCCACGAATATGCCCAATCTGTCCCATATGGAATTTCCCAAATCAAAGCTCCA
GCTTTGCATTCCCAAGGATACACTGGGAGCAATGTCAAGGTGGCTGTTATTGATTCAGGC
ATAGACTCCAGTCACCCAGACCTGAATGTCCGTGGAGGTGCTTCATTTGTACCATCGGAG
ACTAATCCATATCAAGATGGATCTTCACACGGTACGCATGTAGCTGGTACGATCGCAGCA
CTTAATAATTCTATTGGAGTTTTGGGAGTAGCACCATCTGCTTCACTCTATGCTGTGAAA
GTATTGGACTCTACAGGCTCGGGTCAATACTCATGGATCATCAACGGTATCGAATGGGCT
ATATCTAATAACATGGATGTGATCAACATGTCGCTGGGGGGGCCAACTGGATCTACAGCT
CTGAAGACCGTTGTTGATAAAGCTGTTAGTAGTGGTATTGTGGTTGCAGCTGCCGCTGGC
AATGAAGGCAGTTCTGGCAGTACTAGTACTGTAGGCTACCCTGCAAAATATCCTTCCACT
ATTGCCGTTGGTGCGGTAAACTCTTCAAACCAAAGAGCTTCATTTAGTTCTGTGGGGTCA
GAACTCGATGTCATGGCTCCGGGTGTGTCCATTCAAAGTACTTTACCGGGAGGAACCTAT
GGAGCCTACAATGGTACTTCAATGGCAACTCCTCATGTGGCTGGGGCAGCAGCACTAATC
TTATCAAAGCATCCGACCTGGACGAATGCGCAGGTCAGGGATCGTTTAGAAAGCACTGCG
ACTTACCTTGGAATTCTTTCTACTACGAAAAGGGCTGATTAATGTTTCAGGCTGCTGCT
CAA
```

**Protein Sequence:**

```
MRSKKLWISLLFALTLIFTMAFSNMSAQAAGKSSTEEKYIVGFKQTMSAMSSAKKKDVIS
EKGGKVQKQFKYVNAAAATLDEKAVKELKKDPSVAYVEEDHIAHEYAQSVPYGISQIKAP
ALHSQGYTGSNVKVAVIDSGIDSSHPDLNVRGGASFVPSETNPYQDGSSHGTHVAGTIAA
LNNSIGVLGVAPSASLYAVKVLDTGSGQYSWIINGIEWAISNNMDVINMSLGGPTGSTA
LKTVVDAKAVSSGIVVAAAAGNEGSSGSTSTVGYPKYPSTIavgavNssNQRASFSSVGS
ELDVMAPGVSIQSTLPGGTYGAYNGTSMATPHVAGAAALILSKHPTWTNAQVRDRLESTA
TYLGNSFYYGKGLINVQAAAQ
```





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	1.16	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	55.22	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.21	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.57	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.12	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.5	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.09	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.08	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.89	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1.07	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.28	<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	0.7	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.06	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.43	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.43	<a href="#">[51]</a>
COUSIN18			0.35	
CBI	Codon Bias Index	-1~1	0.18	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.34	<a href="#">[71]</a>

RCA	Relative Codon Adaptation	$\geq 0$	1.06	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.18	<a href="#">[9]</a>
B	Codon Usage Bias	$0 \sim 2$	0.24	<a href="#">[10]</a>

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

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	$0 \sim 1$	0.49	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.58	<a href="#">[2]</a>
P2	P2 Index	$0 \sim 1$	0.59	<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	$0 \sim 1$	0.4	<a href="#">[1]</a>
GC	GC Content		0.46	
GC1	GC Content at the First Position of Synonymous Codons		0.5	
GC2	GC Content at the Second Position of Synonymous Codons		0.48	
ENcp	Effective Number of Codon Pairs	$20 \sim 61$	32.73	<a href="#">[2]</a>
CPS	Codon Pair Score	$-1 \sim 1$	0.04	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	$0.5 \sim 1$	0.74	<a href="#">[5]</a>

**Gene Name:** Hyaluronidase-1

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

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

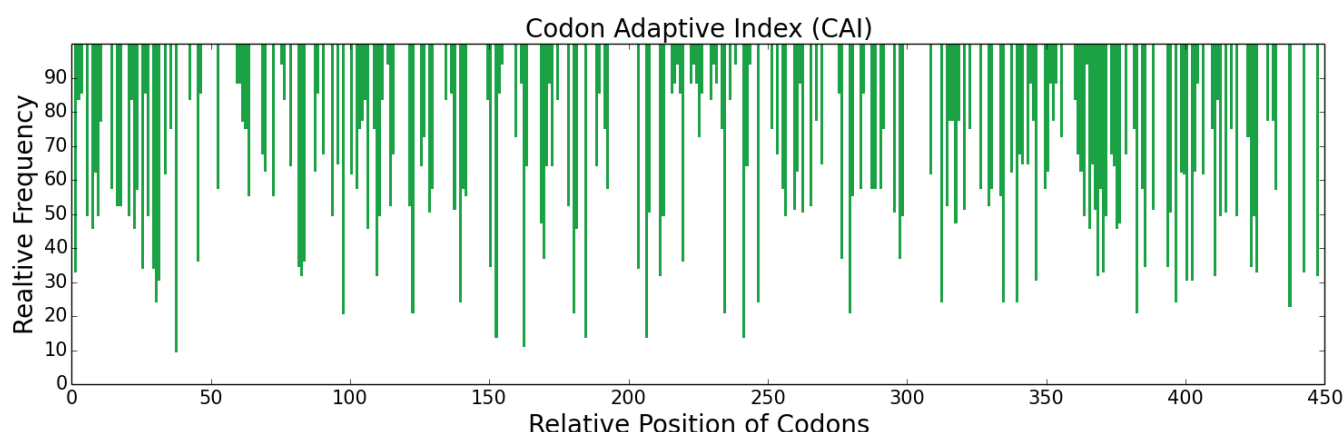
**DNA Sequence Length:** 1350

**DNA Sequence:**

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GTTGTTTCTTAACCAACCCTTCACTACTATTTGGAACGCCAACACTGAATGGTGTATGAAA
AAACACGGAGTCGATGTTGATATTTCCATCTTTGATGTGCGTTACTAATCCTGGTCAGACT
TTTCGTGGCCCCAACATGACTATCTTCTACTCCTCTCAATTAGGTACCTACCCGTACTAC
ACATCTGCCGGAGAGCCTGTGTTTGGAGGCTTACCTCAAAATGCATCCTTGAACGCTCAT
TTGGCAGCAACTTTTCAGGACATTCTTGCCGCTATGCCAGAACCTAGATTCAAGTGGTCTC
GCCGTCATTGATTGGGAAGCTTGGAGACCTCGTTGGGCGTTCAATTGGGATACTAAGGAC
ATTTATCGCCAGAGATCTAGAGCTCTGGTACAGAAACAGCATCCTGATTGGTTGGCACCA
CGAGTGGAAGCTGCCGGCTCAAGATCAGTTCGAAGGAGCCGCTGAAGAATGGATGGCTGGT
ACTTTGAAGCTAGGTCAAGCGCTTAGACCACAAGGCTTATGGGGTTTCTATAAATTTCCCC
GAATGTTATAATTATGACTTCAAGTCTCCTAATTATACTGGACGATGTCCTTTGAATATT
TGTGCGCAGAATGATCAACTCGGTTGGTTGTGGGGACAATCCAGAGCCTTATACCCAAGT
ATCTATCTTCCAGCTGCATTGGAGGGTACCAAGAAGACTCAAAATGTTTCGTACAACATCGA
GTCGCTGAAGCCTTCAGAGTTGCCGCCGGTGCCGGAGATCCAAAGCTTCCAGTATTACCA
TACATGCAATTGTTTTACGATATGACAAACCATTTTCTCCCAGCAGAGGAGCTGGAGCAT
AGTTTGGGAGAATCTGCTGCCCAAGGTGCAGCCGGTGTGTCTCTGGGTTTCATGGCTC
TCCACCTCTACCAAGAGTCGTGTCAAGCCATCAAAGAGTATGTTGACACTACTTTGGGT
CCTTCCATCTTAAATGTGACCAGTGGCGCCAGGTTATGTTCCCAGGTGCTGTGTTCCGGT
CATGGACGATGTGCCCGTAGACCAAGTTACCCAAAGGCTCGTCTTATTCTCAACTCAACA
TCGTTTTTCGATCAAACCAACACCAGGTGGAGGCCCTTAACTCTTCAAGGAGCTTTATCT
TTGGAAGACCGTTTAAGGATGGCTGTTGAGTTTGAGTGCAGATGTTACAGAGGGTGGAGA
GGTACTAGGTGTGAACAATGGGGCATGTGG
```

**Protein Sequence:**

```
MRPFSLEVSLHLPWMAAHLLPVCTLFLNLLSMTQGSRDVPVVPNPFTTIWNANTEWCMK
KHGVDVDISIFDVVTNPGQTFRGPNTIFYSSQLGTYPPYTSAGEPVFGGLPQNASLNAH
LARTFQDILAAMPEPRFSGLAVIDWEAWRPRWAFNWDTKDIYRQRSRALVQKQHPDWLAP
RVEAAAQDQFEGAAEEWMAGTLKLGQALRPQGLWGFYNFPECYNYDFKSPNYTGRCPINI
CAQNDQLGWLWGQSRALYPSIYLPAALEGTKKTKMFVQHRVAEAFRVAAGAGDPKLPVLP
YMQLFYDMTNHFLPAEELEHSLGESAAQGAAGVVLWVSWLSTSTKESCQAIKEYVDTTLG
PSILNVTSGARLCSQVLCSGHGRCARRPSYPKARLILNSTSFSIKPTPGGGPLTLQGALS
LEDRLRMAVEFECRCYRGWRGTRCEQWGMW
```



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	1.22	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	50.12	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.26	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.69	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.14	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.43	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.13	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.12	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.81	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1.13	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.44	<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	0.72	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.04	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.47	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.96	<a href="#">[51]</a>
COUSIN18			1.18	
CBI	Codon Bias Index	-1~1	0.22	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.16	<a href="#">[71]</a>

RCA	Relative Codon Adaptation	$\geq 0$	1.13	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.18	<a href="#">[9]</a>
B	Codon Usage Bias	$0 \sim 2$	0.23	<a href="#">[10]</a>

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

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	$0 \sim 1$	0.48	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.55	<a href="#">[2]</a>
P2	P2 Index	$0 \sim 1$	0.59	<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	$0 \sim 1$	0.41	<a href="#">[1]</a>
GC	GC Content		0.47	
GC1	GC Content at the First Position of Synonymous Codons		0.52	
GC2	GC Content at the Second Position of Synonymous Codons		0.49	
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	$0.5 \sim 1$	0.75	<a href="#">[5]</a>

**Gene Name:** Laccase

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

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

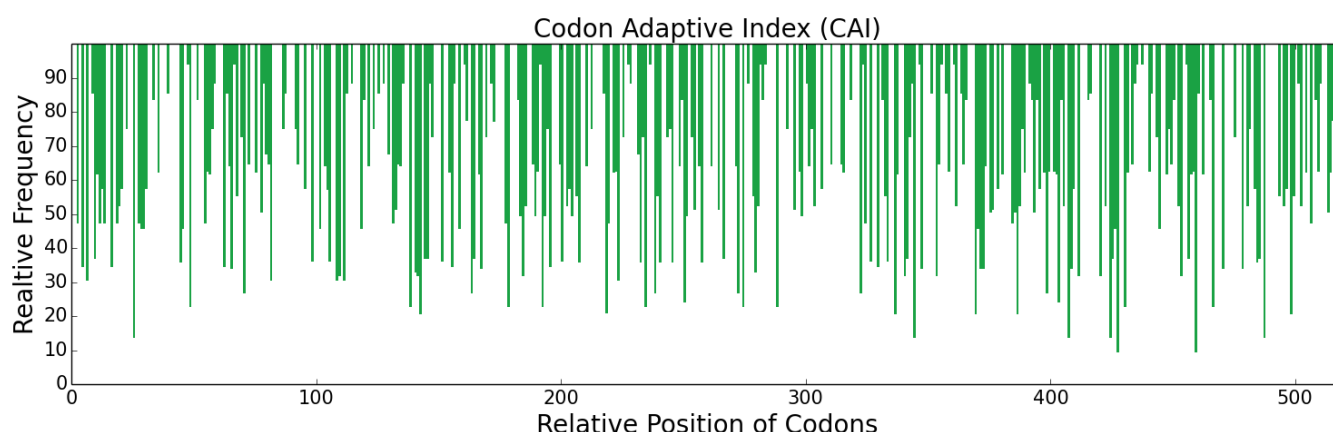
**DNA Sequence Length:** 1557

**DNA Sequence:**

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GCCATTGGACCAGTTGCGTCTCTGGTGGTGGCCAACGCTCCTGTTTCACCAGATGGTTTC
TTGAGAGATGCTATAGTGGTTAATGGGGTTGTTCCCTTCTCCACTGATCACAGGAAAAAAG
GGTGATCGTTTTCCAGCTAAATGTCGATGACACGTTGACCAACCATTCAATGCTTAAATCC
ACCTCGATTTCATTGGCATGGATTCTTTCAAGCTGGAACCAACTGGGCCGATGGTCCCGCT
TTTGTGAACCAGTGCCCCATTGCTTCGGGCCATTTCGTTCTTGATGATTTTCATGTGCCT
GATCAGGCTGGAACCTTCTGGTATCATTCCCATCTGAGTACCCAGTATTGTGATGGGTTG
AGGGGCCCCGTTTGTAGTATATGACCCAAAGGATCCCCATGCTTCACGTTATGATGTGGAT
AATGAGTCTACGGTAATTACACTAACTGACTGGTATCACACTGCTGCTAGACTGGGGCCA
AGATTTTCCTTTAGGCGCAGATGCTACCTTAATCAATGGGTTAGGACGTTCTGCTTCTACC
CCCACTGCAGCCTTAGCTGTCATAAACGTTTCAGCATGGAAAAGAGATACAGATTCCGACTG
GTTTCAATCTCGTGTGACCCAAATTATACTTTTTCCATAGACGGGCATAATTTGACGGTC
ATAGAAGTTGACGGAATAAACTCTCAGCCTCTCTTAGTTGACAGTATTCAGATATTTGCT
GCTCAGAGATACAGTTTTGTATTGAACGCTAACCAGACGGTTGGGAACTATTGGGTCAGG
GCAAAATCCTAATTTTGGTACTGTTGGGTTTGCTGGTGGAATTAACAGTGCTATCTTAAGA
TATCAGGGGAGCACCAGTTGCCGAACCAACTACCACTCAAACCTACCTCAGTTATTCCTTTG
ATTGAAACGAATCTGCATCCCTTGGCTCGTATGCCTGTCCCCGGTTCTCCGACACCAGGT
GGCGTAGACAAAGCGTTGAATCTAGCTTTTAACTTCAACGGCACCAATTTTTTTCATCAAC
AATGCAACTTTTACCCCTCCAACGTTCCGGTGCTACTACAGATTCTTAGTGGTGCCCAA
ACAGCTCAAGATCTGCTTCCGGCAGGATCAGTTTATCCTCTTCCTGCCATTCAACGATC
GAAATCACACTCCCTGCAACTGCGCTAGCCCCAGGCGCTCCACATCCTTTCCATTTGCAT
GGCCATGCATTTGCGGTAGTGCGGTCTGCTGGGTCAACTACCTATAATTACAATGATCCA
ATCTTCAGAGACGTGGTTTCTACAGGAACCCCTGCTGCAGGCGATAATGTAACAATCCGG
TTCCAAACAGATAACCCTGGGCCATGGTTTCTACATTGTCATATTGACTTTCATCTAGAT
GCAGGATTTGCCATAGTATTTGCGGAAGATGTTGCTGATGTCAAGGCAGCCAACCCGGTC
CCAAAAGCATGGTCAGATCTGTGTCCTATCTATGATGGTCTTTCAGAGGCCAATCAA
```

**Protein Sequence:**

```
MGLQRFSSFFVTALVARSLAAIGPVASLVVANAPVSPDGFLRDAIVVNGVVPSPLITGKK
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DQAGTFWYHSHLSTQYCDGLRGPFVVYDPKDPHASRYDVNNESTVITLTDWYHTAARLGP
RFPLGADATLINGLGRSASTPTAALAVINVQH GKRYRFRFLVSI SCDPNYTFSIDGHNLTV
IEVDGINSQPLLVD SIQIFAAQRYSFVLNANQTVGNYWVRANPNFGTVGFAGGINSAILR
YQGAPVAEPTTTQTTSVIPLIETNLHPLARMPVPGSPTPGGVDKALNLAFNFGNTNFFIN
NATFTPTVPVLLQILSGAQTAQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPFHLH
GHAFVVR SAGSTTYNYNDPIFRDVVSTGTPAAGDNVTIRFQTDNPGPWFLHCHIDFHLD
AGFAIVFAEDVADVKAANPVPKAWSDLCP IYDGLSEANQ
```



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	1.18	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	52.96	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.16	<a href="#">[41]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.53	<a href="#">[51]</a>
CDC	Codon Deviation Coefficient	0~1	0.1	<a href="#">[61]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.47	<a href="#">[71]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.14	<a href="#">[81]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.1	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.88	<a href="#">[111]</a>
P	Codon Preference	$\geq 1$	1.08	<a href="#">[121]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.3	<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	0.69	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.06	<a href="#">[21]</a>
FOP	Frequency of Optimal Codons	0~1	0.42	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.7	<a href="#">[51]</a>
COUSIN18			0.65	
CBI	Codon Bias Index	-1~1	0.15	<a href="#">[61]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.32	<a href="#">[71]</a>

RCA	Relative Codon Adaptation	$\geq 0$	1.04	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.2	<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="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.56	<a href="#">[2]</a>
P2	P2 Index	$0 \sim 1$	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	$0 \sim 1$	0.38	<a href="#">[1]</a>
GC	GC Content		0.47	
GC1	GC Content at the First Position of Synonymous Codons		0.56	
GC2	GC Content at the Second Position of Synonymous Codons		0.46	
ENcp	Effective Number of Codon Pairs	$20 \sim 61$	37.18	<a href="#">[2]</a>
CPS	Codon Pair Score	$-1 \sim 1$	0.07	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	$0.5 \sim 1$	0.74	<a href="#">[5]</a>



**Gene Name:** Renin

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

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

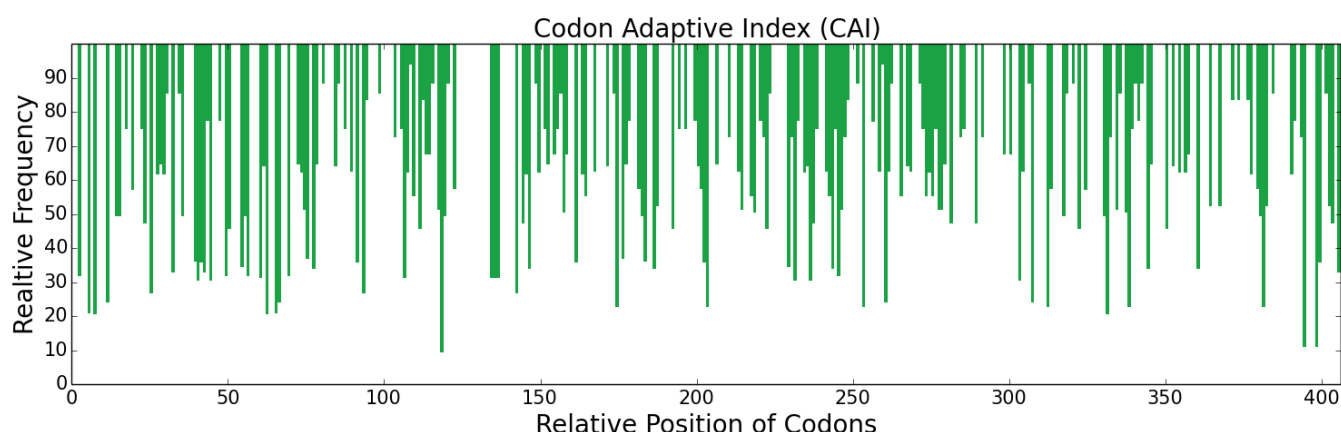
**DNA Sequence Length:** 1218

**DNA Sequence:**

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AGCCAGCCGATGAAGCGACTCACTTTGGGCAACACTACCTCAAGTGTAAATCTAACCAAC
TATATGGATACTCAGTATTACGGAGAAAATCGGTATAGGTACGCCTCCACAACTTTCAAG
GTTGTTTTTGGACTGGAAGCTCAAATGTCTGGGTGCCTTCCTCCAAATGTAGTCGGTTA
TATACTGCCTGTGTTTACCATAAGTTGTTTGATGCTTCTGATAGCAGCAGCTACAAGCAT
AACGGTACGGAAGTACACTAAGATATTCAACTGGAACCGTTTCCGGATTCCCTTTCCCAA
GATATAATTACAGTCGGTGGTATCACTGTTACTCAGATGTTCTGGGGAAGTAACCGAGATG
CCAGCCTTACCCTTTATGCTAGCAGAATTTGATGGTGTGGTTGGAATGGGATTTATTGAG
CAGGCCATAGGGAGAGTTACCCCAATTTTTGACAACATTATCAGTCAAGGTGTCCTTAAG
GAGGACGTGTTCTCTTTTTACTACAACCGTGACTCGGAGAACTCACAGTCGCTGGGAGGT
CAAATCGTCCTAGGAGGCAGTGACCCCTCAACATTATGAAGGGAACTTTCACTACATCAAT
CTCATCAAAACTGGTGTCTGGCAGATCCAAATGAAAGGAGTCTCAGTCGGAAGTAGTACC
TTGCTGTGTGAAGACGGATGTTTGGCTCTGGTTGACACTGGTGCTTCTTACATTTCCGGT
TCCACTTCTTCGATCGAAAAACTCATGGAAGCTTTGGGGGCCAAGAAGAGATTATTCGAT
TATGTTGTGAAGTGCAACGAAGGTCCAACCTTTACCGGACATTAGTTTCCATCTTGGGGGA
AAAGAGTATACTCTAACCTCTGCTGATTACGTGTTTCAGGAATCATACTCATCCAAGAAG
CTATGTACTTTGGCAATTCATGCAATGGATATTCCTCCACCTACTGGTCCTACATGGGCC
TTAGGGGCAACTTTCATTAGAAAGTTTTACACAGAGTTTGACCGCAGAAACAACCGCATA
GGTTTCGCACTGGCTAGG
```

**Protein Sequence:**

```
MDGWRRMPRWGLLLLLLWGSCTFGLPTDTTTTFKRIFLKRMPSSIRESLKERGVDMARLGPEW
SQPMKRLTLGNTTSSVILTNYMDTQYYGEIGIGTPPQTFKVVFDTGSSNVWVPSSKCSRL
YTACVYHKLFDAASDSSSYKHNGTELTLRYSTGTVSGFLSQDIITVGGITVTQMFGEVTEM
PALPFMLAEFDGVVGMGFIEQAIGRVTPIFDNIISQGVLKEDVFSFYNNRDSSENSQSLGG
QIVLGGSDPQHYEGNFHYINLIKTVWQIQMKGVSVGSSTLLCEDGCLALVDTGASYISG
STSSIEKLMEALGAKKRLFDYVVKCNEGPTLPDISFHLGGKEYTLTSADYVFQESYSSKK
LCTLAIHAMDIPPTGPTWALGATFIRKFYTEFDRRNNRIGFALAR
```



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	1.13	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	54.99	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.18	<a href="#">[4]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.51	<a href="#">[5]</a>
CDC	Codon Deviation Coefficient	0~1	0.1	<a href="#">[6]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.51	<a href="#">[7]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.11	<a href="#">[8]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.08	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.87	<a href="#">[11]</a>
P	Codon Preference	$\geq 1$	1.08	<a href="#">[12]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.26	<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	0.7	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.05	<a href="#">[2]</a>
FOP	Frequency of Optimal Codons	0~1	0.45	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	1.85	<a href="#">[5]</a>
COUSIN18			2.72	
CBI	Codon Bias Index	-1~1	0.19	<a href="#">[6]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.28	<a href="#">[7]</a>

RCA	Relative Codon Adaptation	$\geq 0$	1.1	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	$0 \sim \sqrt{2}$	0.15	<a href="#">[9]</a>
B	Codon Usage Bias	$0 \sim 2$	0.2	<a href="#">[10]</a>

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

Index	Description	Range	Value	Reference
tAI	tRNA Adaptation Index	$0 \sim 1$	0.5	<a href="#">[11]</a>
gtAI	Genetic tRNA Adaptation Index	$0 \sim 1$	0.57	<a href="#">[2]</a>
P2	P2 Index	$0 \sim 1$	0.6	<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	$0 \sim 1$	0.46	<a href="#">[11]</a>
GC	GC Content		0.45	
GC1	GC Content at the First Position of Synonymous Codons		0.45	
GC2	GC Content at the Second Position of Synonymous Codons		0.44	
ENcp	Effective Number of Codon Pairs	$20 \sim 61$	38.39	<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: Avidin

Reference Source: Codon Usage Database - Kazusa

Expression Host Organism: Pichia pastoris (budding yeasts)

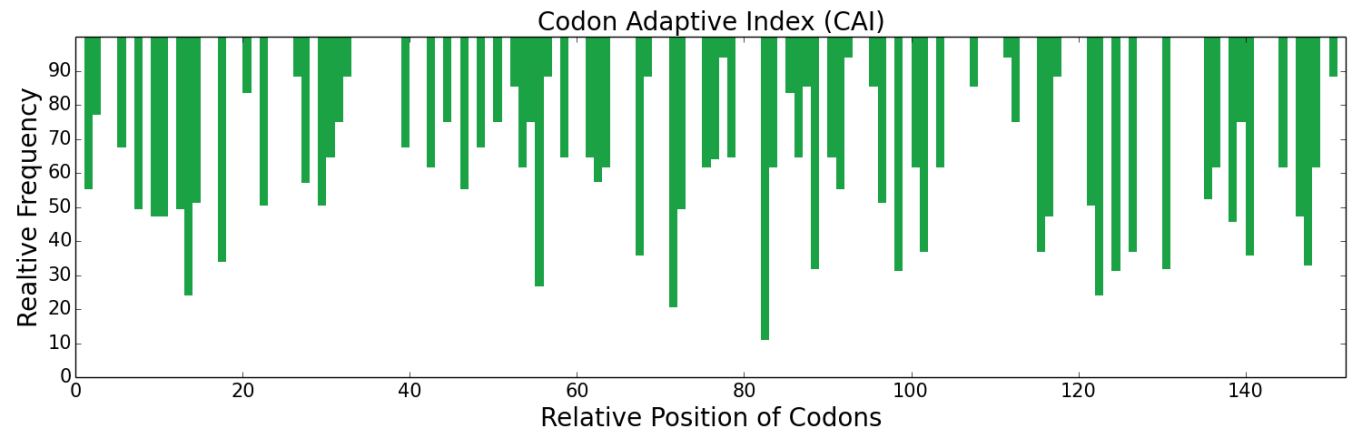
DNA Sequence Length: 456

DNA Sequence:

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AACATGACAATTGGAGCTGTCAACTCCAGAGGAGAATTCACAGGAACGTATATTACCGCT  
GTTACCGCCACATCTAACGAAATAAAAGAATCTCCGTTACATGGTACACAGAATACCATT  
AACAAAGCGCACACAACCTACCTTCGGCTTTACCGTCAATTGGAAGTTCAGTGAAAGCACT  
ACAGTATTTACAGGTCAATGTTTCATTGATAGAAATGGAAAGGAAGTACTGAAAACATG  
TGGCTTCTCAGAAGCTCTGTAAACGATATTGGCGATGATTGGAAGGCAACAAGAGTGGGA  
ATAAACATTTTTTACAAGACTGAGGACACAAAAAGAA

Protein Sequence:

MVHATSPLLLLLLLLLSLALVAPGLSARKCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYITA  
VTATSNEIKESPLHGTQNTINKRTQPTFGFTVNWKFSESTTVFTGQCfidrngkeVLKTM  
WLLRSSVNDIGDDWKATRVGINIFTRLRTQKE



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	1.5	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	43.73	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	≥0	0.42	<a href="#">[41]</a>

DCBS	Directional Codon Bias Score	$\geq 1$	1.86	<a href="#">[5]</a>
CDC	Codon Deviation Coefficient	0~1	0.18	<a href="#">[6]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.47	<a href="#">[7]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.31	<a href="#">[8]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.25	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.7	<a href="#">[11]</a>
P	Codon Preference	$\geq 1$	1.26	<a href="#">[12]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.54	<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	0.73	<a href="#">[1]</a>
CFD	Codon Frequency Distribution	0~1	0.03	<a href="#">[2]</a>
FOP	Frequency of Optimal Codons	0~1	0.47	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	1.75	<a href="#">[5]</a>
COUSIN18			1.06	
CBI	Codon Bias Index	-1~1	0.23	<a href="#">[6]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.4	<a href="#">[7]</a>
RCA	Relative Codon Adaptation	$\geq 0$	1.12	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.36	<a href="#">[9]</a>
B	Codon Usage Bias	0~2	0.46	<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	0.48	<a href="#">[1]</a>
gtAI	Genetic tRNA Adaptation Index	0~1	0.57	<a href="#">[2]</a>
P2	P2 Index	0~1	0.57	<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	0.38	<a href="#">[1]</a>
GC	GC Content		0.41	
GC1	GC Content at the First Position of Synonymous Codons		0.4	
GC2	GC Content at the Second Position of Synonymous Codons		0.47	

ENcp	Effective Number of Codon Pairs	20~61	24.11	<a href="#">[2]</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="#">[5]</a>

**Gene Name:** GFP

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

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

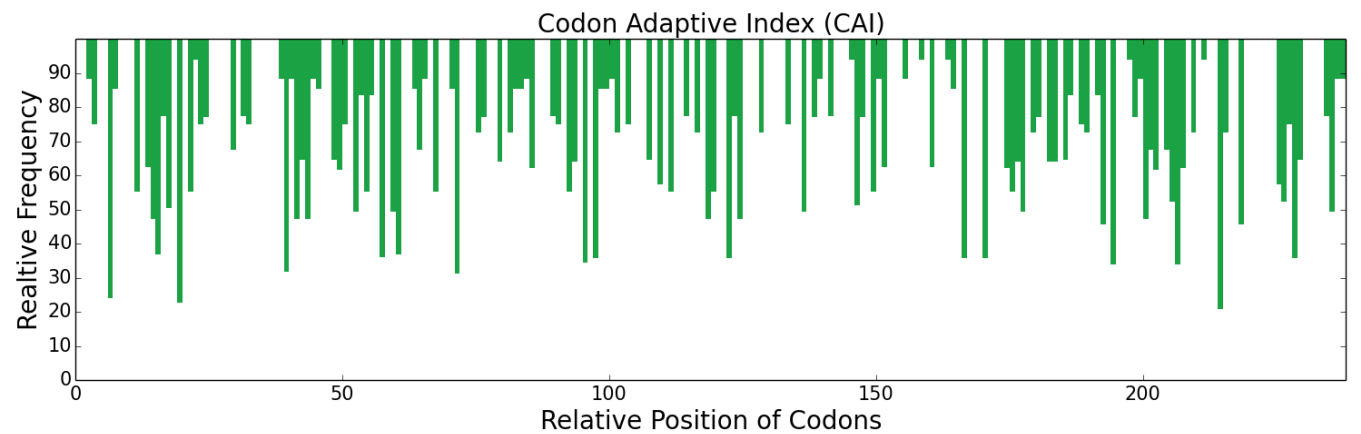
**DNA Sequence Length:** 714

**DNA Sequence:**

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AAACTGACCCTGAAATTCATTTGTACCACAGGAAAAGTTACCTGTCCCTTGGCCCACTTTA  
GTAAGTACTTTCTCCTATGGTGTCCAATGTTTCAGCAGATACCCAGACCACATGAAGCAG  
CATGACTTCTTCAAATCAGCTATGCCAGAGGGATACGTCCAGGAACGTACTATATTCTTC  
AAAGACGATGGAACTACAAGACCAGAGCCGAAGTCAAGTTTGAGGGTGACACTCTGGTC  
AACAGAATAGAGCTGAAGGGTATTGACTTTAAGGAAGATGGAAACATTTTAGGTCACAAA  
TTGGAGTACAACACTACAATAGTCACAACGTCTATATCATGGCTGATAAACAAAAGAATGGT  
ATCAAGGTAAATTTCAAGATAAGACATAACATAGAAGATGGTTCAGTCCAGTTAGCTGAC  
CACTACCAGCAGAACACCCCTATTGGAGACGGTCCTGTGTTGCTACCAGATAATCACTAT  
CTGTCCACACAATCCGCACTATCAAAGGACCCAAATGAAAAGCGAGACCATATGGTGTG  
TTGGAATTTGTTACTGCCGCAGGAATAACCCATGGTATGGATGAGTTATATAAA

**Protein Sequence:**

MSKGEELFTGVVPILEVELDGDVNGHKFSVSSEGEEDATYGKLTCLKFICTTGKLPVPWPTL  
VTTFSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEQDTLV  
NRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNFKIRHNIEDGSGVQLAD  
HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDMVLLEFVTAAGITHGMDELYK



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	1.29	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	48.41	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.3	<a href="#">[4]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.76	<a href="#">[5]</a>
CDC	Codon Deviation Coefficient	0~1	0.14	<a href="#">[6]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.49	<a href="#">[7]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.16	<a href="#">[8]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.13	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.84	<a href="#">[11]</a>
P	Codon Preference	$\geq 1$	1.17	<a href="#">[12]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.36	<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	0.77	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.01	<a href="#">[2]</a>
FOP	Frequency of Optimal Codons	0~1	0.44	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.7	<a href="#">[5]</a>
COUSIN18			0.75	
CBI	Codon Bias Index	-1~1	0.13	<a href="#">[6]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.25	<a href="#">[7]</a>
RCA	Relative Codon Adaptation	$\geq 0$	1.12	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.25	<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	0.54	<a href="#">[11]</a>
gtAI	Genetic tRNA Adaptation Index	0~1	0.62	<a href="#">[2]</a>
P2	P2 Index	0~1	0.66	<a href="#">[3]</a>

### Indices based on complex patterns of codon usage

Index	Description	Range	Value	Reference
			0.45	



GC	GC Content	0~1	0.43	<a href="#">[1]</a>
GC1 GC3	GC Content at the First Position GC Content at the Third Position of Synonymous Codons		0.51	
GC2	GC Content at the Second Position of Synonymous Codons		0.32	
ENcp	Effective Number of Codon Pairs	20~61	20.61	<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	0.77	<a href="#">[5]</a>

**Gene Name:** RFP

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

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

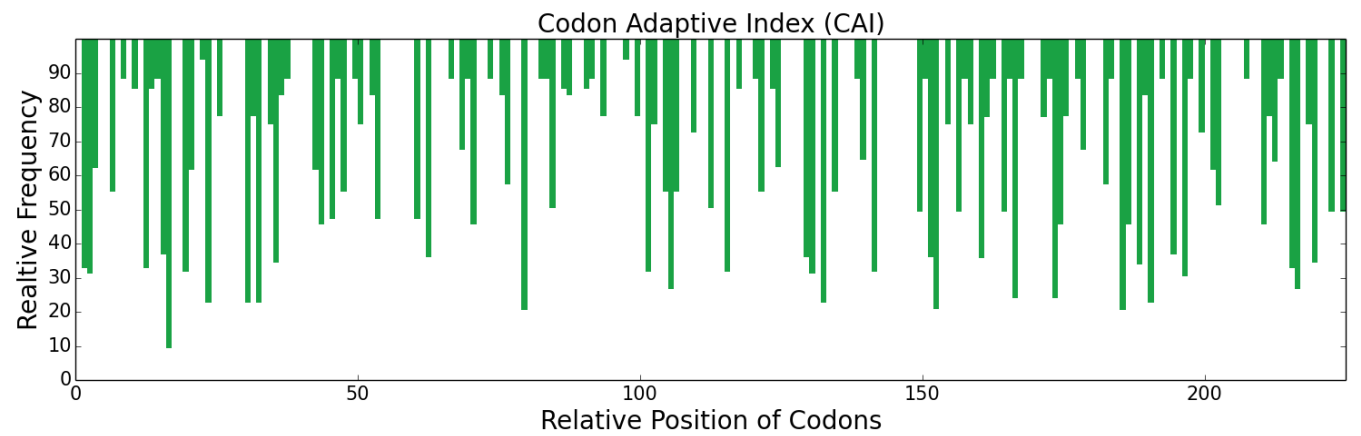
**DNA Sequence Length:** 675

**DNA Sequence:**

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ACAGTTAATGGGCATGAGTTTGAAATTGAAGGGGAGGGGGAAGGACGTCCTTATGAAGGT  
CATAACACAGTGAAGCTGAAAGTCACTAAAGGAGGTCCTCTGCCATTTGCTTGGGATATT  
CTGTCTCCCCAATTTCAATATGGTTCCAAAGTGTACGTTAAACATCCTGCCGATATTCCG  
GATTACAAAAAAGCTTTCTTTCCCTGAAGGTTTCAAATGGGAGAGAGTTATGAATTTTGAG  
GATGGCGGAGTTGTACGGTCACTCAAGACTCTTCTCTCAAGATGGCTGTTTCATTTAC  
AAAGTCAAGTTCATCGGTGTTAACTTTCCAGCGATGGGCCAGTCATGCAAAAGAAAACC  
ATGGGCTGGGAAGCTTCTACTGAAAGATTATATCCCCGAGATGGAGTTTTAAAAGGAGAA  
ATACACAAAGCTTTAAAGCTCAAAGATGGTGGTCACTATCTCGTGGAGTTTAAATCCATT  
TACATGGCCAAAAGCCGGTGCAACTACCTGGGTACTATTACGTAGATTGCGAAATTGGAC  
ATTACAAGTCATAACGAAGATTATACTATTGTGGAGCAGTATGAAAGGACGGAAGGACGT  
CATCATTTATTTT

**Protein Sequence:**

MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDI  
LSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIY  
KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSI  
YMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL



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	1.22	<a href="#">[11]</a>
ENC	Effective Number of Codons	20~61	56.95	<a href="#">[2, 3]</a>
RCBS	Relative Codon Bias Strength	$\geq 0$	0.29	<a href="#">[4]</a>
DCBS	Directional Codon Bias Score	$\geq 1$	1.7	<a href="#">[5]</a>
CDC	Codon Deviation Coefficient	0~1	0.15	<a href="#">[6]</a>
MILC	Measure Independent of Length and Composition	-1~1	-0.54	<a href="#">[7]</a>
ICDI	Intrinsic Codon Deviation Index	0~1	0.23	<a href="#">[8]</a>
SCUO	Synonymous Codon Usage Order	0~1	0.14	<a href="#">[9, 10]</a>
Ew	Weighted Sum of Relative Entropy	0~1	0.82	<a href="#">[11]</a>
P	Codon Preference	$\geq 1$	1.11	<a href="#">[12]</a>
MCB	Maximum-likelihood Codon Bias	$\geq 0$	0.29	<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	0.72	<a href="#">[11]</a>
CFD	Codon Frequency Distribution	0~1	0.06	<a href="#">[2]</a>
FOP	Frequency of Optimal Codons	0~1	0.45	<a href="#">[3, 4]</a>
COUSIN59	Codon Usage Similarity Index	$\infty$	0.38	<a href="#">[5]</a>
COUSIN18			1.46	
CBI	Codon Bias Index	-1~1	0.14	<a href="#">[6]</a>
Dmean	Mean Dissimilarity-based Index	0~2	0.45	<a href="#">[7]</a>
RCA	Relative Codon Adaptation	$\geq 0$	1.08	<a href="#">[8]</a>
CUFS	Codon Usage Frequency Similarity	0~ $\sqrt{2}$	0.28	<a href="#">[9]</a>
B	Codon Usage Bias	0~2	0.38	<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	0.5	<a href="#">[11]</a>
gtAI	Genetic tRNA Adaptation Index	0~1	0.57	<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
			0.39	

GC	GC Content	0~1	0.41	<a href="#">[1]</a>
GC1 GC3	GC Content at the First Position GC Content at the Third Position of Synonymous Codons		0.52	
GC2	GC Content at the Second Position of Synonymous Codons		0.33	
ENcp	Effective Number of Codon Pairs	20~61	29.32	<a href="#">[2]</a>
CPS	Codon Pair Score	-1~1	0.07	<a href="#">[3]</a> , <a href="#">[4]</a>
Codon Volatility	Codon Volatility	0.5~1	0.77	<a href="#">[5]</a>