

Visual Gene Developer 1.0 Build 606 [Sample construct - GFP v3.vgd]

File Edit Function Data Analysis Tool Network computing Window Help

New Open Save Project Explorer Toolbox Workspace

Project Explorer

Project

- Codon usage & W-table
- Gene construct
- Configuration
- Gene optimization
- Layer view

Toolbox

- Refresh
- Pre-defined tool
 - CAI and GC content
 - Codon usage table
 - Repeated sequence
 - Sequence comparison
 - mRNA structure (fast)
 - mRNA structure (slow)
- User-defined tool
 - GC content profile v2
 - mRNA profile v2
 - CAI profile v2
 - Codon bias diagram

Codon Usage Calculation

- Refresh Save as Copy
- Triplet AA Abbrev Sum
- TTT Phe F 00006
- TCT Ser S 00003
- TAT Tyr Y 00004
- TGT Cys C 00000
- TTC Phe F 00006
- TCC Ser S 00002
- TAC Tyr Y 00008
- TGC Cys C 00002

Gene Construct View

- Setting Hide Activate Deactivate
- GFP (714 bp) 6Histag (18 bp) Stop
- 760 770 780 790 800 810 820 830
- T A A C A G C T G C T A G G A T T A C A C A T G G C A T G G A C T A T A C A A A C A C C A C C A T C A T C A T T G A T A
- V T A A R I T H G M D E L Y C A H H H H H H

Workspace

- Copy Paste Clear Parse Back translation
- 780 790 800 810 820
- GACGGGAACCTCAAGACACGCTGCTGAAGTCAAGTTGAAGGTGATACCCCTTGTTA
- ATAGAATCGAGTTAAAGGTATTGATTTAAAGAAAGATGGAAACATTCTTGGACA
- CAAAATCGATACAACTATACTACATATTGTATACATCATCCGACAAACCA
- AAGAATGGCATCAAGTTAACTTCAAAATTAGACACACCACTTAAAGATGGAAAGG
- TTCAATTAGCACCACTTATCAACAAATATCTCC
- TTTACCGACAGCACTTACCTGTCCACCACTCT
- GAAAGAGAGATCACATGATCTTCTTGAAGTTGT
- ATGGCATGGATGAACATAACAA

Gene analysis

- Parameter Value
- w-table file Target m
- CAI 0.7898
- Nc 44.583
- Overall GC content (%) 38.9356
- GC content at 1st place (%) 51.2605
- GC content at 2nd place (%) 31.9328
- GC content at 3rd place (%) 33.6135

mRNA optimization

- Analyze Optimize Stop
- Parameter Value
- Target W-table ID Target m
- Start location 1
- End location 99
- Window size 30
- Step size 9
- Lowest Gibbs Energy -0.2
- Highest Gibbs Energy 0
- Gibbs Energy Unit Average G

Codon optimization

- Perform Restore Align Copy
- Target codon usage Target map for N benth
- Maximum number of mutations 30
- Result
- Be
- ATAGGTAAGGAGAGAAGCACTTTTCATCTGGAGTGGGT
- AATTAGTCCGTAGATGGCGCATGTTAATGGGCAAA

Neural Network Con

- Open Network
- Topology setting
- Parameter
- Number of input vari
- Number of output var
- Number of hidden lay
- Node # of 1st hidden
- Node # of 2nd hidden
- Node # of 3rd hidden
- Node # of 4th hidden
- Node # of 5th hidden
- Neural Network Ma

Organism Nicotiana benthamiana

Source Kazusa codon database (w

Fraction basis Number basis

Triplet	Amino acid	Abbrev	Fraction
TAA	Stop	*	0.320
TGA	Stop	*	0.390

Access to Kazusa codon usage web data

Keyword coli

Conversion table 1: Stan

Result Status: Now

mitochondrion Colinus cristatus [gbvrt]

Yersinia enterocolitica [gbbct]: 516

Scoliopteryx libatrix [gbinv]: 2

Escherichia coli O157:H7 EDL933 [gb

Escherichia coli O127:H6 [gbbct]: 1

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mRNA Structure View

- Setting Copy
- Structure Energy Probability
- 0 150 300 450 600 750 900
- 50 150 250 350 450 550 650 750 850 950

mRNA Gibbs free

Visual Gene Developer - Network computing Server

- Start Disconnect all IP address 192.168.
- # IP address Connection Status
- 1 192.168.1.101 Connected R