

Graphical Codon Usage Analyser

“each triplet position vs. usage table”



sequencename ← ime zaporedja (poljubno)

originating organism ← izvorni organizem

sequence ← zaporedje (SAMO KODIRAJOČA REGIJA)

color options
 Threshold 1: Few used codons highlight codons used less than % in ← obarvanost za frekvenco < 20 %
 Threshold 2: Very few used codons highlight codons used less than % in ← obarvanost za frekvenco < 10 %
 display non highlighted codons in

Codon usage table to apply ← organizem, za katerega analiziramo rabo kodonov

new in version 2.0
 relative adaptiveness read more...
 frequency (like in gcua version 1.0)

outputformat

Webcutter

Iskanje restriksijskih mest – razvrstitev unikatnih mest po mestu rezanja

Please enter a title for this sequence:
 ← ime zaporedja (poljubno)

Paste the DNA sequence into the box below
 ← zaporedje

Please select the type of analysis you would like
 Linear sequence analysis ← tip zaporedja/analize (linearna ali krožna DNA)
 Circular sequence analysis
 Find sites which may be introduced by silent mutagenesis

Please indicate how you would like the restriction sites displayed
 Map of restriction sites
 Table of sites, sorted alphabetically by enzyme name
 Table of sites, sorted sequentially by base pair number ← rezultat naj bo tabela restriksijskih mest, razvrščenih po lokaciji v zaporedju

Please indicate which enzymes to include in the display
 All enzymes
 Enzymes not cutting
 Enzymes cutting once ← upoštevamo le tiste restriktaze, ki znotraj danega zaporedja režejo zgolj 1x
 Enzymes cutting exactly times
 Enzymes cutting at least times, and at most times
 Rainbow highlights for enzymes from the polylinker

Please indicate which enzymes to include in the analysis
 All enzymes in the database
 Only enzymes with recognition sites equal to or greater than bases long ← upoštevamo le tiste restriktaze, katerih prepoznavno mesto je dolgo najmanj 6 bp

Only the following enzymes:

Use the command, control, or shift key to select multiple entries

OligoCalc

Načrtovanje začetnih oligonukleotidov

Oligo Calc: Oligonucleotide Properties Calculator

Enter Oligonucleotide Sequence Below
OD calculations are for single-stranded DNA or RNA

Nucleotide base codes

ATG GCG CCC CCG CAG GTC ←

Reverse Complement Strand(5' to 3') is:

GAC CTG CCG GGG CGC CAT ←

5' modification (if any) 3' modification (if any) Select molecule
 ssDNA

50 nM Primer 1 Measured Absorbance at 260 nanometers

50 mM Salt (Na⁺)

Calculate Swap Strands BLAST mfold

Physical Constants

Length: 18 Molecular Weight: 5461.64 GC content: 78% 1 59.4 °C (Basic)

1 ml of a sol'n with an Absorbance of 1 at 260 nm 2 65.3 °C (Salt Adjusted)

is 5.693 micromolar and contains 31.1 micrograms. 3 59.04 °C (Nearest Neighbor)

Thermodynamic Constants Conditions: 1 M NaCl at 25 °C at pH 7.

RlnK 33.40 cal/(*K*mol) deltaH 167.3 Kcal/mol

deltaG 28.9 Kcal/mol deltaS 430.2 cal/(*K*mol)

Deprecated Hairpin/self-dimerization calculations

5 (Minimum base pairs required for single primer self-dimerization) Check Self-Complementarity

4 (Minimum base pairs required for a hairpin)

zaporedje oligonukleotida (5'→3')

obratno komplementarno zaporedje oligonukleotida (5'→3')

tip zaporedja/analize (linearna ali krožna DNA)

delež GC

T_m (upoštevamo "salt adjusted")

preverimo tvorbo dimerov in sekundarnih struktur

dolžina oligonukleotida

Primer3

Načrtovanje začetnih oligonukleotidov

Primer3web version 4.0.0 - Pick primers from a DNA sequence.

disclaimer code

cautions

Select the **Task** for primer selection generic

Paste source sequence below (5'→3', string of ACGTNa_gnt -- other letters treated as N -- numbers and blanks ignored). FASTA format ok. Please N-out undesirable sequence (vector, ALUs, LINEs, etc.) or use a **Mispriming Library (reposit library)** NONE

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GCCCTCCAGCCGCAATATATTTTCCCAAATTTTAAACAAAAGCTTCAAGCTTCTCATTAATCTCTAGATACATCACTGGAAGTTCCTCCAAT
TMCAGACAGCCGCTGACAGCTTCMAACATTTTATTGTGTTATATCTTAACCTACACACATAGCACTTCCGATATCTCTTTTAACTTGAGACA
GTTCCATTCATTGTTTTTTTCATCATCATAAATAAATCAACTTGTACATCTGCTCCACCAATATCATCCGCGTAAACGATCACTATGGGAGAGCC
GCCCCGATTAAGCTTACAGCTGCCCGCCGAGCTCCGGCTTGGGGCTTCTTTCGCGCCGAGCGGGGACTTTCCGCACTGACAGAAAGTCTGTCT
DTGAAACAGCAGCTGCTGATACTGCTTTCATATATATATCATTCATGCTACAGCTGTCTCTTTGGACAGAAAGACTATCTTTCCGTAAGGCTGGCTCCTCA
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CAAGGCTTTCAGGCTGCAAAATTTAGCAAGTCTTTGATACAAATATTTTATCAACTGCTGTCGAATTTCTCAAAATTCGAAATTCGAATATGTC
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CCGAGACCCGTAACAGCCGCTTCTGCGCTTTTCATAGGCTCCGCCCTCCAGCAGCACATAAATGACGCTCAAGCTCAGAGTGGCGAAACCCG
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GCCCTTTTCGCTAATGCTTTCAGCTCAGCCGCTTACAGAGCAGCACTTATGCTGCTGCAAGCCAGCCTGTAAGAGGATTTAGAGAGGAGGCTATGAGCC
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TTCCCGGCTCAATCCGCTATCCCGCCATAGCAAACTTAAAGTCTTATATTGAAAGCTCTTCCGCGCAAACTCTTCCGCAAGCTTCCGCTTCCGCT
TTTTCAGCTGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
CGAAAGAGGCAAGAGCCGAGCCAGCAAAATTTGAATACACTTCTTCTTTTGAATATTAAGAGTATTAGGCTTATCTCTATGAGGAGCATATAT
TTGATTTTTCGAAATATTAACAAATAGGCTTCCGCGACATTTCCCGCAAAAGCTGCACTTTCAGAAAGCTATTTATATATGATCACTAACTTAAAG
TAGGCTTACAGAGCC

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Force Left Primer Start 352 Force Right Primer Start 1296

Force Left Primer End -100 Force Right Primer End -100

General Primer Picking Conditions

Upload the settings from a file Choose File no file selected

Primer Size Min 13 Opt 23 Max 25

Primer T_m Min 57.0 Opt 59.0 Max 62.0 Max T_m Difference 5

Product T_m Min -100 Opt 0.0 Max 1000

Primer GC% Min 30.0 Opt 50.0 Max 70.0

zaporedje (matrica)

parametri, s katerimi izrecno povemo, katero regijo želimo pomnožiti (*left primer* = smerni oligo; *right primer* = protismerni oligo)

POZOR pri "right primer start/end"!

splošni parametri za izbor oligonukleotidov (dolžina, T_m, ...)