CodonGenie: optimised ambiguous codon design tools

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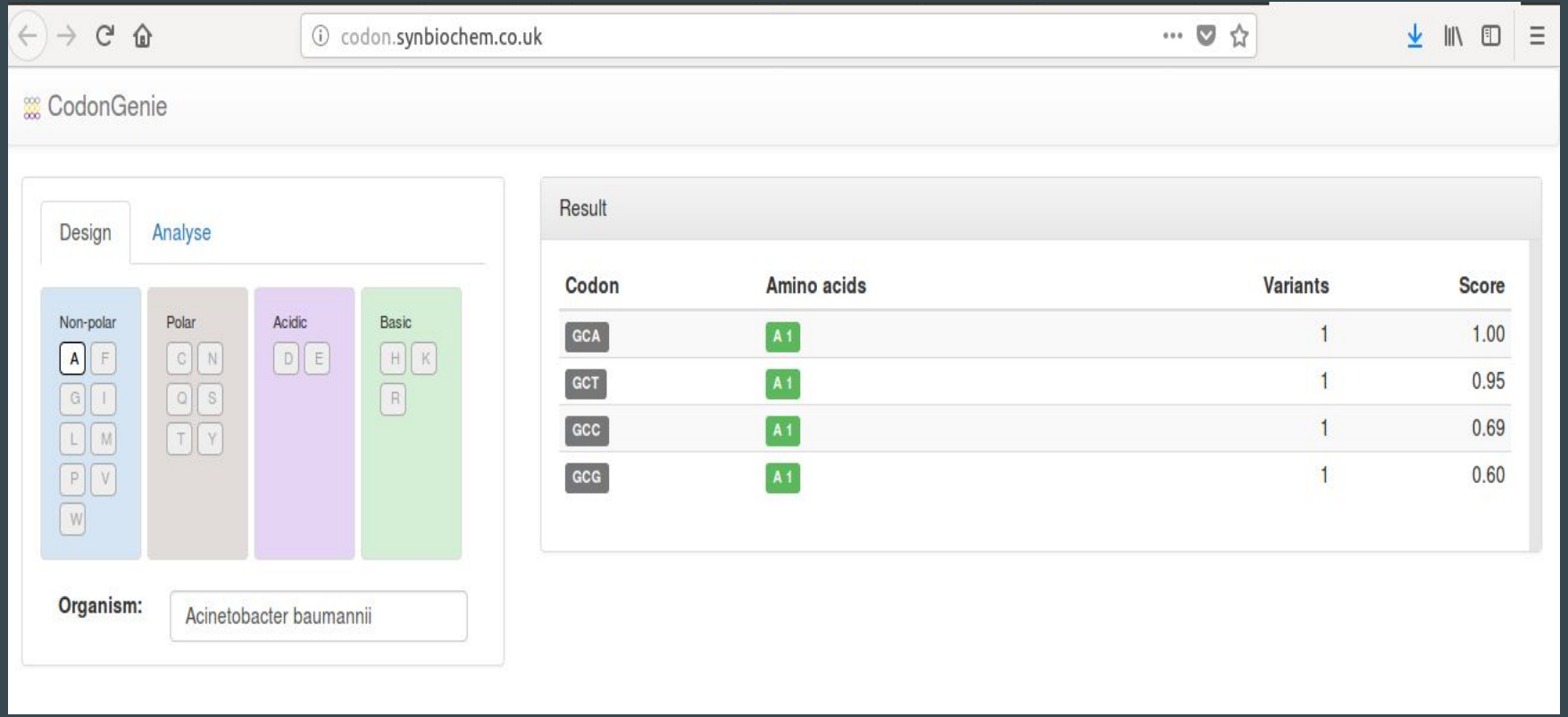
CodonGenie
Design
Analyse
Non-polar
A F G I L M P V W
Polar
C N Q S T Y
Acidic
D E
Basic
H K R
Organism:
Organism

CodonGenie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CodonGenie
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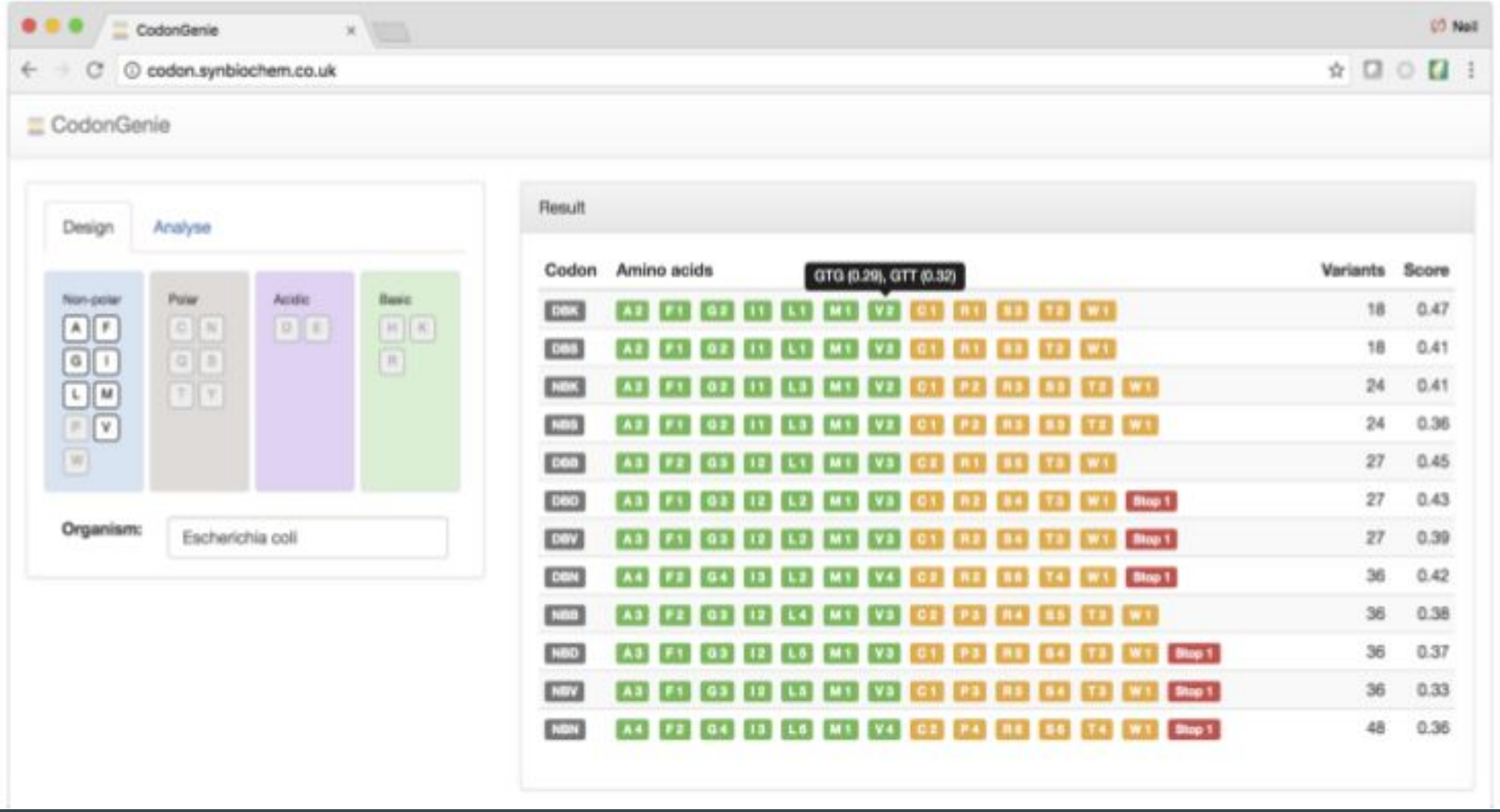
Analyse
Non-polar
A F G I L M P V W
Polar
C N Q S T Y
Acidic
D E
Basic
H K R
Organism:
Acinetobacter baumannii
Result
Codon
Amino acids
Variants
Score
GCA
A 1
1
1.00
GCT
A 1
1
0.95
GCC
A 1
1
0.69
GCG
A 1
1
0.60


CodonGenie
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CodonGenie
Design
Analyse
Non-polar
A F G I L M P V W
Polar
C N Q S T Y
Acidic
D E
Basic
H K R
Organism:
Escherichia coli
Result
Codon
Amino acids
GTG (0.29), GTT (0.32)
Variants
Score
DBK A2 F1 G2 I1 L1 M1 V2 C1 R1 S3 T2 W1 18 0.47
DBS A2 F1 G2 I1 L1 M1 V2 C1 R1 S3 T2 W1 18 0.41
NBK A3 F1 G2 I1 L3 M1 V2 C1 P2 R3 S3 T2 W1 24 0.41
NBS A3 F1 G2 I1 L3 M1 V2 C1 P2 R3 S3 T2 W1 24 0.36
DSB A3 F2 G3 I2 L1 M1 V3 C2 R1 S3 T3 W1 27 0.45
DBO A3 F1 G2 I2 L2 M1 V3 C1 R2 S4 T3 W1 Stop 1 27 0.43
DBV A3 F1 G2 I2 L2 M1 V3 C1 R2 S4 T3 W1 Stop 1 27 0.39
DBN A4 F2 G4 I3 L2 M1 V4 C2 R2 S4 T4 W1 Stop 1 36 0.42
NSB A3 F2 G3 I2 L4 M1 V3 C2 P3 R4 S5 T3 W1 36 0.38
NBO A3 F1 G3 I2 L5 M1 V3 C1 P3 R3 S4 T3 W1 Stop 1 36 0.37
NBV A3 F1 G3 I2 L5 M1 V3 C1 P3 R3 S4 T3 W1 Stop 1 36 0.33
NBN A4 F2 G4 I3 L5 M1 V4 C2 P4 R5 S5 T4 W1 Stop 1 48 0.36

Table 1 Comparison of codon usage frequencies for ambiguous codons encoding F, I, L, M and V in *Escherichia coli* and *Streptomyces coelicolor*. Specific codons from two variant codons DTK and DTS are given, along with their codon usage frequency in the two organisms. For the amino acids F, I and V, there is a preference for codons with T in the third ("wobble") position in *E. coli*, and a preference for C in the wobble position for *S. coelicolor*. This preference is reflected in the differences in scores for the ambiguous codons for the two organisms.

Amino acid	Codon	Ambiguous codon	Codon usage frequency	
			E. coli	*S. coelicolor*
F	TTC	DTS	0.36	0.97
	TTT	DTK	0.64	0.03
I	ATC	DTS	0.31	0.95
	ATT	DTK	0.47	0.03
L	TTG	DTK and DTS	0.13	0.03
M	ATG	DTK and DTS	1.00	1.00
V	GTC	DTS	0.19	0.58
	GTG	DTK and DTS	0.29	0.36
	GTT	DTK	0.32	0.02

Conclusión

CodonGenie, es un servidor web que se encuentra disponible gratuitamente en el siguiente enlace: http://codon.synbiochem.co.uk, este servidor fue creado para apoyar aplicaciones en la mutagénesis de proteínas, diseñando codones ambiguos.