



Εικονική κλωνοποίηση γονιδίου και δημιουργία βιβλιοθηκών μεταλλαγμάτων

Πρωτεϊνική Μηχανική-2^ο Σεμινάριο
15.05.2026

Διβάρης Παναγιώτης (Α.Μ. 1281)
Πατούνη Τατιάνα (Α.Μ. 1295)

Υδρολάσες

- Κατηγορία ενζύμων E.C. 3
- Κατάλυση αντιδράσεων υδρόλυσης

Κύριες Υποκατηγορίες

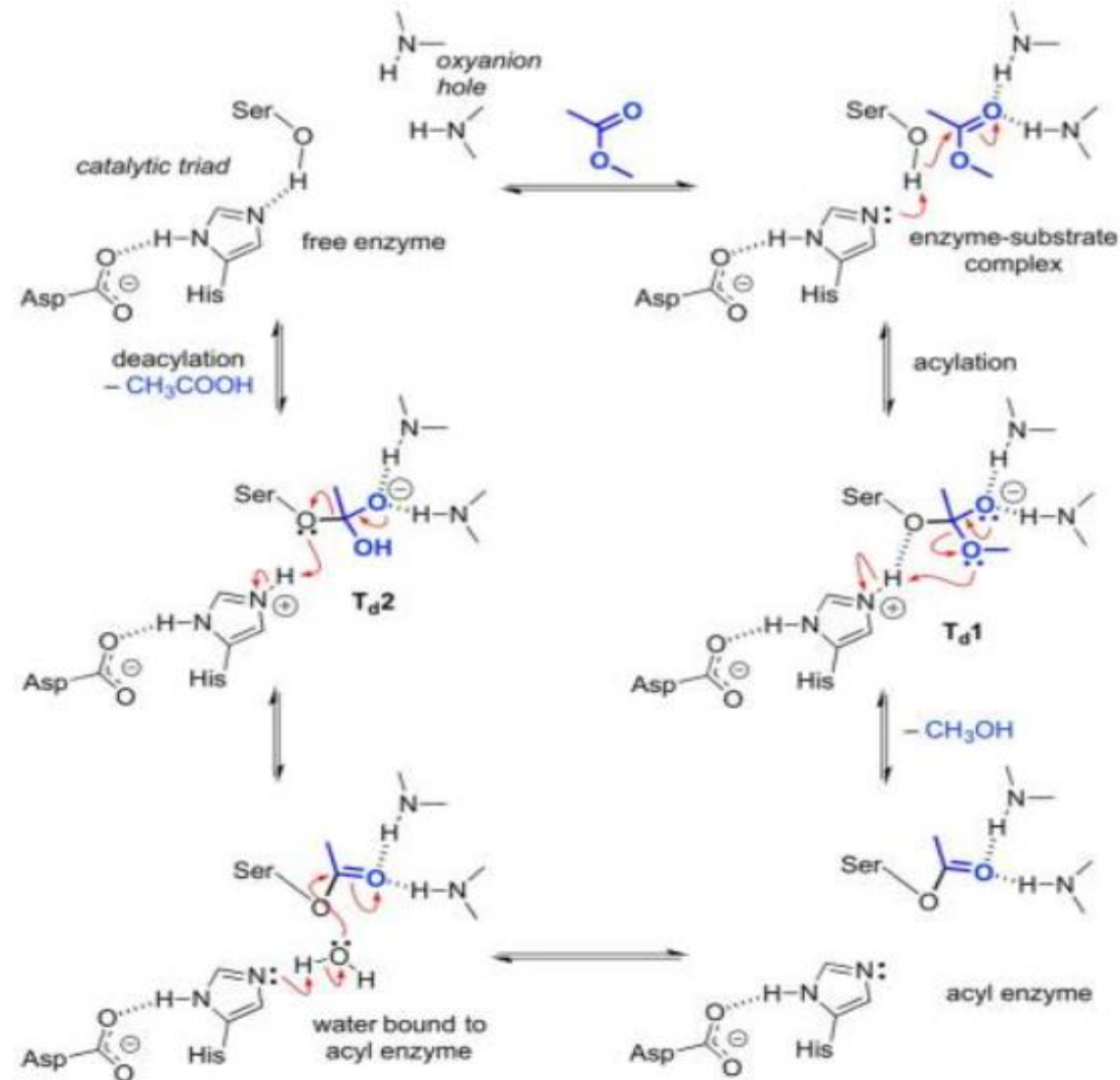
1. Πρωτεάσες
2. Λιπάσες/ Εστεράσες
3. Γλυκοσιδάσες
4. Φωσφατάσες
5. Νουκλεάσες



Σημασία

- Υγεία και παθοφυσιολογία νοσημάτων
- Χρήση στη βιοτεχνολογία και βιομηχανία τροφίμων
- Αποτελούν φαρμακευτικούς στόχους

Καταλυτικός Μηχανισμός



Πρωτεΐνη ABHDB_HUMAN (Q8NFV4)

- Υποοικογένεια: human-ABHD11
- E.C. 3.1.1.116
- Ειδική λιπάση διακυλογλυκερόλης
- Οργανισμός: *homo sapiens*
- Έκφραση σε ευκαρυωτικά κύτταρα HEK293T με FLAG tag
affinity chromatography purification
- UniParc: UPI00003D7D2C
- 306 Αμινοξέα
- Καταλυτικά αμινοξέα: Ser132-His287 (κατά 3DM)
- Ser132-Asp237-His296

Exasy 

Θεωρητικό pI	9.24
Μοριακό βάρος	33.747 Da
Δείκτης αστάθειας	46.33 (unstable)
Χρόνος ημιζωής (E.coli in vivo)	>10 hours

Αλληλουχίες πρωτεΐνης

Αμινοξική αλληλουχία

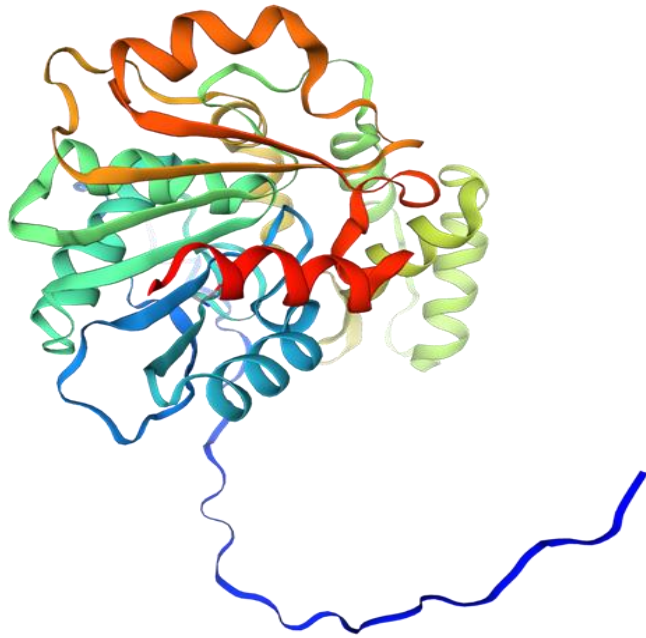
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VFLHGFLFGSKTNFNSIAKILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQ
LGLVPCVVVGHSMSGKTAMLLALQRPVELVERLIAVDISPVESTGVSHFATYVAAMRAINI
ADELPRSRARKLADEQLSSVIQDMAVRQHLLTNLVEVDGRFVWRVNLDAITQHLDKILAF
PQRQESYLGPTLFLGNSQFVHPSHHPEIMRLFPRQMOTVPNAGHWIHADRPQDFIAA
IRGFLV

Γονιδιακή αλληλουχία

ATGCTCCGCTGGACCCGAGCCTGGAGGCTCCCGCGTGAGGGACTCGGCCCCACGGCCCTAGCTTCGCGA
GGGTGCCTGTCGCACCCAGCAGCAGCAGCGGCGGCCGAGGGGGCGCCGAGCCGAGGCCGCTTCCGCTTTC
CTACAGGCTTCTGGACGGGGAGGCAGCCCTCCCGGCCGTCTGCTTTTTTGCACGGGCTCTTCGGCAGCAA
ACTAACTTCAACTCCATCGCCAAGATCTTGGCCCAGCAGACAGGCCGTAGGGTGCTGACGGTGGATGCTC
GTAACCACGGTGACAGCCCCACAGCCCAGACATGAGCTACGAGATCATGAGCCAGGACCTGCAGGACCT
TCTGCCCCAGCTGGGCCTGGTGCCCTGCGTCGTCTGTTGGCCACAGCATGGGAGGAAAGACAGCCATGCTG
CTGGCACTACAGAGGCCAGAGCTGGTGGAACGTCTCATTTGCTGTAGATATCAGCCAGTGGAAGCACAG
GTGTCTCCCACTTTGCAACCTATGTGGCAGCCATGAGGGCCATCAACATCGCAGATGAGCTGCCCCGCTC
CCGTGCCCCGAAAACCTGGCGGATGAACAGCTCAGTTCTGTTCATCCAGGACATGGCCGTGCGGCAGCACCTG
CTCACTAACCTGGTAGAGGTAGACGGGCGCTTCGTGTGGAGGGTGAACCTGGATGCCCTGACCCAGCACC
TAGACAAGATCTTGGCTTTCCACAGAGGCAGGAGTCCTACCTCGGGCCAACACTCTTTCTCCTTGGTGG
AAACTCCCAGTTCTGTGCATCCCAGCCACCACCCTGAGATTATGCGGCTCTTCCCTCGGGCCCAGATGCAG
ACGGTGCCGAACGCTGGCCACTGGATCCACGCTGACCGCCCACAGGACTTCATAGCTGCCATCCGAGGCT
TCCTGGTCTAA

Μοντέλα Ομολογίας

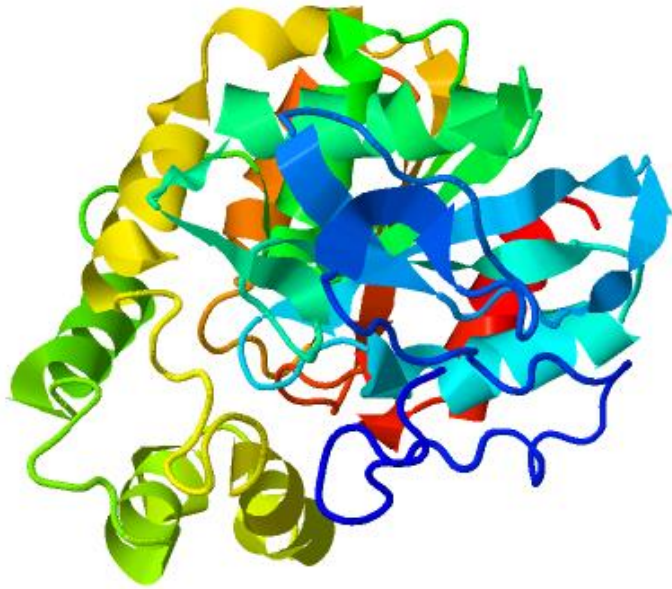
Swiss Model



- AlphaFold DB model of F6R598_CALJA
- Κάλυψη 100%
- GMQE = 0.88
- Ολιγομερική κατάσταση μονομερούς

Μοντέλα Ομολογίας

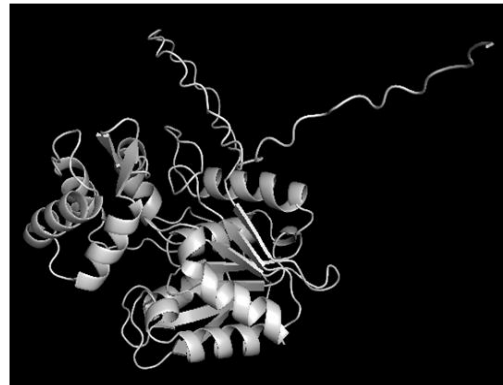
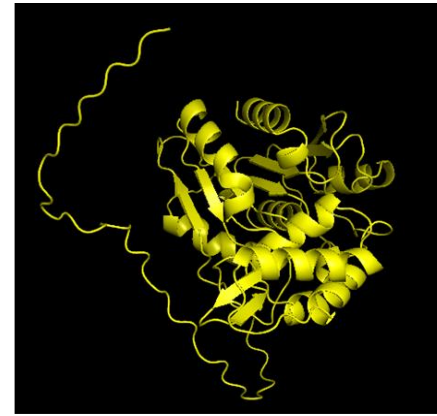
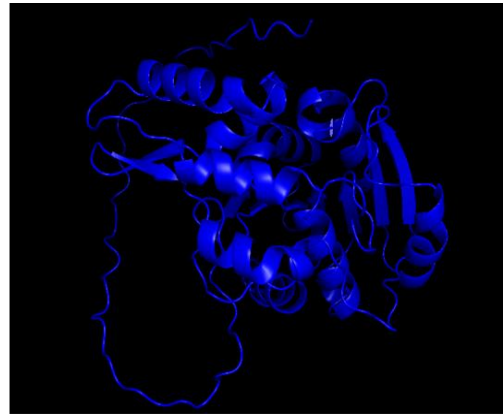
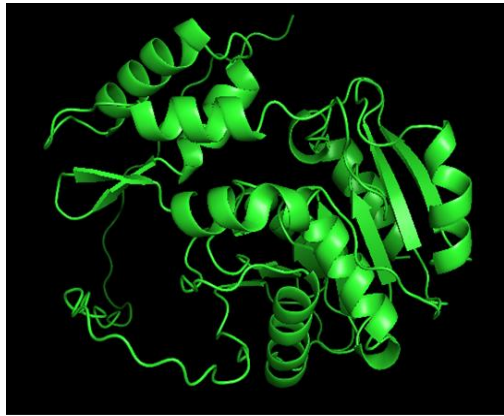
D-I-Tasser



- Με βάση 10 δομές ανάλογων πρωτεϊνών στην PDB
- 5 Ομόλογα μοντέλα
- TM-score=0.75

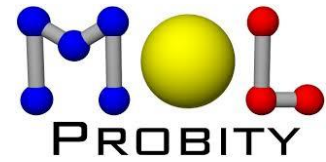
Μοντέλα Ομολογίας

Alpha Fold



Κάλυψη 100%

Σύγκριση μοντέλων ομολογίας



Εργαλείο	Μοντέλο	MOL Probit Score	Ramachandran Outliers
Swiss-Model	1	1.14	7
D-I-Tasser	1	2.72	18
Alpha-Fold	1	1.46	1
	2	1.50	1
	3	1.59	-
	4	1.42	1

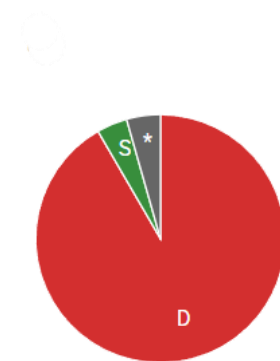
Ανάλυση 3DM

Ζεύγη Συσχετισμών (cut off=0.80)	Συχνότερα Ζεύγη	Ζεύγη στην πρωτεΐνη	Ποσοστό εμφάνισης
27-48	Tyr-Arg	Val-Arg	56.57%
53-64	Ala-Asp	Ser-Asp	12.39%

Συντηρημένα Αμινοξέα		
Αμινοξύ	Οικογένεια	Υποοικογένεια
His87	97.71%	98.39%
Ser32	84.15%	94.11%
Asp64	1.89%	3.96%

Subfamily 2VF2A

Conservation of S
3,96% (47 out of 1.187)

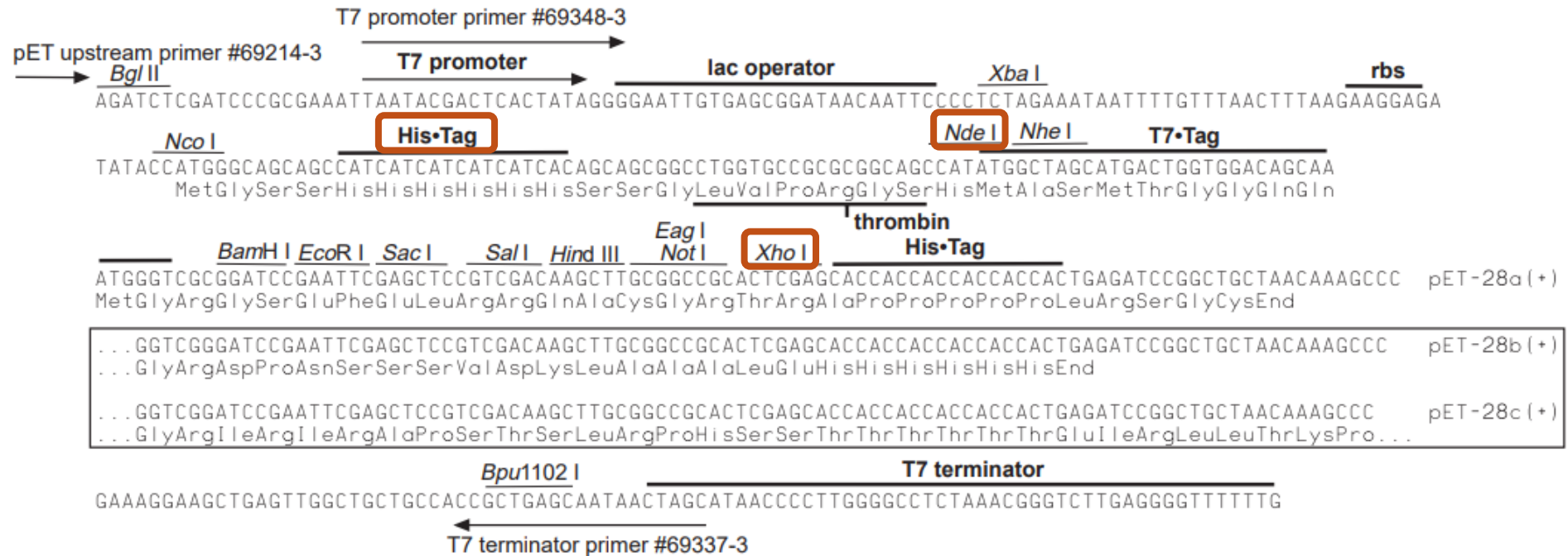




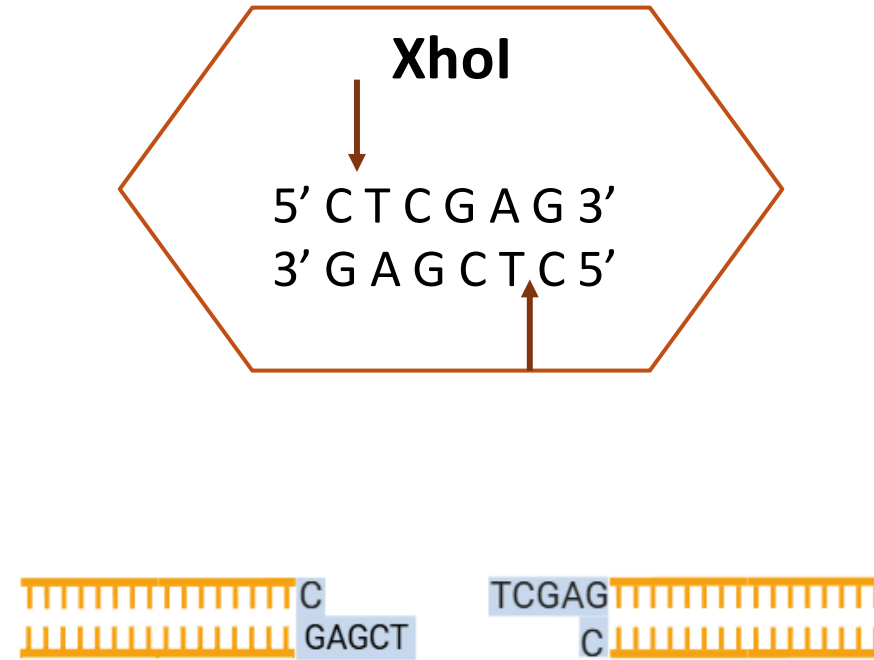
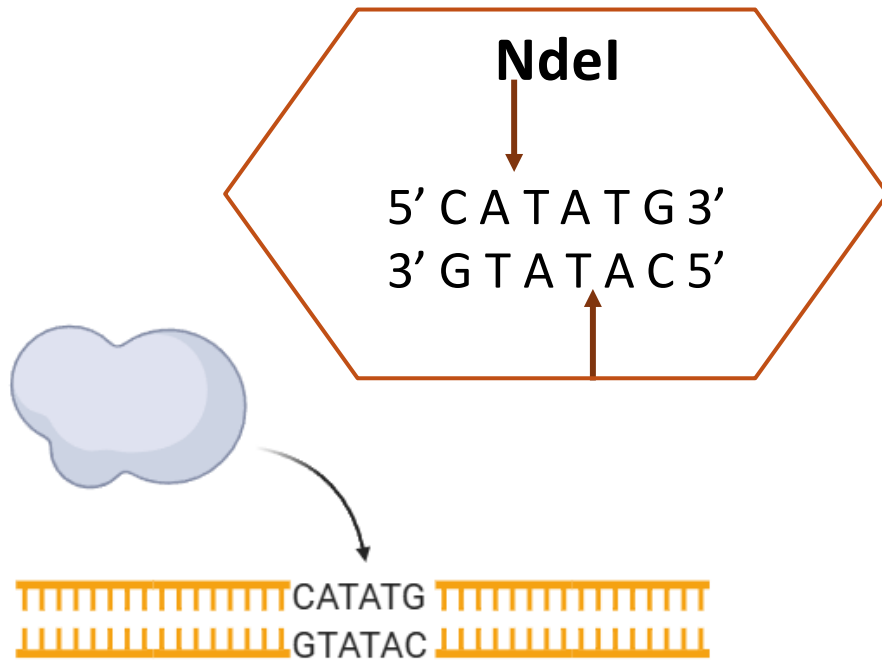
Εικονική Κλωνοποίηση



Πλασμίδιο pET-28b



Περιοριστικά Ένζυμα



Αλληλουχία Πρωτεΐνης

Βελτιωμένη Γονιδιακή Αλληλουχία

ATGCTGCGTTGGACCCGTGCGTGGCGCCTGCCGCGCGAAGGCCCTGGGTCCGCATGGCCCGAGCTTCGCCCGTGTGCCGGTGGCCCCGAGCAGCAGTAGCGG
CGGCCGCGGTGGCGCGGAACCGCGTCCGCTGCCGCTGAGCTATCGCCTTCTGGATGGCGAAGCAGCGCTGCCGGCAGTGGTTTTCTCTGCATGGCCTGTTTG
GTAGCAAAACCAATTTTAATAGCATTTGCCAAAATTCTGGCGCAGCAGACCGGCCGCCGTGTGCTGACCGTGGATGCACGTAACCATGGCGACAGCCCGCAT
AGCCCGGATATGAGCTATGAAATTATGAGCCAGGATCTGCAGGATCTGCTGCCGCAACTGGGCCTGGTTCCGTGCGTGGTGGTTGGCCATTCAATGGGCGG
CAAAACTGCCATGCTGCTGGCGCTGCAGCGCCCGGAACCTGGTGGAACGCCTGATCGCAGTTGATATTAGCCCGGTGGAATCAACCGGTGTGTCACATTTTCG
CGACCTATGTGGCGGCAATGCGCGCCATTAATATTGCCGATGAACTGCCGCGCAGCCGCGCGCGCAAACTGGCGGATGAACAGCTCAGCTCTGTCATTTCAG
GATATGGCCGTACGCCAGCACCTGCTGACCAACCTGGTTGAAGTGGATGGCCGCTTTGTGTGGCGTGTGAACCTGGATGCCCTGACCCAGCATTTGGATAA
AATTCTGGCGTTTCCGCAACGTCAGGAAAGCTACCTGGGTCCGACCCTATTTCTGCTGGGCGGCAACAGTCAGTTTGTACATCCGAGCCATCATCCGGAAA
TTATGCGCCTGTTTTCCGCGTGCCCAGATGCAGACCGTGCCGAACGCCGGCCATTGGATTTCATGCGGATCGTCCGCAGGATTTTATCGCGGCGATTTCGCGGC
TTTCTGGTTTAA

- GC περιεκτικότητα=59.83%
- Βελτιωμένη για *E.coli* K12

Αλληλουχία Πρωτεΐνης

Αμινοξική Αλληλουχία

MLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSGGRGGAEPRPLPLSYRLLDGEAALPAV
VFLHGLFGSKTNFNNSIAKILAQQTGRRVLTVDARNHGDS PHSPDMSYEIMSQDLQDLLPQ
LGLVPCVVVGHSMMGGKTAMLLALQRP ELVERLIAVDISPVESTGVSHFATYVAAMRAIN I
ADELPRSRARKLADEQLSSVIQDMAVRQHLLTNLVEVDGRFVWRVNLDA LTQHLDKILAF
PQRQESYLGPTLFL LGGNSQFVHP SHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFIAA
IRGFLV

Σχεδιασμός Εκκινητών

5' **GATC**CATATG**CTGCGTTGGACCCGTG**CGTGGCGCCTGCCGCGCGAAGGCCTGGGTCCGCATGGCCCGAGCTTCGCCCCGTGTGCCGGT
GGCCCCGAGCAGCAGTAGCGGCGGCCGCGGTGGCGCGGAACCGCGTCCGCTGCCGCTGAGCTATCGCCTTCTGGATGGCGAAGCAGCGC
TGCCGGCAGTGGTTTTCTGCATGGCCTGTTTGGTAGCAAAACCAATTTTAATAGCATTGCCAAAATTCTGGCGCAGCAGACCGGCCGC
CGTGTGCTGACCGTGGATGCACGTAACCATGGCGACAGCCCGCATAGCCCGGATATGAGCTATGAAATTATGAGCCAGGATCTGCAGGA
TCTGCTGCCGCAACTGGGCCTGGTTCCGTGCGTGGTGGTTGGCCATTCAATGGGCGGC AAAACTGCCATGCTGCTGGCGCTGCAGCGCC
CGGAACTGGTGGAACGCCTGATCGCAGTTGATATTAGCCCGGTGGAATCAACCGGTGTGTCACATTTTCGCGACCTATGTGGCGGCAATG
CGCGCCATTAATAATTGCCGATGAACTGCCGCGCAGCCGCGCGCGCAAACCTGGCGGATGAACAGCTCAGCTCTGTCATTCAGGATATGGC
CGTACGCCAGCACCTGCTGACCAACCTGGTTGAAGTGGATGGCCGCTTTGTGTGGCGTGTGAACCTGGATGCCCTGACCCAGCATTTGG
ATAAAATTCTGGCGTTTCCGCAACGTCAGGAAAGCTACCTGGGTCCGACCCTATTTCTGCTGGGCGGCAACAGTCAGTTTGTACATCCG
AGCCATCATCCGGA AATTATGCGCCTGTTTCCGCGTGCCCAGATGCAGACCGTGCCGAACGCCGGCCATTGGATTTCATGCGGATCGTCC
GCAGGATTTTATCGCGGCGATTTCG**CGGCTTTCTGGTTTAA**CTCGAGGACC3'

Σχεδιασμός Εκκινητών

1ος Εκκινητής

5' GATCCATATGCTGCGTTGGACCCGTG 3'

GC content	58%
Length	26 bases
Tm (salt adjusted)	71°C

2ος Εκκινητής (ανάστροφος)

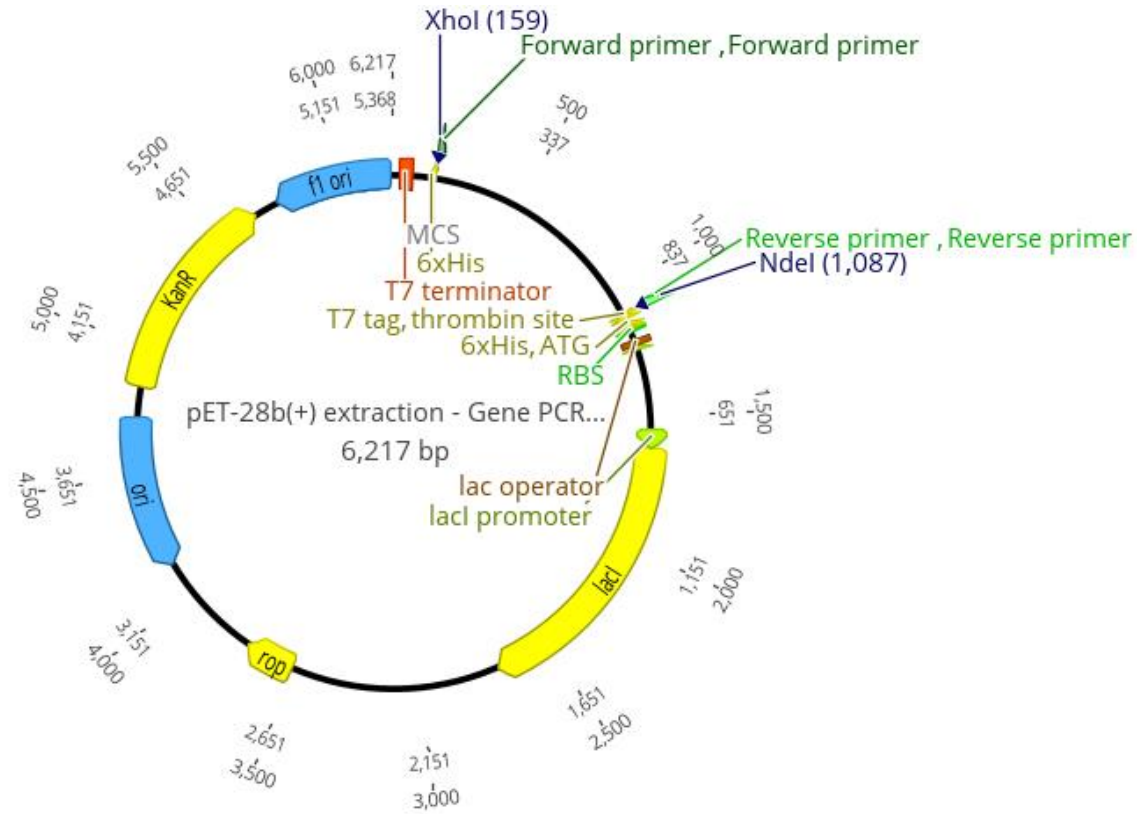
5' GGTCCTCGAGTTAAACCAGAAAGCCG 3'

GC content	54%
Length	26 bases
Tm (salt adjusted)	70°C

- rCutSmart buffer
- Απενεργοποίηση στους 65 °C
- Δεν απαιτείται συμπράγοντας

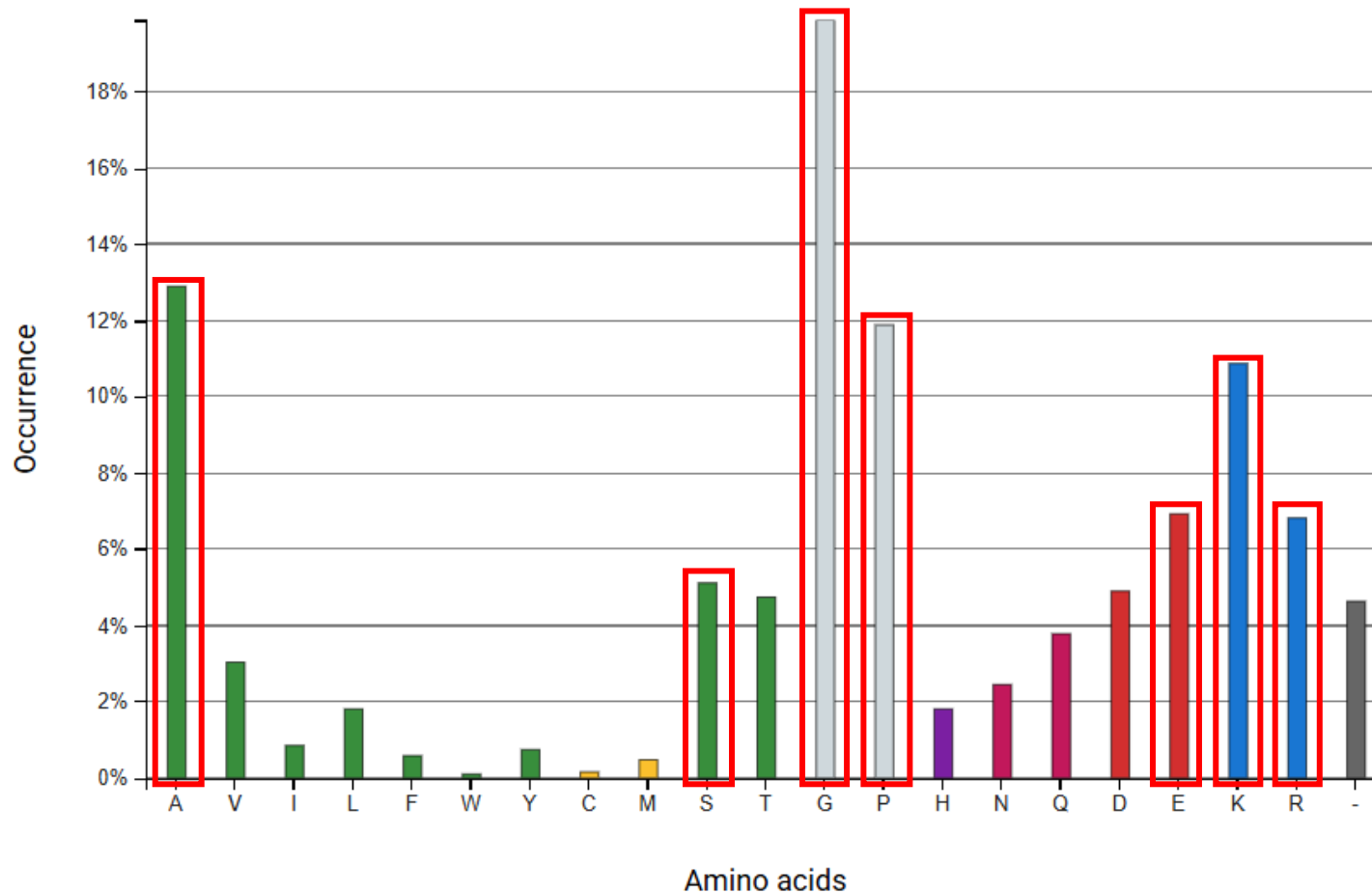
Εικονική Κλωνοποίηση

Ανασυνδυασμός Πλασμιδίου pET28b μέσω Geneious



Σχεδιασμός Βιβλιοθηκών – Θέση 9

Επιτρεπτά αμινοξέα ➡ Συχνότητα εμφάνισης >5%



- Αλανίνη 12.88%
- Σερίνη 5.12%
- Γλυκίνη 19.89%
- Προλίνη 11.90%
- Γλουταμινικό 6.91%
- Λυσίνη 10.90%
- Αργινίνη 6.81%

Σχεδιασμός Βιβλιοθηκών – Θέση 9

1^η θέση: A,G,C

2^η θέση: A,G,C

3^η θέση: T&A or T&G

VVW

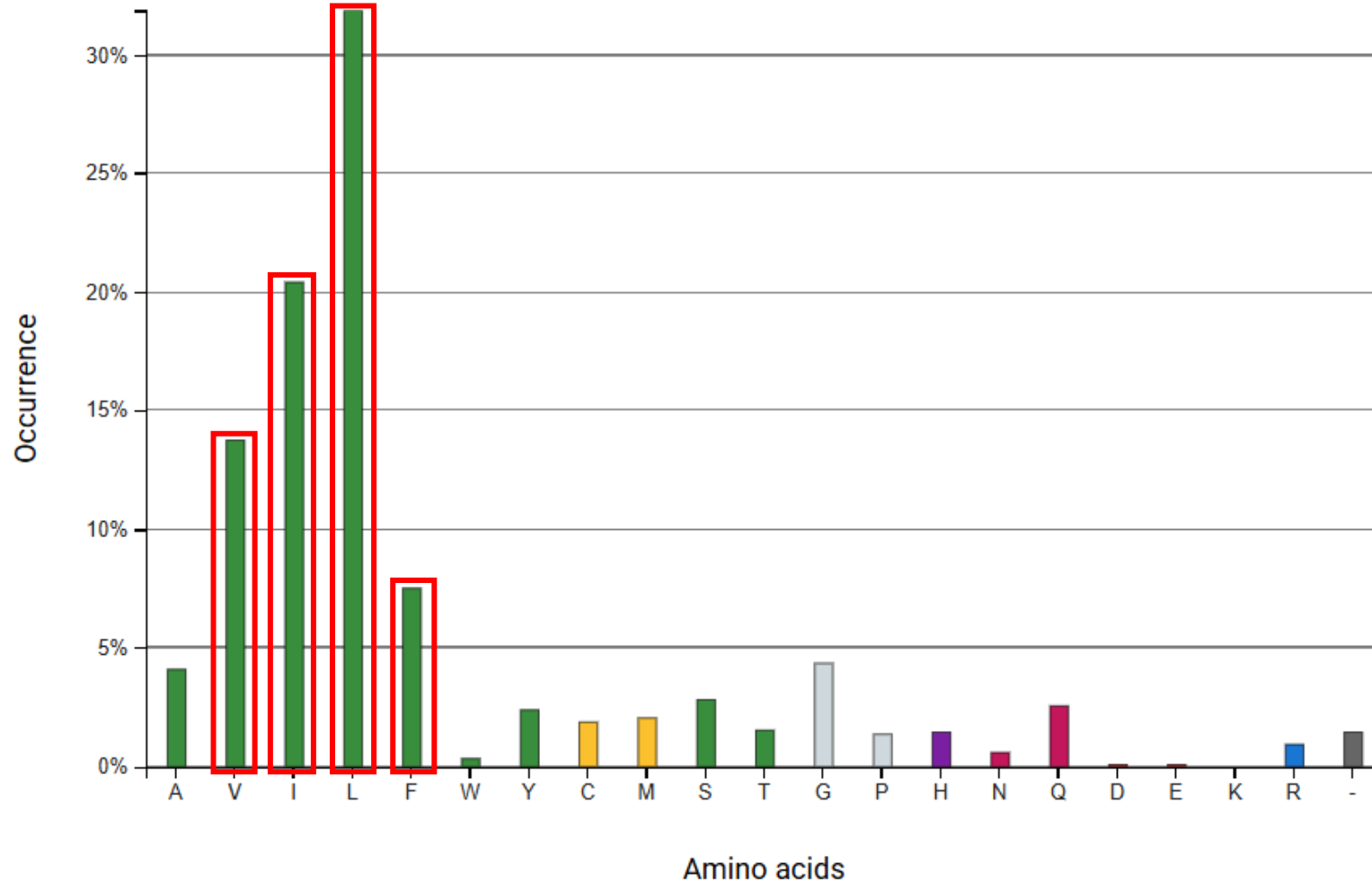
VVK

SECOND POSITION OF THE CODON										
		T		C		A		G		
F	I	TTT	Phe [F]	TCT	Ser [S]	TAT	Tyr [Y]	TGT	Cys [C]	T
		TTC	Phe [F]	TCC	Ser [S]	TAC	Tyr [Y]	TGC	Cys [C]	C
		TTA	Leu [L]	TCA	Ser [S]	TAA	Ter [end]	TGA	Ter [end]	A
		TTG	Leu [L]	TCG	Ser [S]	TAG	Ter [end]	TGG	Trp [W]	G
P	O	CTT	Leu [L]	CCT	Pro [P]	CAT	His [H]	CGT	Arg [R]	T
		CTC	Leu [L]	CCC	Pro [P]	CAC	His [H]	CGC	Arg [R]	C
		CTA	Leu [L]	CCA	Pro [P]	CAA	Gln [Q]	CGA	Arg [R]	A
		CTG	Leu [L]	CCG	Pro [P]	CAG	Gln [Q]	CGG	Arg [R]	G
S	I	ATT	Ile [I]	ACT	Thr [T]	AAT	Asn [N]	AGT	Ser [S]	T
		ATC	Ile [I]	ACC	Thr [T]	AAC	Asn [N]	AGC	Ser [S]	C
		ATA	Ile [I]	ACA	Thr [T]	AAA	Lys [K]	AGA	Arg [R]	A
		ATG	Met [M]	ACG	Thr [T]	AAG	Lys [K]	AGG	Arg [R]	G
N	G	GTT	Val [V]	GCT	Ala [A]	GAT	Asp [D]	GGT	Gly [G]	T
		GTC	Val [V]	GCC	Ala [A]	GAC	Asp [D]	GGC	Gly [G]	C
		GTA	Val [V]	GCA	Ala [A]	GAA	Glu [E]	GGA	Gly [G]	A
		GTG	Val [V]	GCG	Ala [A]	GAG	Glu [E]	GGG	Gly [G]	G

or

SECOND POSITION OF THE CODON										
		T		C		A		G		
F	I	TTT	Phe [F]	TCT	Ser [S]	TAT	Tyr [Y]	TGT	Cys [C]	T
		TTC	Phe [F]	TCC	Ser [S]	TAC	Tyr [Y]	TGC	Cys [C]	C
		TTA	Leu [L]	TCA	Ser [S]	TAA	Ter [end]	TGA	Ter [end]	A
		TTG	Leu [L]	TCG	Ser [S]	TAG	Ter [end]	TGG	Trp [W]	G
P	O	CTT	Leu [L]	CCT	Pro [P]	CAT	His [H]	CGT	Arg [R]	T
		CTC	Leu [L]	CCC	Pro [P]	CAC	His [H]	CGC	Arg [R]	C
		CTA	Leu [L]	CCA	Pro [P]	CAA	Gln [Q]	CGA	Arg [R]	A
		CTG	Leu [L]	CCG	Pro [P]	CAG	Gln [Q]	CGG	Arg [R]	G
S	I	ATT	Ile [I]	ACT	Thr [T]	AAT	Asn [N]	AGT	Ser [S]	T
		ATC	Ile [I]	ACC	Thr [T]	AAC	Asn [N]	AGC	Ser [S]	C
		ATA	Ile [I]	ACA	Thr [T]	AAA	Lys [K]	AGA	Arg [R]	A
		ATG	Met [M]	ACG	Thr [T]	AAG	Lys [K]	AGG	Arg [R]	G
N	G	GTT	Val [V]	GCT	Ala [A]	GAT	Asp [D]	GGT	Gly [G]	T
		GTC	Val [V]	GCC	Ala [A]	GAC	Asp [D]	GGC	Gly [G]	C
		GTA	Val [V]	GCA	Ala [A]	GAA	Glu [E]	GGA	Gly [G]	A
		GTG	Val [V]	GCG	Ala [A]	GAG	Glu [E]	GGG	Gly [G]	G

Σχεδιασμός Βιβλιοθηκών – Θέση 15



- Βαλίνη 13.72%
- Ισολευκίνη 20.44%
- Λευκίνη 31.84%
- Φαινυλαλανίνη 7.52%

Σχεδιασμός Βιβλιοθηκών – Θέση 15

1^η θέση: A,T,G

2^η θέση: T

3^η θέση: T&G or C&G

DTK

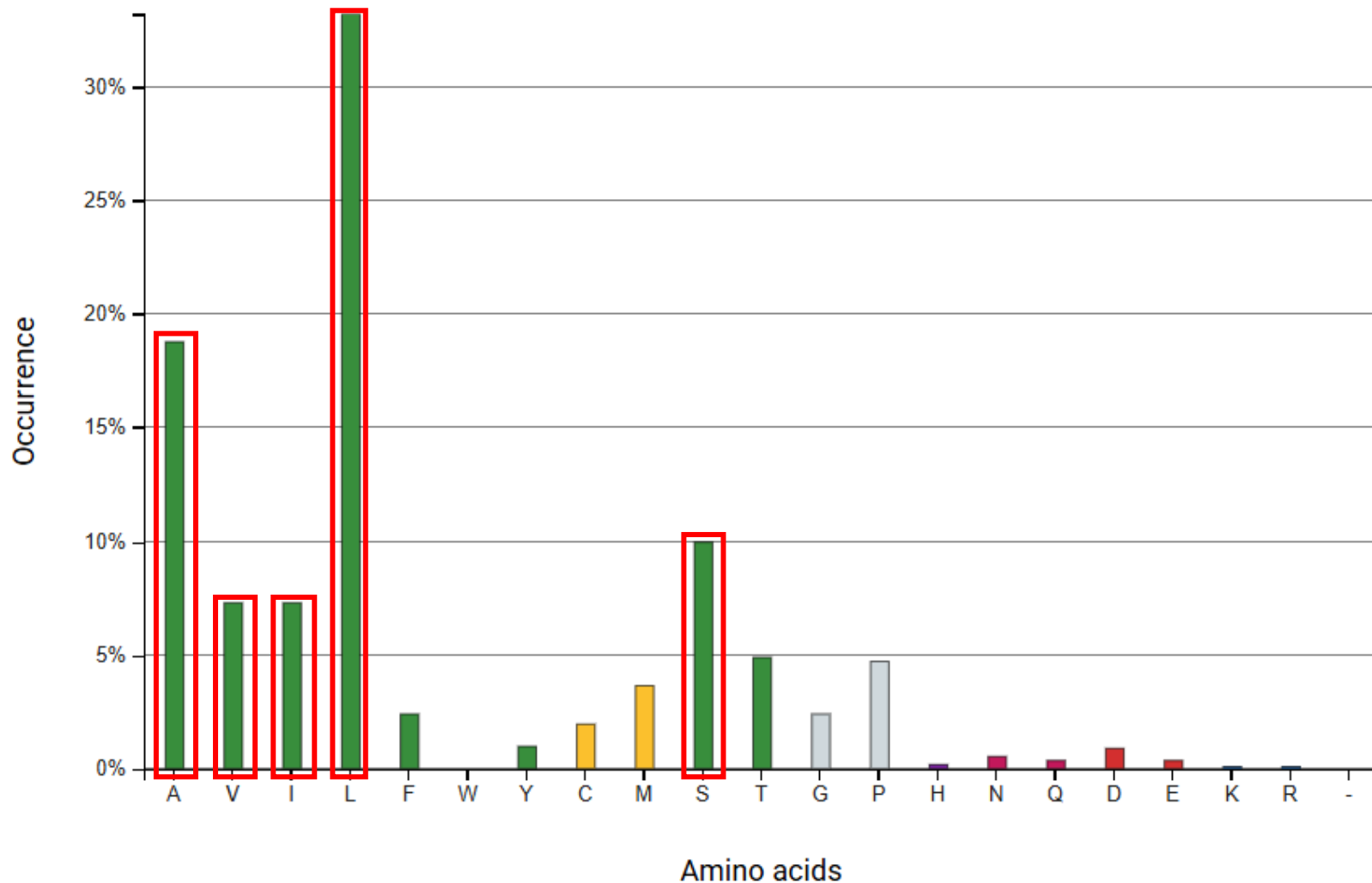
SECOND POSITION OF THE CODON										
		T		C		A		G		
F I R S	T	TTT	Phe [F]	TCT	Ser [S]	TAT	Tyr [Y]	TGT	Cys [C]	T
		TTC	Phe [F]	TCC	Ser [S]	TAC	Tyr [Y]	TGC	Cys [C]	C
		TTA	Leu [L]	TCA	Ser [S]	TAA	Ter [end]	TGA	Ter [end]	A
		TTG	Leu [L]	TCG	Ser [S]	TAG	Ter [end]	TGG	Trp [W]	G
T P O S I T I O N	C	CTT	Leu [L]	CCT	Pro [P]	CAT	His [H]	CGT	Arg [R]	T
		CTC	Leu [L]	CCC	Pro [P]	CAC	His [H]	CGC	Arg [R]	C
		CTA	Leu [L]	CCA	Pro [P]	CAA	Gln [Q]	CGA	Arg [R]	A
		CTG	Leu [L]	CCG	Pro [P]	CAG	Gln [Q]	CGG	Arg [R]	G
	A	ATT	Ile [I]	ACT	Thr [T]	AAT	Asn [N]	AGT	Ser [S]	T
		ATC	Ile [I]	ACC	Thr [T]	AAC	Asn [N]	AGC	Ser [S]	C
		ATA	Ile [I]	ACA	Thr [T]	AAA	Lys [K]	AGA	Arg [R]	A
		ATG	Met [M]	ACG	Thr [T]	AAG	Lys [K]	AGG	Arg [R]	G
	G	GTT	Val [V]	GCT	Ala [A]	GAT	Asp [D]	GGT	Gly [G]	T
		GTC	Val [V]	GCC	Ala [A]	GAC	Asp [D]	GGC	Gly [G]	C
		GTA	Val [V]	GCA	Ala [A]	GAA	Glu [E]	GGA	Gly [G]	A
		GTG	Val [V]	GCG	Ala [A]	GAG	Glu [E]	GGG	Gly [G]	G

DTS

SECOND POSITION OF THE CODON										
		T		C		A		G		
F I R S	T	TTT	Phe [F]	TCT	Ser [S]	TAT	Tyr [Y]	TGT	Cys [C]	T
		TTC	Phe [F]	TCC	Ser [S]	TAC	Tyr [Y]	TGC	Cys [C]	C
		TTA	Leu [L]	TCA	Ser [S]	TAA	Ter [end]	TGA	Ter [end]	A
		TTG	Leu [L]	TCG	Ser [S]	TAG	Ter [end]	TGG	Trp [W]	G
T P O S I T I O N	C	CTT	Leu [L]	CCT	Pro [P]	CAT	His [H]	CGT	Arg [R]	T
		CTC	Leu [L]	CCC	Pro [P]	CAC	His [H]	CGC	Arg [R]	C
		CTA	Leu [L]	CCA	Pro [P]	CAA	Gln [Q]	CGA	Arg [R]	A
		CTG	Leu [L]	CCG	Pro [P]	CAG	Gln [Q]	CGG	Arg [R]	G
	A	ATT	Ile [I]	ACT	Thr [T]	AAT	Asn [N]	AGT	Ser [S]	T
		ATC	Ile [I]	ACC	Thr [T]	AAC	Asn [N]	AGC	Ser [S]	C
		ATA	Ile [I]	ACA	Thr [T]	AAA	Lys [K]	AGA	Arg [R]	A
		ATG	Met [M]	ACG	Thr [T]	AAG	Lys [K]	AGG	Arg [R]	G
	G	GTT	Val [V]	GCT	Ala [A]	GAT	Asp [D]	GGT	Gly [G]	T
		GTC	Val [V]	GCC	Ala [A]	GAC	Asp [D]	GGC	Gly [G]	C
		GTA	Val [V]	GCA	Ala [A]	GAA	Glu [E]	GGA	Gly [G]	A
		GTG	Val [V]	GCG	Ala [A]	GAG	Glu [E]	GGG	Gly [G]	G

or

Σχεδιασμός Βιβλιοθηκών – Θέση 51



- Αλανίνη 18.75%
- Βαλίνη 7.28%
- Ισολευκίνη 7.29%
- Λευκίνη 33.18%
- Σερίνη 9.95%

Σχεδιασμός Βιβλιοθηκών – Θέση 51

1^η θέση: A,T,G

2^η θέση: C,T

3^η θέση: A&G

DYR

SECOND POSITION OF THE CODON										
		T		C		A		G		
FIRST POSITION	T	TTT	Phe [F]	TCT	Ser [S]	TAT	Tyr [Y]	TGT	Cys [C]	T
		TTC	Phe [F]	TCC	Ser [S]	TAC	Tyr [Y]	TGC	Cys [C]	C
		TTA	Leu [L]	TCA	Ser [S]	TAA	Ter [end]	TGA	Ter [end]	A
		TTG	Leu [L]	TCG	Ser [S]	TAG	Ter [end]	TGG	Trp [W]	G
	C	CTT	Leu [L]	CCT	Pro [P]	CAT	His [H]	CGT	Arg [R]	T
		CTC	Leu [L]	CCC	Pro [P]	CAC	His [H]	CGC	Arg [R]	C
		CTA	Leu [L]	CCA	Pro [P]	CAA	Gln [Q]	CGA	Arg [R]	A
		CTG	Leu [L]	CCG	Pro [P]	CAG	Gln [Q]	CGG	Arg [R]	G
	A	ATT	Ile [I]	ACT	Thr [T]	AAT	Asn [N]	AGT	Ser [S]	T
		ATC	Ile [I]	ACC	Thr [T]	AAC	Asn [N]	AGC	Ser [S]	C
		ATA	Ile [I]	ACA	Thr [T]	AAA	Lys [K]	AGA	Arg [R]	A
		ATG	Met [M]	ACG	Thr [T]	AAG	Lys [K]	AGG	Arg [R]	G
	G	GTT	Val [V]	GCT	Ala [A]	GAT	Asp [D]	GGT	Gly [G]	T
		GTC	Val [V]	GCC	Ala [A]	GAC	Asp [D]	GGC	Gly [G]	C
		GTA	Val [V]	GCA	Ala [A]	GAA	Glu [E]	GGA	Gly [G]	A
		GTG	Val [V]	GCG	Ala [A]	GAG	Glu [E]	GGG	Gly [G]	G

Σχεδιασμός Βιβλιοθηκών – Συνδυαστική βιβλιοθήκη

Amino acids [AA] encoded in each position					
	1	2	3	4	5
Ala [A]	2	0	2	0	0
Arg [R]	3	0	0	0	0
Asn [N]	1	0	0	0	0
Asp [D]	1	0	0	0	0
Cys [C]	0	0	0	0	0
Gln [Q]	1	0	0	0	0
Glu [E]	1	0	0	0	0
Gly [G]	2	0	0	0	0
His [H]	1	0	0	0	0
Ile [I]	0	1	1	0	0
Leu [L]	0	1	2	0	0
Lys [K]	1	0	0	0	0
Met [M]	0	1	1	0	0
Phe [F]	0	1	0	0	0
Pro [P]	2	0	0	0	0
Ser [S]	1	0	2	0	0
Thr [T]	2	0	2	0	0
Trp [W]	0	0	0	0	0
Tyr [Y]	0	0	0	0	0
Val [V]	0	2	2	0	0
Stop	0	0	0	0	0
Codons	18	6	12	0	0
AA	12	5	7	0	0

VVW-DTK-DYR

II. SET % COVERAGE and % WT background		95
		0
Positions Randomized	Codons	Colonies
1		
1 + 2		
1 + 2 + 3	1296	3881
1 + 2 + 3 + 4		
1 + 2 + 3 + 4 + 5		

Σχεδιασμός Βιβλιοθηκών – Συνδυαστική βιβλιοθήκη

Amino acids [AA] encoded in each position					
	1	2	3	4	5
Ala [A]	2	0	2	0	0
Arg [R]	3	0	0	0	0
Asn [N]	1	0	0	0	0
Asp [D]	1	0	0	0	0
Cys [C]	0	0	0	0	0
Gln [Q]	1	0	0	0	0
Glu [E]	1	0	0	0	0
Gly [G]	2	0	0	0	0
His [H]	1	0	0	0	0
Ile [I]	0	1	1	0	0
Leu [L]	0	1	2	0	0
Lys [K]	1	0	0	0	0
Met [M]	0	1	1	0	0
Phe [F]	0	1	0	0	0
Pro [P]	2	0	0	0	0
Ser [S]	1	0	2	0	0
Thr [T]	2	0	2	0	0
Trp [W]	0	0	0	0	0
Tyr [Y]	0	0	0	0	0
Val [V]	0	2	2	0	0
Stop	0	0	0	0	0
Codons	18	6	12	0	0
AA	12	5	7	0	0

VVW-DTK-DYR VS NNK-NNK-NNK

		NNK, NNK, NNK	VVW, DTK, DYR
95% Κάλυψη	Κωδικόνια	32768	1296
	Αποικίες	98163	3881
Επιτρεπτά αα	Θέση 9	7	7
	Θέση 15	4	4
	Θέση 51	5	5
Μη επιτρεπτά αα	Θέση 9	13	5
	Θέση 15	16	1
	Θέση 51	15	2

Amino acids [AA] encoded in each position					
	1	2	3	4	5
Ala [A]	2	2	2	0	0
Arg [R]	3	3	3	0	0
Asn [N]	1	1	1	0	0
Asp [D]	1	1	1	0	0
Cys [C]	1	1	1	0	0
Gln [Q]	1	1	1	0	0
Glu [E]	1	1	1	0	0
Gly [G]	2	2	2	0	0
His [H]	1	1	1	0	0
Ile [I]	1	1	1	0	0
Leu [L]	3	3	3	0	0
Lys [K]	1	1	1	0	0
Met [M]	1	1	1	0	0
Phe [F]	1	1	1	0	0
Pro [P]	2	2	2	0	0
Ser [S]	3	3	3	0	0
Thr [T]	2	2	2	0	0
Trp [W]	1	1	1	0	0
Tyr [Y]	1	1	1	0	0
Val [V]	2	2	2	0	0
Stop	1	1	1	0	0
Codons	32	32	32	0	0
AA	20	20	20	0	0

Σχεδιασμός Βιβλιοθηκών – Συνδυαστική βιβλιοθήκη

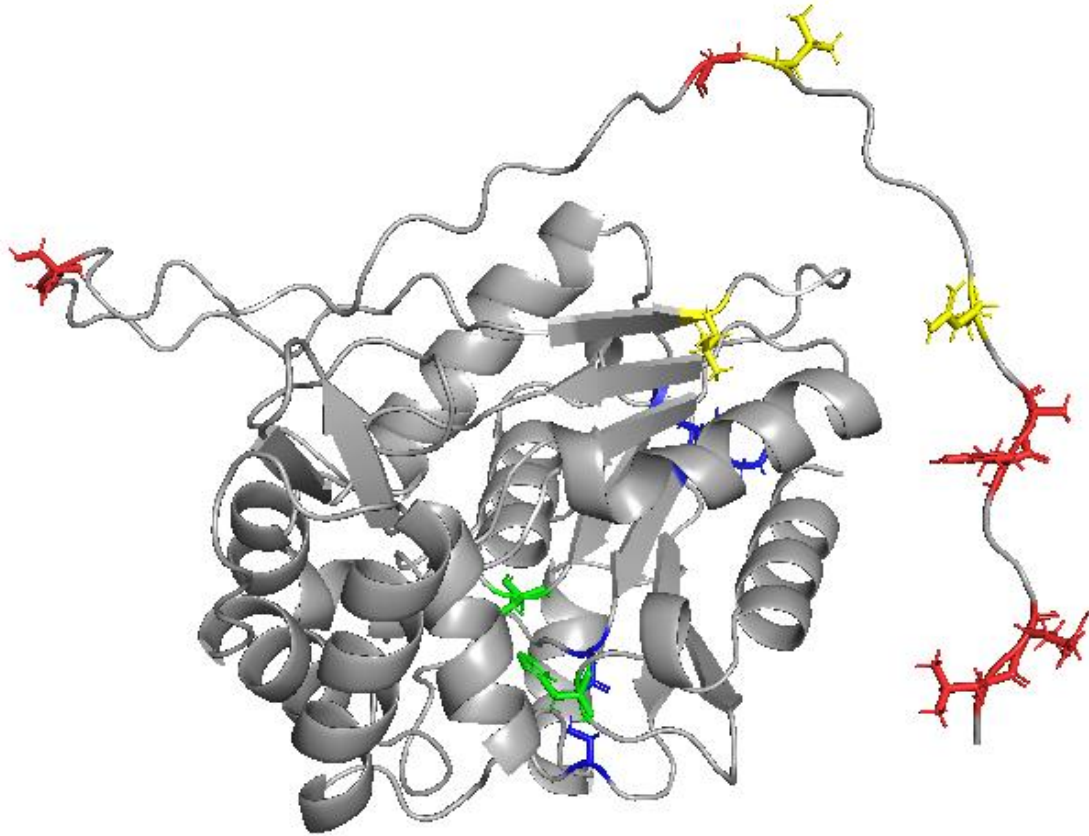
Amino acids [AA] encoded in each position					
	1	2	3	4	5
Ala [A]	2	0	2	0	0
Arg [R]	3	0	0	0	0
Asn [N]	1	0	0	0	0
Asp [D]	1	0	0	0	0
Cys [C]	0	0	0	0	0
Gln [Q]	1	0	0	0	0
Glu [E]	1	0	0	0	0
Gly [G]	2	0	0	0	0
His [H]	1	0	0	0	0
Ile [I]	0	1	1	0	0
Leu [L]	0	1	2	0	0
Lys [K]	1	0	0	0	0
Met [M]	0	1	1	0	0
Phe [F]	0	1	0	0	0
Pro [P]	2	0	0	0	0
Ser [S]	1	0	2	0	0
Thr [T]	2	0	2	0	0
Trp [W]	0	0	0	0	0
Tyr [Y]	0	0	0	0	0
Val [V]	0	2	2	0	0
Stop	0	0	0	0	0
Codons	18	6	12	0	0
AA	12	5	7	0	0

VVW-DTK-DYR VS NDT-NDT-NDT

		NDT, NDT, NDT	VVW, DTK, DYR
95% Κάλυψη	Κωδικόνια	1728	1296
	Αποικίες	5175	3881
Επιτρεπτά αα	Θέση 9	3	7
	Θέση 15	4	4
	Θέση 51	4	5
Μη επιτρεπτά αα	Θέση 9	9	5
	Θέση 15	8	1
	Θέση 51	8	2

Amino acids [AA] encoded in each position					
	1	2	3	4	5
Ala [A]	0	0	0	0	0
Arg [R]	1	1	1	0	0
Asn [N]	1	1	1	0	0
Asp [D]	1	1	1	0	0
Cys [C]	1	1	1	0	0
Gln [Q]	0	0	0	0	0
Glu [E]	0	0	0	0	0
Gly [G]	1	1	1	0	0
His [H]	1	1	1	0	0
Ile [I]	1	1	1	0	0
Leu [L]	1	1	1	0	0
Lys [K]	0	0	0	0	0
Met [M]	0	0	0	0	0
Phe [F]	1	1	1	0	0
Pro [P]	0	0	0	0	0
Ser [S]	1	1	1	0	0
Thr [T]	0	0	0	0	0
Trp [W]	0	0	0	0	0
Tyr [Y]	1	1	1	0	0
Val [V]	1	1	1	0	0
Stop	0	0	0	0	0
Codons	12	12	12	0	0
AA	12	12	12	0	0

Μοντέλο ομολογίας ABHDB_HUMAN (Q8NFV4)



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Σας ευχαριστούμε για την προσοχή σας!

