

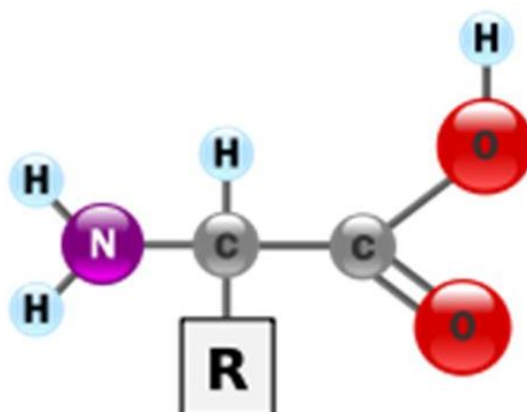
ΑΡΙΣΤΟΤΕΛΕΙΟ ΠΑΝΕΠΙΣΤΗΜΙΟ ΘΕΣΣΑΛΟΝΙΚΗΣ

ΣΧΟΛΗ ΘΕΤΙΚΩΝ ΕΠΙΣΤΗΜΩΝ

ΤΜΗΜΑ ΧΗΜΕΙΑΣ

ΕΡΓΑΣΤΗΡΙΟ ΒΙΟΧΗΜΕΙΑΣ

Άσκηση Δομικής Βιοχημείας



Ονοματεπώνυμο: Καρατζά Μελπομένη

A.E.M.: 8952

Επιβλέπουσα καθηγήτρια: κα. Χολή-Παπαδοπούλου
Θεοδώρα

Αναφορά Αποτελεσμάτων

Κωδικός- Accession number: **P12645**

Πρωτεΐνη: Bone morphogenetic protein 3 - Οστική μορφογενετική πρωτεΐνη

Short name: BMP 3

Οργανισμός: Homo sapiens (Human)

Function – Λειτουργία: ρυθμίζει αρνητικά την οστική πυκνότητα. Ανταγωνίζεται την ικανότητα ορισμένων οστεογόνων BMP να επάγουν διαφοροποίηση και οστεογένεση οστεοπαράγοντων.

Fasta Sequence

```
MAGASRLLFLWLGCFCVSLAQGERPKPPFPELRKAVPGDRTAGGGPDSELQPQDKVSEHM
LRLYDRYSTVQAARTPGSLEGGSQWRPRLREGNTVRSFRAAAAETLERKGLYIFNLTS
LTKSENILSATLYFCIGELGNISLSCPVS GGCSHHAQRKHIQIDLSAWTLKFSRNQSQLL
GHLSVDMASHRDIMSWLSKDITQLLRKAKENEEFLIGFNITSKGRQLPKRRLPFPEPYI
LVYANDAAISEPESVVSSLQGHRNFPTGTVPKWDSHIRAALSIERRKKRSTGVLLPLQNN
ELPGA EYQYKKDEVWEERKPYKTLQAQ APEKSKNKKKQRKGPHRKSQTLQFDEQTLKKAR
RKQWIEPRNCARRYLKVD FADIGWSEWISPKSFDAYYCSGACQFPMPKSLKPSNHATIQ
SIVRAVG VVPGIPECCVPEKMSSLSILFFDENKNVVLKVYPNMTVESACR
```

PTM/Processing

Ακολουθίες DNA και cDNA και mRNA σε τρεις διαφορετικές τράπεζες

δεδομένων

1.EMBL

EMBL mRNA (cDNA clone MGC:116934 IMAGE:40006302), complete cds.

```
TCAGCGTTGGAGTGAGACGGCGCCCGCAGCGCCCTGCGCGGGTGAGGTCCGCGCAGCTGCTG
GGGAAGAGCCACCTGTCAGGCTGCGCTGGGTGAGCGCAGCAAGTGGGGCTGGCCGCTATCTCG
CTGCACCCGGCCGCGCTCCCGGGCTCCGTGCGCCCTCGCCCCAGCTGGTTTGAGATTCAACCCTC
GGCTCCGCCCGCCGGCTCCTTGCGCCTTCGGAGTGTCGCCGACGCGCCGGGAGCCGACGCGC
CGCGCGGGTACCTAGCCATGGCTGGGGCGAGCAGGCTGCTCTTTCTGTGGCTGGGCTGCTTCTG
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GTCCAGTGTCTGGAGGATGCTCCCATCATGCTCAGAGGAAACACATTGAGATTGATCTTTCTGCAT
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CGAGCTTCCTGGGGCAGAATACCAAGTATAAAAAGGATGAGGTGTGGGAGGAGAGAAAGCCTTACA
```

AGACCCTTCAGGCTCAGGCCCTGAAAAGAGTAAGAATAAAAAAGAAACAGAGAAAGGGGCCTCAT
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TCTTTGAAGCCATCAAATCATGCTACCATCCAGAGTATAGTGAGAGCTGTGGGGGTCTTCCTGGG
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GAACTCATTGAATGC

>ENA|AAH96270|AAH96270.1 Homo sapiens (human) bone morphogenetic protein 3
ATGGCTGGGGCGAGCAGGCTGCTCTTTCTGTGGCTGGGCTGCTTCTGCGTGAGCCTGGCGCAGG
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TCTTGAAGAAAAGGACTGTATATCTTCAATCTGACATCGCTAACCAAGTCTGAAAACATTTTGTCTG
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GCTCCCATCATGCTCAGAGGAAACACATTTCAGATTGATCTTTCTGCATGGACCCTCAAATTCAGCAG
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TACCAGTATAAAAAGGATGAGGTGTGGGAGGAGAGAAAGCCTTACAAGACCCTTCAGGCTCAGGC
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AGGAGATACCTCAAGGTAGACTTTGCAGATATTGGCTGGAGTGAATGGATTATCTCCCCCAAGTCC
TTTGATGCCTATTATTGCTCTGGAGCATGCCAGTTCCCCATGCCAAAGTCTTTGAAGCCATCAAATC
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2.GenBank

>ENA|BC096270|BC096270.2 Homo sapiens bone morphogenetic protein 3, mRNA (cDNA
clone MGC:116935 IMAGE:40006303), complete cds.

TCAGCGTTGGAGTGGAGACGGCGCCCGCAGCGCCCTGCGCGGGTGAGGTCCGCGCAGCTGCTG
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GGCTCCGCGCCGGCTCCTTGCGCCTTCGGAGTGTCCCGCAGCGACGCCGGGAGCCGACGCGC
CGCGCGGGTACCTAGCCATGGCTGGGGCGAGCAGGCTGCTCTTTCTGTGGCTGGGCTGCTTCTG
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GAATGTAGTGCTTAAAGTATACCCTAACATGACAGTAGAGTCTTGCGCTTGACAGATAACCTGGCAAA
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3.DDBJ

>ENA|AAH96270|AAH96270.1 Homo sapiens (human) bone morphogenetic protein 3

ATGGCTGGGGCGAGCAGGCTGCTCTTTCTGTGGCTGGGCTGCTTCTGCGTGAGCCTGGCGCAGG
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TTTGATGCCTATTATTGCTCTGGAGCATGCCAGTTCCCCATGCCAAAGTCTTTGAAGCCATCAAATC
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ATACCCTAACATGACAGTAGAGTCTTGCGCTTGACAGATAA

Σύγκριση μεταφρασμένου CCDS με τις τρεις παρακάτω ακολουθίες:

S1: 5'3' Frame 1- Όλη η ακολουθία.

S2: 5'3' Frame 3- Μπλέ ακολουθία.

S3: 5'3' Frame 2-Μπλέ ακολουθία με παραπάνω νουκλεοτίδια για το 5' άκρο.

S4: Μεταφρασμένο CCDS.

	10	20	30	40	50	60
S1xxxx0	MAGASRLLFLWLGCFCVSLAQGERPKPPFPELRKAVPGDRTAGGGPDSELQPQDKVSEHM					
S4xxxx3	MAGASRLLFLWLGCFCVSLAQGERPKPPFPELRKAVPGDRTAGGGPDSELQPQDKVSEHM					
S3xxxx2	-----					

S2xxxx1	-----
Consensus	
Prim. cons.	MAGASRLLFLWLGCFCVSLAQGERPKPPFPELRKAVPGDRTAGGGPDSELQPQDKVSEHM
	70 80 90 100 110 120
S1xxxx0	LRLYDRYSTVQAARTPGSLEGGSQWRPRLREGNTVRSFRAAAATLERKGLYIFNLTS
S4xxxx3	LRLYDRYSTVQAARTPGSLEGGSQWRPRLREGNTVRSFRAAAATLERKGLYIFNLTS
S3xxxx2	-----AAETLERKGLYIFNLTS
S2xxxx1	-----TLERKGLYIFNLTS
Consensus	aaETLERKGLYIFNLTS
Prim. cons.	LRLYDRYSTVQAARTPGSLEGGSQWRPRLREGNTVRSFRAAAAETLERKGLYIFNLTS
	130 140 150 160 170 180
S1xxxx0	LTKSENILSATLYFCIGELGNISLSCPVSGGCSHHAQRKHIQIDLSAWTLKFSRNQSQLL
S4xxxx3	LTKSENILSATLYFCIGELGNISLSCPVSGGCSHHAQRKHIQIDLSAWTLKFSRNQSQLL
S3xxxx2	LTKSENILSATLYFCIGELGNISLSCPVSGGCSHHAQRKHIQIDLSAWTLKFSRNQSQLL
S2xxxx1	LTKSENILSATLYFCIGELGNISLSCPVSGGCSHHAQRKHIQIDLSAWTLKFSRNQSQLL
Consensus	LTKSENILSATLYFCIGELGNISLSCPVSGGCSHHAQRKHIQIDLSAWTLKFSRNQSQLL
Prim. cons.	LTKSENILSATLYFCIGELGNISLSCPVSGGCSHHAQRKHIQIDLSAWTLKFSRNQSQLL
	190 200 210 220 230 240
S1xxxx0	GHLSVDMAKSHRDIMSWLSKDITQLLRKAKENEEFLIGFNITSKGRQLPKRRLPFPEPYI
S4xxxx3	GHLSVDMAKSHRDIMSWLSKDITQLLRKAKENEEFLIGFNITSKGRQLPKRRLPFPEPYI
S3xxxx2	GHLSVDMAKSHRDIMSWLSKDITQLLRKAKENEEFLIGFNITSKGRQLPKRRLPFPEPYI
S2xxxx1	GHLSVDMAKSHRDIMSWLSKDITQLLRKAKENEEFLIGFNITSKGRQLPKRRLPFPEPYI
Consensus	GHLSVDMAKSHRDIMSWLSKDITQLLRKAKENEEFLIGFNITSKGRQLPKRRLPFPEPYI
Prim. cons.	GHLSVDMAKSHRDIMSWLSKDITQLLRKAKENEEFLIGFNITSKGRQLPKRRLPFPEPYI
	250 260 270 280 290 300
S1xxxx0	LVYANDAAISEPESVSSLQGHRNFPTGTVPKWDSHIRAALSIERRKKRSTGVLLPLQNN
S4xxxx3	LVYANDAAISEPESVSSLQGHRNFPTGTVPKWDSHIRAALSIERRKKRSTGVLLPLQNN
S3xxxx2	LVYANDAAISEPESVSSLQGHRNFPTGTVPKWDSHIRAALSIERRKKRSTGVLLPLQNN
S2xxxx1	LVYANDAAISEPESVSSLQGHRNFPTGTVPKWDSHIRAALSIERRKKRSTGVLLPLQNN
Consensus	LVYANDAAISEPESVSSLQGHRNFPTGTVPKWDSHIRAALSIERRKKRSTGVLLPLQNN
Prim. cons.	LVYANDAAISEPESVSSLQGHRNFPTGTVPKWDSHIRAALSIERRKKRSTGVLLPLQNN

	310	320	330	340	350	360
S1xxxx0	ELPGA	EYQYKKDEV	WEERKPYKTLQAQ	AEKSKNKKKQ	RKGPHRKSQTLQ	FDEQTLKKAR
S4xxxx3	ELPGA	EYQYKKDEV	WEERKPYKTLQAQ	AEKSKNKKKQ	RKGPHRKSQTLQ	FDEQTLKKAR
S3xxxx2	ELPGA	EYQYKKDEV	WEERKPYKTLQAQ	AEKSKNKKKQ	RKGPHRKSQTLQ	FDEQTLKKAR
S2xxxx1	ELPGA	EYQYKKDEV	WEERKPYKTLQAQ	AEKSKNKKKQ	RKGPHRKSQTLQ	FDEQTLKKAR
Consensus	ELPGA	EYQYKKDEV	WEERKPYKTLQAQ	AEKSKNKKKQ	RKGPHRKSQTLQ	FDEQTLKKAR
Prim.cons.	ELPGA	EYQYKKDEV	WEERKPYKTLQAQ	AEKSKNKKKQ	RKGPHRKSQTLQ	FDEQTLKKAR

	370	380	390	400	410	420
S1xxxx0	RKQWIEPRNCARRY	LKVDFADIGSEWII	SPKSFDAYYCSGACQ	FMPKSLKPSNHATIQ		
S4xxxx3	RKQWIEPRNCARRY	LKVDFADIGSEWII	SPKSFDAYYCSGACQ	FMPKSLKPSNHATIQ		
S3xxxx2	RKQWIEPRNCARRY	LKVDFADIGSEWII	SPKSFDAYYCSGACQ	FMPK-----		
S2xxxx1	RKQWIEPRNCARRY	LKVDFADIGSEWII	SPKSFDAYYCSGACQ	FMPK-----		
Consensus	RKQWIEPRNCARRY	LKVDFADIGSEWII	SPKSFDAYYCSGACQ	FMPK		
Prim.cons.	RKQWIEPRNCARRY	LKVDFADIGSEWII	SPKSFDAYYCSGACQ	FMPKSLKPSNHATIQ		

	430	440	450	460	470
S1xxxx0	SIVRAVG	VPGIPEPCCVPEK	MSSLSILFFDENK	NNVLKVYPNMTV	ESCACR
S4xxxx3	SIVRAVG	VPGIPEPCCVPEK	MSSLSILFFDENK	NNVLKVYPNMTV	ESCAR-
S3xxxx2	-----				
S2xxxx1	-----				
Consensus					
Prim.cons.	SIVRAVG	VPGIPEPCCVPEK	MSSLSILFFDENK	NNVLKVYPNMTV	ESCA2R

Από την τράπεζα CCDS παίρνουμε την παρακάτω μεταφράσιμη ακολουθία νουκλεοτιδίων και μεταφράζουμε το γαλάζιο πλαίσιο ανάγνωσης που αποτελεί την μεταφράσιμη λειτουργική πρωτεΐνη.

S1 ακολουθία βάσεων DNA

ATGGCTGGGGCGAGCAGGCTGCTCTTTCTGTGGCTGGGCTGCTTCTGCGTGAGCCTGGCGCAGGGAGAGA
GACCGAAGCCACCTTTCCCGGAGCTCCGCAAAGCTGTGCCAGGTGACCGCACGGCAGGTGGTGGCCCCGA
CTCCGAGCTGCAGCCGCAAGACAAGGTCTCTGAACACATGCTGCGGCTCTATGACAGGTACAGCACGGTC
CAGGCGGGCCGGACACCGGGCTCCCTGGAGGGAGGCTCGCAGCCCTGGCGCCCTCGGCTCCTGCGCGAAG
GCAACACGGTTCGAGCTTTGGGGCGGCAGCAGCAGAACTCTTGAAAGAAAAGGACTGTATATCTTCAA
TCTGACATCGCTAACCAAGTCTGAAAACATTTTGTCTGCCACACTGTATTTCTGTATTGGAGAGCTAGGA
AACATCAGCCTGAGTTGTCCAGTGTCTGGAGGATGCTCCCATCATGCTCAGAGGAAACACATTAGATTG
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GGCCAAATCTCATCGAGATATTATGTCCTGGCTGTCTAAAGATATCACTCAACTCCTTGAGGAAGGCCAAA
GAAAATGAAGAGTTTCTCATAGGATTTAACATTACGTCCAAGGGACGCCAGCTGCCAAAGAGGAGGTTAC
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CTTTCCATTGAGCGGAGGAAGAAGCGCTCTACTGGGGTCTTGTGCTCTGCAGAACACGAGCTTCTG
GGGCAGAATACCAAGTATAAAAAGGATGAGGTGTGGGAGGAGAGAAAGCCTTACAAGACCCTTCAGGCTCA
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CACTCAGTATTTTATTCTTTGATGAAAATAAGAATGTAGTGCTTAAAGTATACCCTAACATGACAGTAGA
GTCTTGCGCTTGACAGATAA

FRAME S1 – Μετάφραση – ακολουθία αμινοξέων

5'3' Frame 1

MAGASRLFLWLGCFCVSLAQGERPKPPFPELRKAVPGD
RTAGGGPDSELQPQDKVSEHMLRLYDRYSTVQAARTPGS
LEGGSQPWRPRLREGNTVRSFRAAAAETLERKGLYIFNL
TSLTKSENILSATLYFCIGELGNISLSCPVS GGCSHHAQRK
HIQIDLSAWTLKFSRNQS QLLGHLSDVDMAKSHRDI MSWLS
KDITQLLRKAKENEEFLIGFNITSKGRQLPKRRLPFPEPYIL
VYANDAAISEPESVVSSLQGHRNFPTGTVPKWDSHIRAAL
SIERRKKRSTGVLLPLQNNELPGA EYQYKKDEVWEERKPY
KTLQAQAPEKSKNKKKQ RKGPHRKSQTLQFDEQTLKKAR
RKQWIEPRNCARRY LKVD FADIGWSEWIISP KSF DAY YCS
GACQFP MPKSLKPSNHATI QSIVRAVG VVP GIPEPCCVPE
K MSSL SILFFDENKNVVLKVYPN M TVESCACR Stop

S2-το μπλέ κομμάτι της νουκλεοτιδικής ακολουθίας.

AAACTCTGAAAGAAAAGGACTGTATATCTTCAATCTGACATCGCTAACCAAGTCTGAAAACATTTTGTCTGCCAC
ACTGTATTTCTGTATTGGAGAGCTAGGAAACATCAGCCTGAGTTGTCCAGTGTCTGGAGGATGCTCCCATCATGCT
CAGAGGAAACACATTCAGATTGATCTTTCTGCATGGACCCTCAAATTCAGCAGAAACCAAAGTCAACTCCTTGCC
ATCTGTCAGTGGATATGGCCAAATCTCATCGAGATATTATGTCCTGGCTGTCTAAAGATATCACTCAACTCCTGAG
GAAGGCCAAAGAAAATGAAGAGTTTCTCATAGGATTTAACATTACGTCCAAGGGACGCCAGCTGCCAAAGAGGAGG
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TAAAAAGAAAACAGAGAAAGGGGCTCATCGGAAGAGCCAGACGCTCCAATTTGATGAGCAGACCCTGAAAAGGCA
AGGAGAAAAGCAGTGGATTGAACCTCGGAATTGCGCCAGGAGATACCTCAAGGTAGACTTTGCAGATATTGGCTGGA
GTGAATGGATTATCTCCCCAAGTCCTTTGATGCCTATTATTGCTCTGGAGCATGCCAGTTCCTCATGCCAAAG

FRAME S2

5'3' Frame 3

TLERKGLYIFNLTSLTKSENILSATLYFCIGELGNISLSCPVS
SGGCSHHAQRKHIQIDLSAWTLKFSRNQSQLLGHL SV
D **MAKSHRDI** **MSWLSKDITQLLRKAKENEEFLIGFNITSKGR**
QLPKRRLPFPEPYILVYANDAAISEPESVVSSLQGHNF
TGTVPKWDSHIRAALSIERRKKRSTGVLLPLQNNELPGA
EYQYKKDEVWEERKPYKTLQAQAPEKSKNKKKQRKGPHRK
SQTLQFDEQTLKKARRKQWIEPRNCARRYLKVDFADIGW
SEWIISPKSFDAYYCSGACQFP **MPK**

S3 - Μεταφράζουμε το μπλέ κομμάτι της ακολουθίας με μερικά νουκλεοτίδια πριν από αυτήν.

GCAGCAGAAACTCTTGAAAGAAAAGGACTGTATATCTTCAATCTGACATCGCTAACCAAGTCTGAAAACATTTTGT
CTGCCACACTGTATTTCTGTATTGGAGAGCTAGGAAACATCAGCCTGAGTTGTCCAGTGTCTGGAGGATGCTCCCT
CATGCTCAGAGGAAACACATTGAGATTGATCTTTCTGCATGGACCCTCAAATTCAGCAGAAAC **CAAAGTCAACTCT**
TGGCCATCTGTCAGTGGATATGGCCAAATCTCATCGAGATATTATGTCCTGGCTGTCTAAAGATATCACTCAACTC
TTGAGGAAGGCCAAAGAAAATGAAGAGTTCCCTCATAGGATTTAACATTACGTCCAAGGGACGCCAGCTGCCAAAGA
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TCCATTGAGCGGAGGAAGAAGCGCTCTACTGGGGTCTTGCTGCCTCTGCAGAACACGAGCTTCTGGGGCAGAAT
ACCAATATAAAAAGGATGAGGTGTGGGAGGAGAGAAAGCCTTACAAGACCCTTCAGGCTCAGGCCCCGTGAAAAGAG
TAAGAATAAAAAGAAACAGAGAAAGGGCCTCATCGGAAGAGCCAGACGCTCCAATTTGATGAGCAGACCCTGAAA
AAGGCAAGGAGAAAGCAGTGGATTGAACCTCGGAATTGCGCCAGGAGATACCTCAAGGTAGACTTTGCAGATATTG
GCTGGAGTGAATGGATTATCTCCCCAAGTCCTTTGATGCCTATTATTGCTCTGGAGCATGCCAGTTCCCCATGCC
AAAG

FRAME S3

5'3' Frame 1

A AETLERKGLYIFNLTSLTKSENILSATLYFCIGELGNISLS
CPVSGGCSHHAQRKHIQIDLSAWTLKFSRNQSQLLGHL SV
D **MAKSHRDI** **MSWLSKDITQLLRKAKENEEFLIGFNITSKGR**
QLPKRRLPFPEPYILVYANDAAISEPESVVSSLQGHNF
TGTVPKWDSHIRAALSIERRKKRSTGVLLPLQNNELPGA
EYQYKKDEVWEERKPYKTLQAQAPEKSKNKKKQRKGPHRK
SQTLQFDEQTLKKARRKQWIEPRNCARRYLKVDFADIGW
SEWIISPKSFDAYYCSGACQFP **MPK**

FRAME S4-Μεταφρασμένο CCDS

MAGASRLFLWLGCFCVSLAQGERPKPPFPPELRKAVPGDRTAGGGPDSELQPQDKVS
EHMLRLYDRYSTVQAARTPGSLEGGSQPWRPRLREGNTVRSFRAAAA **ETLERKGLY**
IFNLTSLTKSENILSATLYFCIGELGNISLSCPVSSGGCSHHAQRKHIQIDLSAWTLK
FSRNQSQLLGHL SVDMAKSHRDI **MSWLSKDITQLLRKAKENEEFLIGFNITSKGR**QL
PKRRLPFPEPYILVYANDAAISEPESVVSSLQGHNFPTGTVPKWDSHIRAALSIE
RKKRSTGVLLPLQNNELPGA **EYQYKKDEVWEERKPYKTLQAQAPEKSKNKKKQRKG**P
HRKSQTLQFDEQTLKKARRKQWIEPRNCARRYLKVDFADIGWSEWIISPKSFDAYYC
SGACQFPMPKSLKPSNHATIQSIVRAVGVPVGIPEPCCVPEKMSSLSILFFDENKN **V**
VLKVYPNMTVESCAR

Restriction enzyme map of the pTZ19 vector. The map shows a circular plasmid with a 537 aa linear representation. Various restriction sites are marked with colored vertical lines and labeled with enzyme names. The sites are distributed around the circle, with some clustered together and others well-separated. The map includes a scale bar at the top indicating the 537 aa length and a red arrow at the right end indicating the MspI site.

Restriction sites (clockwise from top left):

- *BsmBI
- *EciI
- *SmaI
- *AvaI
- *TspMI
- BsoBI
- *XmaI
- *BsiEI
- *EagI
- BsgI
- *Esp3I
- *BsmBI
- *BcgI
- NcoI
- BtgI
- KpnI
- Acc65I
- *NaeI
- *NgoMIV
- *BsrFI
- Pf1FI
- Tth111I
- BfuAI
- BspMI
- Tsp45I
- BsiHKA I
- SacI
- Eco53kI
- *BtgZI
- EcoRV
- TaqI
- HincII
- DpnI
- *MboI
- *DpnII
- Sau3AI
- Pf1MI
- *HpyCH4IV
- HindIII
- BsaWI
- *BsrBI
- *AfeI
- BmrI
- AcuI
- BtsI
- SphI
- TfiI
- MslI
- DrdI
- BstZ17I

2 cutters

Number of cuts =

#	Enzyme	Specificity	Sites & flanks	Cut positions (blunt - 5' ext - 3' ext.)
1	AccI	GT ⁺ MK ⁺ AC	list	1401/1403, 1650/1652
2	ApOI	R ⁺ AATT ⁺ Y	list	782/786, 1060/1064
3	BceAI	ACGGC(N) ₁₂ NN ⁺ _A	list	*34/36, *408/410
4	BfaI	C ⁺ TA ⁺ G	list	266/268, 686/688
5	Bpu10I	CC ⁺ TNA ⁺ GC	list	1248/1251, 1569/1572
6	BpuEI	CTTGA(G) _(N) ₁₄ NN ⁺ _A	list	907/905, 1379/1377
7	BsaI	GGTCTCN ⁺ NNNN ⁺ _A	list	*334/338, 442/446
8	BseRI	GAGGGA(N) ₈ NN ⁺ _A	list	976/974, 1232/1230
9	BspQI	GCTCTTCN ⁺ NNN ⁺ _A	list	61/64, 1298/1301
10	BstEII	G ⁺ GTINAC ⁺ C	list	383/388, 966/971
11	EcoNI	CCTNN ⁺ N ₁ NNAGG	list	329/330, 1340/1341
12	EcoO109I	RG ⁺ GNC ⁺ CY	list	1252/1255, 1292/1295
13	HphI	GGTGA(N) ₇ N ⁺ _A	list	54/53, 395/394
14	Hpy99I	⁺ CGWCG ⁺	list	*238/233, *251/246
15	KasI	G ⁺ GCGC ⁺ C	list	*20/24, *528/532
16	MlyI	GAGTC(N) ₅ ⁺	list	404, 1679
17	MscI	TGG ⁺ CCA	list	813, 833
18	MseI	T ⁺ TA ⁺ A	list	927/929, 1644/1646
19	NarI	GG ⁺ CG ⁺ CC	list	*21/23, *529/531
20	NmeAIII	GCCGAG(N) ₁₉ NN ⁺ _A	list	169/167, 514/512
21	NspI	R ⁺ CATG ⁺ Y	list	451/447, 1479/1475
22	PleI	GAGTCNNNN ⁺ N ⁺ _A	list	404/405, 1678/1679
23	PluTI	G ⁺ CGCG ⁺ C	list	*24/20, *532/528
24	PstI	C ⁺ IGCA ⁺ G	list	423/419, 1164/1160
25	SapI	GCTCTTCN ⁺ NNN ⁺ _A	list	61/64, 1298/1301
26	SfcI	C ⁺ TRYA ⁺ G	list	419/423, 1160/1164
27	SfoI	GGC ⁺ GCC	list	*22, *530
28	SmlI	C ⁺ TYRA ⁺ G	list	886/890, 1394/1398

Number of cuts = 3 OK Save as text file

#	Enzyme	Specificity	Sites & flanks	Cut positions (blunt - 5' ext. - 3' ext.)
1	AlwNI	CAG ⁺ NNN ⁺ CTG	list	60/57, 716/713, 1336/1333
2	AvaII	G ⁺ GWC ⁺ C	list	*47/50, *478/481, 774/777
3	BanI	G ⁺ GYRC ⁺ C	list	*20/24, 261/265, *528/532
4	BcoDI	GTCTC ⁺ NNNN ⁺	list	9/13, 334/338, 442/446
5	BsmAI	GTCTC ⁺ NNNN ⁺	list	9/13, 334/338, 442/446
6	BtsCI	GGATG ⁺ NN ⁺	list	728/726, 1210/1208, 1524/1522
7	CviQI	G ⁺ TAC ⁺ C	list	262/264, 469/471, 1583/1585
8	EarI	CTCTTC ⁺ NNN ⁺	list	61/64, 903/906, 1298/1301
9	FokI	GGATG (N) ⁺ g ⁺ NNNN ⁺	list	735/739, 1217/1221, 1511/1515
10	HinfI	G ⁺ ANT ⁺ C	list	410/413, 1564/1567, 1670/1673
11	MspAII	CMG ⁺ CKG ⁺	list	57, 170, 952
12	PvuII	CAG ⁺ CTG ⁺	list	57, 170, 952
13	RsaI	GT ⁺ AC ⁺	list	263, 470, 1584
14	SfaNI	GCATC (N) ⁺ g ⁺ NNNN ⁺	list	713/717, 997/1001, 1444/1448
15	StvI	C ⁺ CWGG ⁺ G	list	270/274, 808/812, 939/943

RestStart
PCRStart

HaeIII
HpaII TaqI
KpnI AvaI HincII HindIII EcoRI SmaI
MspI XhoI TaqI ClaI EcoRV HpaII
RsaI ApaI SalI TaqI AluI TaqI AvaI
XmaI

ggtaccggggccccccctcgaggtcgacggtatcgataagcttgatatcgaattccccggggacaaaatggcaagtaaaa
^10 ^20 ^30 ^40 ^50 ^60 ^70
ccatggccccggggggagctccagctgccatagctattcgaactatagcttaagggggccctgggttttaccggttcatttt

DdeI

tagcctgatgggataggtcttaagtccaacgaaccagtgtcaccactgacacaatgaggaaaaccATGTCACATCTCGCA
^90 ^100 ^110 ^120 ^130 ^140 ^150
atcggactaccctatccgagattcaggttgcttggtcacagtgggtgactgtgttactccttttggtacagtgtagagcgt

M S H L A

TaqI
BstUI
CfoI
HaeIII BstUI HhaI SspI
E L V A S A K A A I S Q A S D V A A L D N V R V E Y L
GAACTGGTTGCCAGTGCGAAGGCGGCCATTAGCCAGGCGTCAGATGTTGCCGCGTTAGATAATGTGCGCGTCGAATATTT
^170 ^180 ^190 ^200 ^210 ^220 ^230
cttgaccaacggtcacgcttccgcggtaatcggtccgcagtcctacaacggcgcaatctattacacgcgcagcttataaa

AluI
PvuII
MboII
HpaII
MseI AluI MspI
G K K G H L T L Q M T T L R E L P P E E R P A A G A V
GGGTAAAAAAGGGCACTTAACCCTTCAGATGACGACCCTGCGTGAGCTGCCGCCAGAAGAGCGTCCGGCAGCTGGTGCGG
^250 ^260 ^270 ^280 ^290 ^300 ^310
cccattttttcccggtgaattgggaagtctactgctgggacgcactcgacggcggtcttctcgcaggccgtcgaccacgcc

BstUI
CfoI CfoI CfoI
HhaI HhaI HhaI
I N E A K E Q V Q Q A L N A R K A E L E S A A L N A
TTATCAACGAAGCGAAAGAGCAGGTTTCAGCAGGCGCTGAATGCGCGTAAAGCGGAAGCTGGAAAGCGCTGCACTGAATGCG
^330 ^340 ^350 ^360 ^370 ^380 ^390
aatagttgcttcgctttctcgtccaagtcgtccgcgacttacgcgcatttcgccttgacctttcgcgcagctgacttacgc

BstUI
CfoI
HhaI HpaII MspI RsaI
R L A A E T I D V S L P G R R I E N G G L H P V T R T
CGTCTGGCGGCGGAAACGATTGATGTCTCTCTGCCAGGTCGTTCGCATTGAAAACGGCGGTCTGCATCCGGTTACCCGTAC
^410 ^420 ^430 ^440 ^450 ^460 ^470

Με κόκκινο πλαίσιο έχουν επισημανθεί τα σημεία αναγνώρισης των EcoR1 και BamH1

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                                     HpaII
                                     MspI
                                     HaeIII
      MboII
TaqI  TaqI      AluI      HpaII  MspI      TaqI      MboII
I  D  R  I  E  S  F  F  G  E  L  G  F  T  V  A  T  G  P  E  I  E  D  D  Y  H  N
CATCGACCGTATCGAAAAGTTTCTTCGGTGAGCTTGGCTTTACCGTGGCAACCGGGCCGGAAATCGAAGACGATTATCATA
      ^490      ^500      ^510      ^520      ^530      ^540      ^550
gtagctggcatagctttcaaagaagccactcgaaccgaaatggcaccgttggcccggccttttagcttctgctaatagtat
-----
                                     CfoI
                                     BstUI
                                     CfoI
                                     BssHII
                                     BstUI
                                     CfoI
                                     HhaI
                                     BssHII
      HpaII  HhaI
TaqI  MspI  HhaI
F  D  A  L  N  I  P  G  H  H  P  A  R  A  D  H  D  T  F  W  F  D  T  T  R  L
ACTTCGATGCTCTGAACATTCTGGTCACCAACCGGCGCGCGCTGACCACGACACTTTCTGGTTTGACACTACCCGCCTG
      ^570      ^580      ^590      ^600      ^610      ^620      ^630
tgaagctacgagacttgtaaggaccagtggtggggccgcgcgcgactggtgctgtgaaagaccaaactgtgatggggcgac
-----
                                     HaeIII
      MboI
      NdeII
      RsaI      RsaI      HinfI      BstUI
L  R  T  Q  T  S  G  V  Q  I  R  T  M  K  A  Q  Q  P  P  I  R  I  I  A  P  G  R
CTGCGTACCCAGACCTCTGGCGTACAGATCCGCACCATGAAAGCCCAGCAGCCACCGATTTCGTATCATCGCGCCTGGCCG
      ^650      ^660      ^670      ^680      ^690      ^700      ^710
gacgcatgggtctggagaccgcatgtctagcgctggtactttcgggtcgtcggtggctaagcatagtagcgggacggc
-----
      HinfI
V  Y  R  N  D  Y  D  Q  T  H  T  P  M  F  H  Q  M  E  G  L  I  V  D  T  N  I  S
TGTTTATCGTAACGACTACGACCAGACTCACACGCCGATGTTCCATCAGATGGAAGGTCTGATTGTTGATACCAACATCA
      ^730      ^740      ^750      ^760      ^770      ^780      ^790
acaaatagcattgctgatgctggtctgagtgctgcggtctacaaggtagtctaccttcagactaacaactatggtttagt
-----
      AluI      MboII
      HinfI
F  T  N  L  K  G  T  L  H  D  F  L  R  N  F  F  E  E  D  L  Q  I  R  F  R  P
GCTTTACCAACCTGAAAGGCACGCTGCACGACTTCCTGCGTAACTTCTTTGAGGAAGATTTGCAGATTTCGCTTCCGTCCT
      ^810      ^820      ^830      ^840      ^850      ^860      ^870
cgaaatggttggactttccgtgcgacgtgctgaaggacgcattgaagaaactccttctaactgtctaagcgaaggcagga
-----
      PstI      AatII
S  Y  F  P  F  T  E  P  S  A  E  V  D  V  M  G  K  N  G  K  W  L  E  V  L  G  C

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Με κόκκινο πλαίσιο έχουν επισημανθεί τα σημεία αναγνώρισης των EcoR1 και BamH1

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TCCTACTTCCCGTTTACCGAACCTTCTGCAGAAGTGGACGTCATGGGTAAAAACGGTAAATGGCTGGAAGTGCTGGGCTG
      ^890      ^900      ^910      ^920      ^930      ^940      ^950
aggatgaaggggcaaatggcttggaagacgtcttcacctgcagtacccatttttgccatttaccgaccttcacgacccgac
-----
                                     HpaII
                                     MspI
                                     TaqI
      G  M  V  H  P  N  V  L  R  N  V  G  I  D  P  E  V  Y  S  G  F  G  F  G  M  G  M
CGGGATGGTGCATCCGAACGTGTTGCGTAACGTTGGCATCGACCCGGAAGTTTACTCTGGTTTCGGCTTCGGGATGGGGA
      ^970      ^980      ^990      ^1000     ^1010     ^1020     ^1030
gccctaccacgtaggcttgcaaacgcattgcaaccgtagctgggccttcaaagagaccaaagccgaagccctaccct
-----
                                     MboI
                                     MboII      TaqI      NdeII
      E  R  L  T  M  L  R  Y  G  V  T  D  L  R  S  F  F  E  N  D  L  R  F  L  K  Q
TGGAGCGTCTGACTATGTTGCGTTACGGCGTCACCGACCTGCGTTTCTTCGAAAACGATCTGCGTTTCCTCAAACAG
      ^1050     ^1060     ^1070     ^1080     ^1090     ^1100     ^1110
acctcgagactgatacaacgcaatgccgcagtggtggacgcaagtaagaagcttttgctagacgcaaaggagttgtc
-----
      DraI                                     HpaII
      MseI                                     MspI
      F  K  Z
TTTAAATAAaggcaggaatagattatgaaattcagtgaaactgtggttacgcgaatgggtgaacccggcgattgatagcgat
      ^1130     ^1140     ^1150     ^1160     ^1170     ^1180     ^1190
aaattttattccgtccttatctaatactttaagtcacttgacaccaatgcgcttaccacttgggccgctaactatcgcta
-----
                                     SpeI
                                     BamHI
      CfoI                                     HaeIII      SacII
      HhaI                                     MboI      NdeII      XbaI      NotI      BstUI
cgcgctggcaaatcaaatcactatggcgggcctggaagttgggggatccactagttctagagcgggccgccaccgcggtgga
      ^1210     ^1220     ^1230     ^1240     ^1250     ^1260     ^1270
cgcgaccgttttagtttagtgataccgcccggaccttcaacccctaggtgatcaagatctcgccggcggtggcgccacct
-----
      SacI
      AluI                                     HinfI      HaeIII
      S  L  A  V  V  L  Q  R  R  D  W  E  N  P  G
gctccaattcgccctatagtgagtcgtattacaATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCTTGGC
      ^1290     ^1300     ^1310     ^1320     ^1330     ^1340     ^1350
cgagggttaagcgggatatactcagcataatgttaagtgaccggcagcaaaatgttgacgactgacccttttgggaccg
-----
                                     MboI
                                     NdeII
      MseI                                     AluI      MboII
      PvuII                                     HaeIII      PvuI
V  T  Q  L  N  R  L  A  A  H  P  P  F  A  S  W  R  N  S  E  E  A  R  T  D  R  P
GTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCC
      ^1370     ^1380     ^1390     ^1400     ^1410     ^1420     ^1430
caatggggttgaattagcggaacgtcgtgtaggggaaagcggtcgcaccgcattatcgcttctccgggcgtggctagcggg
-----

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Με κόκκινο πλαίσιο έχουν επισημανθεί τα σημεία αναγνώρισης των EcoR1 και BamH1

```

          CfoI          CfoI          MseI          CfoI          CfoI
          HhaI          HhaI          HhaI          HhaI          HhaI
          BstUI
S  Q  Q  L  R  S  L  N  G  E  W
TTCCTCAACAGTTGCGCAGCCTGAATGGCGAATGGgacgcgcctctgtagcggcgccattaagcgcggcggtgtggtggtta
      ^1450      ^1460      ^1470      ^1480      ^1490      ^1500      ^1510
aaggggtgtcaacgcgtcggtgacttaccgcttaccctgcgcgggacatcgccgcgtaattcgcgccgccccacaccaccaat
-----
          CfoI          CfoI          CfoI          MboII
          HhaI          HhaI          HhaI
          BstUI
cgcgcgagcgtgaccgctacacttgccagcgccctagcgcccgctcctttcgctttcttcccttcctttctcgccacgttc
      ^1530      ^1540      ^1550      ^1560      ^1570      ^1580      ^1590
gcgcgctcgactggcgcgatgtgaacggtcgcgggatcgcgggcgaggaaaagcgaaaagaagggaaggaagcggtgcaag
-----
          NaeI          HpaII          MspI          AluI          TaqI
cgcggtttccccgtcaagctctaaatcgggggctcccttttaggggtccgatttagtgctttacggcacctcgaccccaa
      ^1610      ^1620      ^1630      ^1640      ^1650      ^1660      ^1670
cggccgaaaaggggcagttcgagatttagcccccgagggaatccaagcctaaatcacgaaatgccgtggagctgggggtt
-----
          HaeIII          HinfI
aaaacttgattaggggtgatggttcacgtagtgggccatcgccctgatagacgggtttttcgccctttgacgttggagtcca
      ^1690      ^1700      ^1710      ^1720      ^1730      ^1740      ^1750
ttttgaactaatcccactaccaagtgcaccccgtagcgggactatctgccaaaaagcgggaaactgcaacctcaggt
-----
          MseI          HinfI
cgttctttaaatagtggaactcttgtttccaaactggaacaacactcaaccctatctcggtctattcttttgatttataaggg
      ^1770      ^1780      ^1790      ^1800      ^1810      ^1820      ^1830
gcaagaaattatcacctgagaacaaggttgaccttgttgtgagttgggatagagccagataagaaaactaaatattccc
-----
          MseI          HaeIII          MseI          AluI          MseI          BstUI          MseI          MseI          SspI
attttgccgatttcggcctattgggttaaaaaatgagctgatttaacaaaaatttaacgcgaattttaacaaaatattaac
      ^1850      ^1860      ^1870      ^1880      ^1890      ^1900      ^1910
taaaacggctaaagccggataaccaattttttactcgactaaattgtttttaattgcgcttaaaattgttttataattg
-----
          BstUI          CfoI          HhaI
gcttacaatttaggtggcacttttcggggaaatgtgcgcggaacccctatttggtttttttctaaatacattcaaatat
      ^1930      ^1940      ^1950      ^1960      ^1970      ^1980      ^1990
cgaatgttaaatccaccgtgaaaagcccctttacacgcgccttggggataaacaataaaaaagatttatgtaagtttata
-----
          SspI          MboII          M  S  I  Q  H  F  R
gtatccgctcatgagacaataaccctgataaatgcttcaataatattgaaaaaggaagagtATGAGTATTCAACATTTC
      ^2010      ^2020      ^2030      ^2040      ^2050      ^2060      ^2070
cataggcgagtagtactctgttattgggactatttacgaagttattataacttttctctcactcataagttgtaagg
-----

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Με κόκκινο πλαίσιο έχουν επισημανθεί τα σημεία αναγνώρισης των EcoR1 και BamH1

```

V A L I P F F A A F C L P V F A H P E T L V K V K D
GTGTCGCCCTTATTCCCTTTTTCGCGCATTTCCTCTGTTTTCCTCAGCCAGAAACGCTGGTGAAAAGTAAAAGAT
^2090 ^2100 ^2110 ^2120 ^2130 ^2140 ^2150
cacagcggaataagggaacacgacgtaaacggaaggacacacgagtggttcttgcgaccactttcattttcta
-----
MboI MboI MboI MboI
NdeII NdeII NdeII NdeII
A E D Q L G A R V G Y I E L D L N S G K I L E S F R P
GCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAGAGTTTTCGCCC
^2170 ^2180 ^2190 ^2200 ^2210 ^2220 ^2230
cgacttctagtcaaccacgctgctcacccaatgtagcttgacctagagttgtcgccattctaggaactctcaaaagcggg
-----
BstUI
CfoI
HhaI
HpaII
MspI
E E R F P M M S T F K V L L C G A V L S R I D A G G Q E
CGAAGAACGTTTCCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAG
^2250 ^2260 ^2270 ^2280 ^2290 ^2300 ^2310
gcttcttgcaaaaggttactactcgtgaaaatttcaagacgatacaccgcgcataatagggcataactgcggcccggttc
-----
RsaI
ScaI
DdeI
Q L G R R I H Y S Q N D L V E Y S P V T E K H L T D
AGCAACTCGGTGCGCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGAT
^2330 ^2340 ^2350 ^2360 ^2370 ^2380 ^2390
tcgttgagccagcggcgtatgtgataagagtcttactgaaccaactcatgagtggtcagtgcttttcgtagaatgccta
-----
MboI
HaeIII
NdeII
G M T V R E L C S A A I T M S D N T A A N L L L T T I
GGCATGACAGTAAGAGAATTATGCAGTGCCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACTTCTGACAACGAT
^2410 ^2420 ^2430 ^2440 ^2450 ^2460 ^2470
ccgtactgtcattctcttaatacgtcacgacggtattggtactcattgtgacgcggttgaatgaagactggttgcta
-----
AluI
PvuI
AluI
MboI
MboI
HpaII
NdeII NdeII MspI
G G P K E L T A F L H N M G D H V T R L D R W E P E L
CGGAGGACCGAAGGAGCTAACCGCTTTTTCGACAAACATGGGGGATCATGTAACCTCGCCTTGATCGTTGGGAACCGGAGC
^2490 ^2500 ^2510 ^2520 ^2530 ^2540 ^2550
gcctcctggcttcctcgattggcgaaaaaacgtggtgtacccctagtagcattgagcgggaactagcaacccttgccctcg
-----
CfoI
HhaI
MseI
N E A I P N D E R D T T M P V A M A T T L R K L L T
TGAATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACCTATTAAC
^2570 ^2580 ^2590 ^2600 ^2610 ^2620 ^2630
acttacttcggtatggtttgctgctgcactgtggtgctacggacatcggtaccggttggtgcaacgcgtttgataattga
-----
HpaII
MspI
MseI

```

user@mint:~\$ window focus()

Με κόκκινο πλαίσιο έχουν επισημανθεί τα σημεία αναγνώρισης των EcoR1 και BamH1


```

      AluI      VspI
G E L L T L A S R Q Q L I D W M E A D K V A G P L L R
GGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACCTTCTGCG
      ^2650      ^2660      ^2670      ^2680      ^2690      ^2700      ^2710
ccgcttgatgaatgagatcgaagggccgttggttaattatctgacctacctccgctattttcaacgtcctggtgaagacgc
-----
      HaeIII
CfoI      HpaII
HhaI      MspI      HpaII      BstUI
S A L P A G W F I A D K S G A G E R G S R G I I A A L
CTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCAC
      ^2730      ^2740      ^2750      ^2760      ^2770      ^2780      ^2790
gagccgggaaggccgaccgaccaaataacgactatttagacctcgccactcgacccagagcgccatagtaacgtcgtg
-----
      HaeIII      HinfI
G P D G K P S R I V V I Y T T G S Q A T M D E R N R
TGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGA
      ^2810      ^2820      ^2830      ^2840      ^2850      ^2860      ^2870
accccggtctaccattcgggagggcatagcatcaatagatgtgctgcccctcagtcggttgatacctacttgctttatct
-----
      DdeI
MboI
NdeII      MseI
Q I A E I G A S L I K H W Z
CAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAAactgtcagaccaagtttactcatatatacttttagattga
      ^2890      ^2900      ^2910      ^2920      ^2930      ^2940      ^2950
gtctagcgactctatccacggagtgactaattcgtaaccattgacagtcctggttcaaatagagtatatatgaaatctaact
-----
      MboI
      DraI
      MseI
      MboI
      MboII
      MseI
      DraI
      MseI
      MseI
      NdeII
      NdeII
      MboII
      MseI
tttaaaacttcatttttaatttaaaggatctaggtgaagatcctttttgataatctcatgacaaaaatcccttaacgtg
      ^2970      ^2980      ^2990      ^3000      ^3010      ^3020      ^3030
aaattttgaagtaaaaattaaattttcctagatccacttctaggaaaaactattagagtactggttttaggggaattgcac
-----
      MboII
      MboI
      MboI
      MboI
      BstUI
      DdeI
      NdeII
      NdeII
      NdeII
      CfoI
      HhaI
agttttcgtttccactgagcgtcagaccccgtagaaaaagatcaaaagatccttcttgagatccttttttctgcgcgtaatc
      ^3050      ^3060      ^3070      ^3080      ^3090      ^3100      ^3110
tcaaaagcaaggtgactcgcagtcctggtggcatcttttctagtttctagaagaactctaggaaaaaagacgcgcattag
-----
      MboI
      NdeII
      HpaII
      MspI
      AluI
tgctgcttgcaaacaaaaaaaccaccgctaccagcggtggtttgtttgccggatcaagagctaccaactctttttccgaa
      ^3130      ^3140      ^3150      ^3160      ^3170      ^3180      ^3190
acgacgaacgtttgttttttgggtggcgatggtcgccaccaaacaacggcctagttctcgatggttgagaaaaaggctt
-----

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Με κόκκινο πλαίσιο έχουν επισημανθεί τα σημεία αναγνώρισης των EcoR1 και BamH1

```

-----
                                CfoI
                                HhaI
                                MboII
                                HaeIII
ggtaactggcttcagcagagcgcagataccaaatactgttcttctagtgtagccgtagttagccaccacttcaagaact
^3210      ^3220      ^3230      ^3240      ^3250      ^3260      ^3270
ccattgaccgaagtcgtctcgcgtctatggtttatgacaagaagatcacatcggcacatccggtggtgaagttcttga
-----
                                                                HpaII
                                                                MspI
ctgtagcaccgcctacatacctcgtctctgctaactcctgttaccagtggtgctgctgccagtggcgataagtcgtgtcttacc
^3290      ^3300      ^3310      ^3320      ^3330      ^3340      ^3350
gacatcgtggcggtatgtatggagcgagacgattaggacaatggtcaccgacgacggtcaccgctattcagcacagaatgg
-----
                                HpaII
                                MspI
                                CfoI
                                HhaI
                                AluI
HinfI
gggttggactcaagacgatagttaccggataaggcgcagcgggtcgggtgaacggggggttcgtgcacacagcccagctt
^3370      ^3380      ^3390      ^3400      ^3410      ^3420      ^3430
cccaacctgagttctgctatcaatggcctattccgcgtcgcagcccagcttgcccccaagcacgtgtgtcgggtcgaa
-----
                                DdeI
                                AluI
                                CfoI
                                HhaI
ggagcgaacgacctacaccgaactgagatacctacagcgtgagctatgagaaagcgcacgcttcccgaaggagaaagg
^3450      ^3460      ^3470      ^3480      ^3490      ^3500      ^3510
cctcgtcttgctggatgtggttgactctatggatgtcgcactcgatactctttcgcggtgcgaagggttccctctttcc
-----
                                HpaII
                                MspI
                                CfoI
                                HhaI
                                AluI
cggacaggtatccggtaagcggcaggggtcggaacaggagagcgcacgagggagcttccaggggaaacgcctggtatctt
^3530      ^3540      ^3550      ^3560      ^3570      ^3580      ^3590
gcctgtccataggccattcgcgtcccagccttgtcctctcgcgtgctccctcgaagggtccccctttgcggaccatagaa
-----
                                TaqI
tatagtctctgctgggtttcgccacctctgacttgagcgtcgatttttgtgatgctcgtcagggggggcggagcctatggaa
^3610      ^3620      ^3630      ^3640      ^3650      ^3660      ^3670
atatcaggacagcccaaagcgggtggagactgaactcgcagctaaaaacactacgagcagtcccccgcctcggtacacctt
-----
                                HaeIII
                                BstUI
                                HaeIII
                                HaeIII
aaacgccagcaacgcggcctttttacggttcctggccttttgctggccttttgctcacatgttctttcctgcgttatccc
^3690      ^3700      ^3710      ^3720      ^3730      ^3740      ^3750
tttgcggtcgtttgcgccggaaaaatgccaaaggaccggaaaaacgaccggaaaaacgagtgtagaagaaggacgcaataggg
-----
                                                                HinfI
                                HinfI
                                AluI
                                CfoI
                                HhaI
ctgattctgtggataaccgtattaccgccttttgagtgcgtgataccgctcgcgcagccgaacgaccgagcgcagcgag
^3770      ^3780      ^3790      ^3800      ^3810      ^3820      ^3830
-----

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Με κόκκινο πλαίσιο έχουν επισημανθεί τα σημεία αναγνώρισης των EcoR1 και BamH1


```

                                MboII
                                CfoI
                                HhaI
                                BstUI
                                CfoI
                                HhaI
                                HinfI
                                MseI
                                AluI
                                PvuII
                                BstUI
                                HaeIII
                                VspI
                                A P N T Q T A S P R A L A D S L M Q L
tcagtgcgagcgaggaagcggaagaGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTTCATTAAATGCAGCTG
^3850 ^3860 ^3870 ^3880 ^3890 ^3900 ^3910
agtcactcgctccttcgccttctcgcgggttatgcggttggcggagaggggcgcgcaaccggctaagtaattacgtcgac
-----
                                CfoI
                                HhaI
                                MseI
                                VspI
                                AluI
A R Q V S R L E S G Q Z
GCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAgcgcaacgcaattaatgtgagttagctcactcattaggcaccccc
^3930 ^3940 ^3950 ^3960 ^3970 ^3980 ^3990
cgtgctgtccaaagggtgaccttttcgccggtcactcgcggttgcgttaattacactcaatcgagtgagtaatccgtgggg
-----
                                HpaII
                                MspI
                                AluI
                                M
aggctttacacttttatgcttcggctcgatgtgtgtggaattgtgagcggataacaatttcacacaggaaacagctAT
^4010 ^4020 ^4030 ^4040 ^4050 ^4060 ^4070
tccgaaatgtgaaatacgaaggccgagcatacaacacaccttaacactcgccctattgttaaagtggtcctttgtcgata
-----
                                RestEnd
                                PCREnd
                                TaqI
                                AluI
                                MseI
                                AluI
T M I T
GACCATGATTACGccaagctcgaaattaaccctcactaaagggaacaaaagct
^4090 ^4100 ^4110 ^4120 ^413
ctggtactaatgcggttcgagctttaattgggagtgatttccttgttttcga
-----

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Με κόκκινο πλαίσιο έχουν επισημανθεί τα σημεία αναγνώρισης των EcoR1 και BamH1

Τέλος, εξετάσαμε την τριτοταγή δομή της πρωτεΐνης που έχει αναλυθεί με X-ray diffraction και 2.21Å resolution ακολουθώντας τα παρακάτω βήματα:

- ✓ Αποθήκευση του αρχείου pdb της BMP-3
- ✓ Άνοιγμα αρχείου μέσω του προγράμματος Raswin
- ✓ Εύρεση εντολών για την απεικόνιση χαρακτηριστικών στο μόριο της πρωτεΐνης από το αρχείο Word του Raswin Help
- ✓ Επιλογή στο πρόγραμμα:
 - Ribbons & Structure
 - Εντολή: Rasmol Command line→select cys →color blue
- ✓ Export file

