Biochimie

2008/2009

1er Semestre

1) Décrire la réaction enzymatique permettant la transformation de l'acide phosphoenolpyruvique en acide pyruvique.

2) Expliquer la construction des plasmides recombinants et leur détection.

3) Indiquer les particularités d'un enzyme allostérique par rapport à un enzyme michaelien. Donner deux exemples d'enzymes, allostérique et michaélien, rencontrés dans le cycle de Krebs ou la glycolyse.

4) Organisation des gènes des chaines légères kappa des immunoglobulines et mécanisme de leur expression

5) Exercice (annexe ci-joint)

a) A partir de la séquence D'ADNc, trouver la position du codon initiateur et du premier codon stop en donnant le triplet de bases pour chacun

b) A partir de la séquence d'ADNc et de la position respective de chaque amorce sur cet ADNc, donner exactement la taille du fragment d'ADN qui serait amplifié par PCR et le nom de l'enzyme permettant l'amplification.

c) Donner, a partir de la carte de restriction, le nombre et la taille des fragments générés apres digestion enzymatique du fragment par Ban I

Merci à f54.henny

LOCUS NM_000962 5093 bp mRNA linear PRI 21-DEC-2008
DEFINITION Homo sapiens prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1), transcript variant 1,mRNA.

CDS 136..1935

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   1 aggtgacagc tggagggagg agcgggggtg gagccggggg aagggtgggg aggggatggg
  61 ctggagctcc gggcagtgtg cgaggcgcac gcacaggagc ctgcactctg cgtcccgcac
 121 cccagcagcc gcgccatgag ccggagtctc ttgctctggt tcttgctgtt cctgctcctg
 181 ctcccgccgc tccccgtcct gctcgcggac ccaggggcgc ccacgccagt gaatccctgt
 241 tgttactatc catgccagca ccagggcatc tgtgtccgct tcggccttga ccgctaccag
 301 tgtgactgca cccgcacggg ctattccggc cccaactgca ccatccctgg cctgtggacc
 361 tggctccgga attcactgcg gcccagcccc tctttcaccc acttcctgct cactcacggg
 421 cgctggttct gggagtttgt caatgccacc ttcatccgag agatgctcat gcgcctggta
 481 ctcacagtgc gctccaacct tatccccagt ccccccacct acaactcagc acatgactac
 541 atcagctggg agtctttctc caacgtgagc tattacactc gtattctgcc ctctgtgcct
 601 aaagattgcc ccacacccat gggaaccaaa gggaagaagc agttgccaga tgcccagctc
 661 ctggcccgcc gcttcctgct caggaggaag ttcatacctg acccccaagg caccaacctc
 721 atgtttgcct tctttgcaca acacttcacc caccagttct tcaaaacttc tggcaagatg
 781 ggtcctggct tcaccaaggc cttgggccat ggggtagacc tcggccacat ttatggagac
 841 aatctggagc gtcagtatca actgcggctc tttaaggatg ggaaactcaa gtaccaggtg
 901 ctggatggag aaatgtaccc gccctcggta gaagaggcgc ctgtgttgat gcactacccc
 961 cgaggcatcc cgccccagag ccagatggct gtgggccagg aggtgtttgg gctgcttcct
1021 gggctcatgc tgtatgccac gctctggcta cgtgagcaca accgtgtgtg tgacctgctg
1081 aaggctgagc accccacctg gggcgatgag cagcttttcc agacgacccg cctcatcctc
1141 ataggggaga ccatcaagat tgtcatcgag gagtacgtgc agcagctgag tggctatttc
1201 ctgcagctga aatttgaccc agagctgctg ttcggtgtcc agttccaata ccgcaaccgc
1261 attgccatgg agttcaacca tctctaccac tggcacccca tcatgcctga ctccttcaag
1321 gtgggctccc aggagtacag ctacgagcag ttcttgttca acacctccat gttggtggac
1381 tatggggttg aggccctggt ggatgccttc tctcgccaga ttgctggccg gatcggtggg
1441 ggcaggaaca tggaccacca catcctgcat gtggctgtgg atgtcatcag ggagtctcgg
1501 gagatgcggc tgcagccctt caatgagtac cgcaagaggt ttggcatgaa accctacacc
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1621 gacattgatg cgttggagtt ctaccctgga ctgcttcttg aaaagtgcca tccaaactct
1681 atctttgggg agagtatgat agagattggg gctccctttt ccctcaaggg tctcctaggg
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1801 aacattgtca agacggccac actgaagaag ctggtctgcc tcaacaccaa gacctgtccc
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2581 gtgggctgta ttcacgccat tggttggaag ctaccagagc tctatcccca tccaggtctt
2641 gactcatggc agctgtttct catgaagcta ataaaattcg ctttctaaag ttacctgtta
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2881 actgcccttt tcaggaagct ctcttaaaat acccattgcc ccagacctgg aagatataac
2941 attcagttcc caccatctga ttaaaacaac ttcctccctt acagagcata caacagaggg
3001 ggcacccggg gaggagagca catactgtgt tccaatttca cgcttttaat tctcatttgt
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3061 tctcacacca acagtgtgaa gtgcgtggta taatctccat ttcaaaacca aggaagcagc
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3181 attcctggtt tgactcagtt ccaggcctga tcttgcctgt ctggctcagg gtcaaagaca
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3361 taatcaatac agacaaggtt ctgcccttat ggagctcaca ctccagtggc agacaaacag
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3481 acccccctctg ctctgtcctc ccctattgcg ctctcaagac cagagaccca acagcagtga
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3661 acactttggg cttagtattt ctcaggaaga gctatggccc agaaacaaca ggggaaacta
3721 gagttcggtc tgacagtcct tggggttaag tctcctgtct tatggtccag aaactcctgt
3781 ttctccttag ttggctggaa actgctccca tcattccttc tggcctctgc tgaatgcagg
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4681 gtgaagaatc ttaatgcttg taatttaaac atttgttcct ggagttttga tttggtggat
4741 gtgatggttg gttttatttg tcagtttggt tgggctatag cacacagtta tttaatcaaa
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4861 tgactttaag tgaaagagat tacttaaata atttgggtga gctgcacctg attagttgaa
4921 aggcctcaag aacaaacact gcagtttcct ggaaaagaag aaactttgcc tcaagactat
4981 agccatcgac tcctgcctga gtttccagcc tgctagtctg ccctatggat ttgaagtttg
5041 ccaaccccaa caattgtgtg aattaatttc taaaaataaa gctatataca gcc
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AMORCE SENS

> ref|NM_000962.2| UEGM Homo sapiens prostaglandin-endoperoxide synthase 1 (prostaglandin
G/H synthase and cyclooxygenase) (PTGS1), transcript variant
1, mRNA
Length=5093

GENE ID: 5742 PTGS1 | prostaglandin-endoperoxide synthase 1 (prostaglandin G/H
synthase and cyclooxygenase) [Homo sapiens] (Over 100 PubMed links)

Score = 40.1 bits (20), Expect = 0.014
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

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Query  1    CCGGCCCCAACTGCACCATC  20
            ||||||||||||||||||||
Sbjct  326  CCGGCCCCAACTGCACCATC  345
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AMORCE ANTISENS

> ref|NM_000962.2| UEGM Homo sapiens prostaglandin-endoperoxide synthase 1 (prostaglandin
G/H synthase and cyclooxygenase) (PTGS1), transcript variant
1, mRNA
Length=5093

GENE ID: 5742 PTGS1 | prostaglandin-endoperoxide synthase 1 (prostaglandin G/H
synthase and cyclooxygenase) [Homo sapiens] (Over 100 PubMed links)

Score = 40.1 bits (20), Expect = 0.014
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1     CTGAGTGGCTATTTCCTGCA  20
             ||||||||||||||||||||
Sbjct  1186  CTGAGTGGCTATTTCCTGCA  1205
```

CARTE DE RESTRICTION

Table by Enzyme Name

Enzyme name	No. cuts	Positions of sites	Recognition sequence	
AccB1I	2	384 611	g/gyrcc	More info
Alw21I	2	733 766	gwgcw/c	More info
AspHI	2	733 766	gwgcw/c	More info
BanI	2	384 611	g/gyrcc	More info
Bbv12I	2	733 766	gwgcw/c	More info
BsaAI	2	726 851	yac/gtr	More info
BsgI	2	16 857	gtgcag	More info
BshNI	2	384 611	g/gyrcc	More info
BsiHKAI	2	733 766	gwgcw/c	More info
Bsp143II	2	98 615	rgcgc/y	More info
Bsp19I	2	292 482	c/catgg	More info
BstDSI	2	292 482	c/crygg	More info
BstH2I	2	98 615	rgcgc/y	More info
DsaI	2	292 482	c/crygg	More info
Eco64I	2	384 611	g/gyrcc	More info
HaeII	2	98 615	rgcgc/y	More info
MspA1I	2	220 860	cmg/ckg	More info
NcoI	2	292 482	c/catgg	More info
NspBII	2	220 860	cmg/ckg	More info
PvuII	2	220 860	cag/ctg	More info
XcmI	2	576 678	ccannnnn/nnnntgg	More info