



**UNIVERSIDAD DE BARCELONA  
FACULTAD DE FARMACIA  
DEPARTAMENTO DE BIOQUÍMICA Y BIOLOGÍA MOLECULAR**

**ESTUDIO DE LOS MECANISMOS DE INHIBICIÓN  
DE LA ACTIVIDAD CARNITINA  
PALMITOILTRANSFERASA 1**

**ASSIA BENTEBIBEL**

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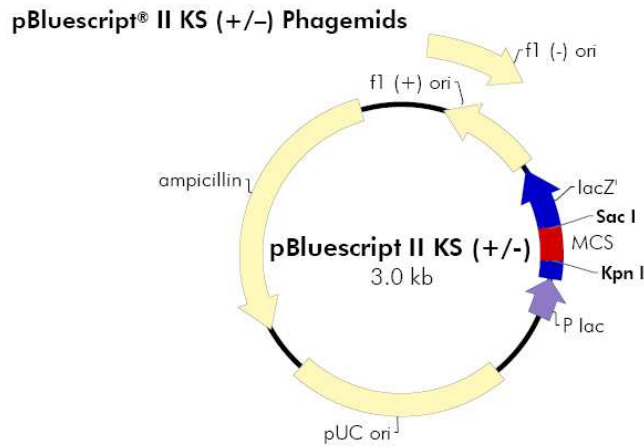
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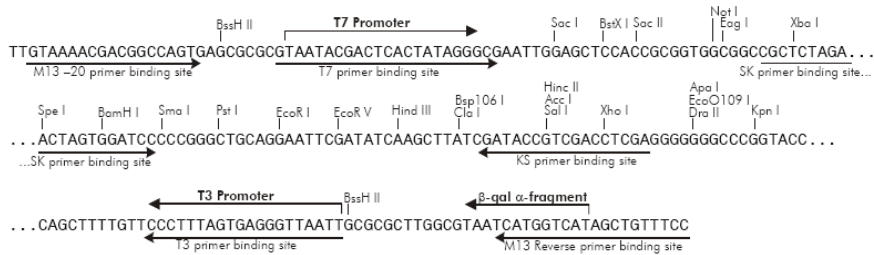
## **APÉNDICES**

## 1. MAPA DE RESTRICIÓN DE LOS VECTORES PLASMÍDICOS

❖ *Vector Bluescript (pBS)* (Stratagene, ref. 212205) para subclonaje



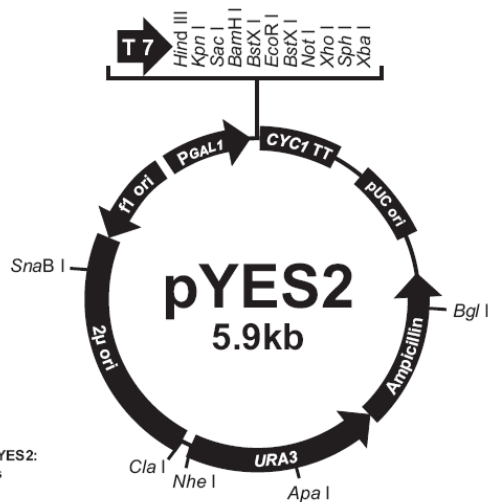
**pBluescript II KS (+/-) Multiple Cloning Site Region**  
(sequence shown 598–826)



❖ *Vector pYES 2.0* (Invitroge, ref. V825-20) de expresión en *S. cerevisiae*

**Map of pYES2**

The figure below summarizes the features of the pYES2 vector. The sequence for pYES2 is available for downloading from our Web site ([www.invitrogen.com](http://www.invitrogen.com)) or from Technical Service (see page 17).



**Comments for pYES2:**  
5856 nucleotides

GAL1 promoter: bases 1-451  
T7 promoter/priming site: bases 475-494  
Multiple cloning site: bases 501-600  
CYC1 transcription terminator: bases 608-856  
pUC origin: bases 1038-1711  
Ampicillin resistance gene: bases 1856-2716 (C)

## 2. OLIGONUCLEÓTIDOS

OLIGONUCLEÓTIDOS	SECUENCIA (5' → 3')
CPT1A	
CPT1A.C608A.for	5' GAG ACT GTA CGC TCC <u>GCC</u> ACT TAT GGA GTC CTG C 3'
CPT1A.C608A.rev	5' G CAG GAC TCC ATA AGT GGC GGA GCG TAC AGT CTC 3'
CPT1A.R243T.for	5' GAA TAT ATC TAC CTG <u>ACG</u> GGC CGA GGG CCG CTC 3'
CPT1A.R243T.rev	5' GAG CGG CCC TCG GCC CGT CAG GTA GAT ATA TTC 3'
CPT1A.W682A.for	5' GAG GTA TTG TCT GAG CCA <u>GCG</u> AGG TTG TCT ACG AGC 3'
CPT1A.W682A.rev	5' GCT CGT AGA CAA CCT CGC TGG CTC AGA CAA TAC CTC 3'
CPT1A.A478G.for	5' CAC TCC TGG GCG GAG <u>GGG</u> CCC ATC GTG GGC CAT TTG 3'
CPT1A.A478G.rev	5' CAA ATG GCC CAC GAT GGG CCC CTC CGC CCA GGA GTG3'
CPT1A.M593S.for	5' CTC ACA TAT GAG GCC TCC <u>AGT</u> ACC CGG CTC TTC CGA GAA GG 3'
CPT1A.M593S.rev	5' CC TTC TCG GAA GAG CCG GGT ACT GGA GGC CAC ATA TGT GAG 3'
CPT1A.M593R.for	5' CTC ACA TAT GAG GCC TCC <u>AGG</u> ACC CGG CTC TTC CGA GAA GG 3'
CPT1A.M593R.rev	5' CC TTC TCG GAA GAG CCG GGT CCT GGA GGC CAC ATA TGT GAG 3'
CPT1A.M593K.for	5' CTC ACA TAT GAG GCC TCC <u>AAG</u> ACC CGG CTC TTC CGA GAA GG 3'
CPT1A.M593K.rev	5' CC TTC TCG GAA GAG CCG GGT CTT GGA GGC CAC ATA TGT GAG 3'

OLIGONUCLEÓTIDOS	SECUENCIA (5' → 3')
CPT1B	
CPT1B.HindIII.ATG.for	5' TCG ATA AGC TTA TAA AAT GGC GGA AGC ACA CCA GGC AG 3'
CPT1B.HindIII.rev	5' GGG ACA GGA AGC TTG GGC 3'
CPT1B.AAAA.for	5' CGA CAG GCA TCT TCC TCT TCC GAC AAA C 3'
CPT1B.AAAA.rev	5' GTT TGA CGG AAG AGG AAG ATG CCT GTC G 3'
CPT1B-MseI.rev	5' CTT GTT GGC TCG TGT TCT TAA TAA GC 3'
CPT1B.H473A.for	5' CAG CTG GGC CTC AAC ACA GAA <u>GCC</u> TCA TGG GCA GAT GCT CCC 3'
CPT1B.H473A.rev	5' GGG AGC ATC TGC CCA TGA GGC TTC TGT GTT GAG GCC CAG CTG 3'
CPT1B.H477A.for	5' AAC ACA GAA CAC TCA TGG GCA <u>GCT</u> GCT CCC ATC ATC GGT CAC CTC 3'
CPT1B.H477A.rev	5' GAGGTGACCGATGATGGGAGCAGCTGCCCCATGAGTGTCTGTGTGTT 3'
CPT1B.R655N.for	5' GCC ATG ACA GGG GCT GGG ATC GAC <u>AAC</u> CAC CTC TTC TGC CTC 3'
CPT1B.R655N.rev	5' GAG GCA GAA GAG GTG GTT GTC GAT CCC AGC CCC TGT CAT GGC 3'
CPT1B.TET602-604VDN.for	5' ATG TTC CGA GAG GGG CGG <u>GTA GAC AAT</u> GTG CGT TCC TGT ACT AGC 3'
CPT1B.TET602-604VDN.rev	5' GCT AGT ACA GGA ACG CAC ATT GTC TAC CCG CCC CTC TCG GAA CAT 3'
CPT1B.H279A.for	5' G GGA AAC ACC GTT <u>GCC</u> GCC ATG AT 3'
CPT1B.H279A.rev	5' AT CAT GGC GGC AAC GGT GTT TCC C 3'
CPT1B.H483A.for	5' GCT CCC ATC ATC GGT <u>GCC</u> CTC TGG GAG TTC G 3'
CPT1B.H483A.rev	5' C GAA CTC CCA GAG GGC ACC GAT GAT GGG AGC 3'
CPT1B.M593S.for	5' CTG ACC TAT GAG GCC TCC <u>AGC</u> ACA AGA ATG TTC CGA GAG 3'
CPT1B.M593S.rev	5' CTC TCG GAA CAT TCT TGT GCT GGA GGC CTC ATA GGT CAG 3'
CPT1B.COT GGG709-711QGV.for	5' AATCATCTGGGTGCTCAAGGTGTCCTTTGGTCCTGTGGCC 3'
CPT1B.COT GGG709-711QGV.rev	5' GGCCACAGGACCAAAGACACCTTGAGCACCCAGATGATT 3'
CPT1B.CrAT GGG709-711VMF.for	5' AATCATCTGGGTGCTGTAATGTTCCTTTGGTCCTGTGGCC 3'
CPT1B.CrAT GGG709-711VMF.rev	5' GGCCACAGGACCAAAGAACATTACAGCACCCAGATGATT 3'

Los nucleótidos marcados en negrita corresponden a la secuencia para una eficiente traducción de las proteínas en levaduras.

Los nucleótidos subrayados son los mutados con el fin de cambiar un amino ácido original por otro de interés (tal y como se indica en el nombre del oligonucleótido). Los otros oligonucleótidos, se utilizaron para la secuenciación del cDNA.

### 3. SECUENCIAS

#### 3.1 Secuencia de CPT1A de rata

Secuencia de la carnitina palmitoiltransferasa I de hígado de rata (CPT1A), publicada por Esser (Esser, 1993), con número de acceso en GeneBank Data Libraries L07736.

DEFINICIÓN: mRNA de carnitina palmitoiltransferasa I, cDNAs completos.

NÚMERO DE ACCESO: L07736

FUENTE: cDNA correspondientes a mRNA de hígado de macho adulto de *Rattus norvegicus*.

AUTORES: Esser, V., Britton, C.H., Weis, B.C., Foster, D.W. and McGarry, J.D.

TÍTULO: Cloning, sequencing and expression of a cDNA encoding rat liver carnitine palmitoyltransferase I. Direct evidence that a single polypeptide is involved in inhibitor interaction and catalytic function.

PUBLICACIÓN: *J. Biol. Chem.* **268**, 5817-5822 (1993).

ZONA CODIFICANTE: 103 – 2424 (773 aminoácidos).

```
"MAEAHQAVAFQFTVTPDGIDLRLSHEALKQICLSGLHSWKKKFIRFKNGIITGVFPA
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VAVIMTMRYSLKVL LLSYHGWMFAEHGKMSRSTKIWMAMVKVLSGRKPMLYSFQTS LPR
LPVPAVKD TVSRYLESVRPLMKEEDFQRMTALAQDFAVNLGPKLQWYLK LKSWWATNY
VSDWWEYIYLRGRGPLMVNSNYAMEMLYITP THIQ AARAGNTIHA ILLYRRTL DRE
ELKPIRLLGSTIPLCSAQWERLFNTSRIPGEETDTIQHIKDSRHIVVYHRGRYFKVWL
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EKHQHLYRLAMTGAGIDRHLFCLYV VSKYLAVDSPFLKEVLSEPWRLSTSQTPQQQVE
LDFEKNPDYVSCGGGFGPVADDGYGVSYIIVGENFIHFHISSKFSSPETDSHRFGKH
LRQAMMDIITLFGLTINSKK"
```



RECuento DE BASES: 1109 a; 1115 c; 1121 g; 1032 t

1 agtcggtcga ctccgagctc agtgaggacc taaagcagag gactgtggtg cggaggacag  
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121 gctgtggcct tccagttcac cgtcaccccc gatggcattg acctccgcct gagccaagaa  
181 gccctcaaac agatctgcct gtcggggctg cactcctgga agaagaagtt catccggttc  
241 aagaatggca tcatcactgg tgtgttcccc gcgaatccgt ccagctggct tatcgtggtg  
301 gtgggtgtga tttcatccat gcatgccaaa gtggaccctt ccctgggcat gatcgcaaaag  
361 atcagtcgga ccctagacac cactggccgc atgtcaagcc agacgaagaa cattgtgagc  
421 ggctcctct ttggtacagg gctctgggtg gcagtcacatca tgaccatgag ctactcgtg  
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721 caggattht gctgcaacct cggacccaaa ttgcagtggt atttgaagct aaaatcctgg  
781 tgggcccaca attacgtgag tgactgggtg gaagaatata tctacctgag gggccgaggg  
841 ccgctcatgg tcaacagcaa ctactacgac atggagatgc tgtacatcac cccaacctat  
901 atccaggcag cgagagctgg caacaccatc cacgccatac tgctgtatcg tcgcacatta  
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2101 cttgacgtcg actcacctt cctgaaggag gtattgtctg agccatggag gttgtctacg  
2161 agccagactc ctcagcagca ggtggagctc tttgacttht agaaaaacc tgactatgtg  
2221 tctgtggag gggcttht gcccgttgc gatgacggct atggtgtctc ctacattata  
2281 gtgggagaga atthtcatca cttccatatt tcttccaagt tctctagccc tgagacagac  
2341 tcacaccgct ttgggaagca cttgagacaa gccatgatgg acattatcac cttgtthtggc  
2401 ctacacatca atthtcaaaaa gtaaacctt gaccacacg gaaggaaaa ggaccctcgt

2461 gatacaaac aaatgaatag atgttgctcc tgaccatagg acaggcagaa aattgctctt  
2521 ataaaactca gttttccttc cagaagggtt accgtcagtc tccctagaac aacagtaggc  
2581 ttcacgtgtg aattgtgacc ctactacatc cagagatgcc ttggctccag gaatattggg  
2641 cacagtcccc tgatgtcttt tgaatcggct cctactggat aaagggattt aaatgctggg  
2701 gaattcctgg attctggggg ttgtttcttc acatgtggtg gaggtgacag acttcctcag  
2761 tggtgaccct gtgaataactt gggcgtctga ctccaccag gcagtgtgag catcaccttg  
2821 tggaaagaga aagtgtcttc agagccagca gaggcaacag ctgtagctaa cacatctgta  
2881 acacactaat ggaatgggta ggctgggga ttaaggttct gctatgagtg acagccactg  
2941 tccctttgga agttcacatt tccaggaagc agagtaccac ctcccagtg ccaccttctt  
3001 cacacatctt caaaaccag tgccttaaag aaggggcca ttggcaagcg ggaccataga  
3061 gaagacttag catctgtgaa gcctttgggt ggatatgtga ggatgctgct tccccttact  
3121 ggttctgca taaagatgtc ctaagtaag cacttcccc acccctagaa aatgaggtcc  
3181 ttggngaagg caggatgct ggagtctcat tgcctgccag ttccattaag ccacaaaata  
3241 gcagacatgt gtccacagag ggaggggctt ggtagtcaa ggctgcatag ctggacaaca  
3301 gcgggagagt gtggcttctt gtatttgaca gctgttgga agaggagtga gaccctggtc  
3361 accaagtcag acatactgac acaggcagcc aaagctcacg gagccaggag atatagatag  
3421 atactggctt gtattctggc agatacacc ctgggcttat cttctaatacc caccagtc  
3481 gattccaacc agagtcaaat tccatagaag gctaggtcat tttggcgaca gactcaggg  
3541 tctcaagtaa tgggtgcttt taccacatg ccatcctca gtgggagtgc ctttcttgaa  
3601 agcatccaat gggctaaagc agctctacca agtctgtttg gtatttaatg taaacattag  
3661 cattaatgga gtggtctctc ctacctgca ccatcctgct ctgacaagct tagctctccg  
3721 aggtttacat catgtattta tttccagtg ccctttggc cttgtttgat tctgcccct  
3781 gtgccagaag tggcccagaa gtgaggggtg gggtagaccag cagtgcagag aggtgctggc  
3841 tgaacagttc atgtgtgtct tatgggtata catgtataaa ttttgaatg taaaaaaaa  
3901 aatcatacct aaaagggcca aagttttttt tttttttact aaaaccaaga aaacaaaaga  
3961 caacataaag acataagcag aaacaaactg ttgtaagtca gagcggcctg actctcgctg  
4021 ctgtgaccac tcaccaacct gtgttactca gagtagccc gctagtgcc gagtgggaca  
4081 ttcctctctc aggtttocag tgccttgct gctcctgagc agttaccaat gcaatttcgc  
4141 attccttaca aggcagaaga gtgggctctc actgtatgtg ttcaaaggag gaggtaagac  
4201 tattgtgtat ttaatttaat gtggaacaaa atatagtctt accgcagcca aggttcaaat  
4261 ttgggttctt aatctgtcca ttgcatgtaa ataccatatc tgtttggata taaatcttag  
4321 aagtgcagtg gtgagcgaat gtagctggcc attaataaaa cattaatact gtctact

### 3.2 Secuencia de CPT1B de rata

Secuencia de la carnitina palmitoiltransferasa I de músculo de rata (CPT1A), publicada por Yamazaki (Yamazaki, 1995), con número de acceso en GeneBank Data Libraries [D43623](#).

DEFINICIÓN: mRNA de carnitina palmitoiltransferasa 1, cDNAs completos.

NÚMERO DE ACCESO: D43623

FUENTE: cDNA correspondientes a mRNA de músculo de macho adulto de *Rattus norvegicus*.

AUTORES: Yamazaki,N., Shinohara,Y., Shima,A. and Terada,H.

TÍTULO: High expression of a novel carnitine almitoyltransferase I like protein in rat brown adipose tissue and heart: isolation and characterization of its cDNA clone.

PUBLICACIÓN: *FEBS Lett.* **363** (1-2), 41-45 (1995).

ZONA CODIFICANTE: 27 – 2345 (772 aminoácidos).

"MAEAHQAVAFQFTVTPDGVDFRLSREALRHIYLSGINSWKKRLIRIKNGILRGVYPGS  
PTSWLVVVMATVGSNYCKVDISMGLVHCIQRCLPTRYGSYGTPQTETLLSMVIFSTGVW  
ATGIFLFRQTLKLLLSYHGWMFEMHSKTSHATKIWAICVRLSSRRPMLYSFQTSPLPKL  
PVPSVPATIHRYLDSVRPLLDDEAYFRMESLAKEFQDKIAPRLQKYLVLKSWWATNYVS  
DWWEYVYLRGRSPIMVDSNYAMDFVLIKNTSQQAARLGNTVHAMIMYRRKLDREEIK  
PVMALGMVPMCSYQMERMFNTTRIPGKETDLLQHLSESRHVAVYHKGRFFKVWLYEGSC  
LLKPRDLEMQFQRILDDTSPQPGEKLAALTAGRVEWAEARQKFFSSGKNKMSLDTI  
ERAAFFVALDEDSHCYNPDDEASLSLYGKSLHGCNRYNRWFDKSFITLISCKNGQLGLNT  
EHSWADAPIIGHLWEFVLATDTFHLGYTETGHCVGEPNTKLPQPQRMQWDIPEQCQTAI  
ENSYQVAKALADDVELYCFQFLPFGKGLIKKCRTPDAFVQIALQLAHFRDKGKFLTY  
EASMRMFREGRTETVRSCTSESTAFVRAMMTGSHKEQDLQDLFRKASEKHQNMRYLAM  
TGAGIDRHLFCLYIVSKYLGVRSPFLDEVLSEPWLSLSTSQIPQFQICMFDPKQYPNHLG  
AGGGFGPVADHGYGVSYMIAGENTMFFHVSSKLSSETNALRFGNHIRQALLDIADLFFK  
ISKTDSD "

RECuento de bases: 656 a; 788 c; 727 g; 642 t

1 ctgagctgtg ctgactaaac cccaggatgg cggaaagcaca ccaggcagta gctttccagt  
61 tcaactgtgac cccagacggg gtcgacttcc ggcttagtgc ggaggctctg agacacatct  
121 acctgtctgg aatcaactcc tggagaagaac gccttattcg aatcaagaat ggtatcctta  
181 ggggtgtgta ccctggcagc cctaccagct ggctgggtgt tgtcatggca acagttggtt  
241 ccaactactg caaagtggac atctccatgg ggctgggtcca ttgcatccag agatgcctcc  
301 cgacaaggta tggctcctac gggacccac agaccgagac acttctcagt atggctcatct  
361 tctccaccgg agtctgggag acaggcattt ttttattccg acaaaccctg aagctgctgc  
421 tttcctatca tgggtggatg ttcgagatgc acagcaagac cagccatgcc accaagatct  
481 gggctatctg tgttcgtctc ctgtccagcc ggcggccat gctctatagc ttccaacat  
541 cactgcccga gcttctgtc cccagtgtgc cagccacaat tcaccggtagc ttggattctg  
601 tgcggccctt gctggatgac gaagcctatt tccgcatgga gtcggtggcc aaagaattcc  
661 aggacaagat tgccccaga ctgcagaaat acctggtgct gaagtcattg tgggcaacca  
721 actatgtaag tgactggtag gaagagtacg tctacctcg aggcaggagc cccatcatgg  
781 tgaacagcaa ctattacgcc atggatcttg tgcttattaa gaacacgagc caacaagcag  
841 cacgtttggg aaacaccgtt cacgcatga tcatgtatcg ccgcaactg gaccgagaag  
901 agatcaagcc ggtaatggca ctgggtatgg taccatgtg ctctaccag atggagagga  
961 tgttcaacac tacacgcatc ccaggcaaag agacagactt gctacagcac ctctcagaga

1021 gcaggcacgt ggctgtctac cacaaaggtc gcttcttcaa ggtttggctc tatgagggct  
1081 cgtgcctgct caagccccga gacctcgaga tgcagttcca gagaatcctc gatgacacct  
1141 ccccgcctca gcctggagag gaaaagctgg cagccctcac cgcaggagga agggtagagt  
1201 gggcagaagc acgtcagaag ttcttttagct ctggcaagaa caagatgtcc ctggatacca  
1261 tcgaacgtgc tgetttcttt gtggccctgg acgaagactc tcaactgttac aaccctgatg  
1321 acgagggccag tctcagcctc tacggcaaat ccctgctgca cggcaactgc tataacaggt  
1381 ggttcgacaa atctttcact ctcatctcct gcaagaatgg ccagctgggc ctcaacacag  
1441 aacactcatg ggcagatgct cccatcatcg gtcacctctg ggagttcgtc ctggccactg  
1501 atacctttca cctgggctac acggagacag gacactgtgt gggatgaacc aacaccaagt  
1561 tgccgcccgc tcagcggatg cagtgggaca ttcccagca gtgccagaca gccatcgaga  
1621 attcgtacca agtagccaag gcctggctg atgatgtgga gttatactgc ttccagttct  
1681 tacccttcgg caaaggcctg atcaagaagt gtcggaccag ccctgatgcc tttgtgcaga  
1741 ttgccctgca gctggctcat ttccgggaca aaggcaagtt ctgcctgacc tatgagggct  
1801 ccatgacaag aatgttccga gaggggaggga cagagactgt gcgttctctg actagcgagt  
1861 ccacggcctt tgtgcccggc atgatgacgg ggtcccataa gaaacaagac ctccaagacc  
1921 tcttccggaa agcctccgaa aaacacccaa acatgtaccg cctagccatg acaggggctg  
1981 ggatcgacag gcacctcttc tgctctaca tcgtctcca gtacttaggg gttagatctc  
2041 ctttctgga cgaggtgctt tcggaacct ggagcctctc caccagccag atccccagt  
2101 tccagatctg catgtttgac ccaaagcagt accccaatca tctgggtgct ggaggtggct  
2161 ttggtcctgt ggccgaccac ggatacgggg tttcctacat gatcgagggc gaaaacacaa  
2221 tgttcttcca tgtttccagc aagttatcga gttcagaaac gaacgccctg cgcttcggga  
2281 accacatccg tcaagcactg ctggatatcg ccgacctttt caaaatttcc aagactgaca  
2341 gctgagacca ggagacacac cagctgcctt ttggtcccca cctgggtggag gaagaggtct  
2401 gtggccagtt cacaggcata aggggtggca tgcacacgtg cccagttctg agaccagctc  
2461 cagcgcaggg gctccccagg cagacactgc tcctccaggc ccggtcgagg tgggattgga  
2521 gtgggtgaggg aactttgatc ttttttttcc ccccggctct ggtagatgct aataaaaata  
2581 aggctgtata attctctctc agcccttagg tgctatggt tggtagaga actagaaggc  
2641 ctttcccctg ccctgctca ggttaggggtg gtggcgactg aagggccggg tgaatgttca  
2701 taatggcttt ttacctgctt tgaatgtgt gcttttctg aataatgagg acttcgagag  
2761 tgctgtccaa cctctcatgt gcacttggaa taaattctta cttagaacc ttt

#### 4. DEFICIENCIAS HUMANAS EN CPT1A y CPT2

Posición	Mutación	Observación	Referencia
Arg <sup>123</sup> (exón 4)	R123C	Mobilidad aberrante.	Brown, 2001
Ala <sup>275</sup> (exón 8)	A275T	↓ eficiencia catalítica y estabilidad de la proteína.	Gobin, 2002
Cys <sup>304</sup> (exón 9)	C304W	↓ estabilidad de la proteína y no hay actividad CPT1	Gobin, 2003
Arg <sup>316</sup> (exón 9)	R316G	Actividad CPT1 no detectable.	Bennett, 2004
Phe <sup>343</sup> (exón 10)	F343V		
Arg <sup>357</sup> (exón 10)	R357W	↓ estabilidad y actividad de la proteína.	Brown, 2001
Glu <sup>360</sup> (exón 10)	E360G	↓ estabilidad de la proteína y no hay actividad CPT1.	Ogawa, 2002
Del 1183_1185 (exón 11)	delR395	↓ estabilidad de la proteína, no hay actividad CPT1 y se deleciona la Arg <sup>395</sup> .	Brown, 2001 Bonfont, 2004
Ala <sup>414</sup> (exón 11), altamente conservado	A414V	Residuo posiblemente del centro catalítico del enzima y de unión del palmitoil-CoA. ↓ eficiencia catalítica y estabilidad de la proteína.	Gobin, 2002 Gobin, 2003
Asp <sup>454</sup> (exón 12)	D454G	↓ estabilidad, actividad y nivel (Western Blot) de la proteína	LIJ, 1998
Gly <sup>465</sup> (exón 12)	G465W		
Pro <sup>479</sup> (exón 12)	P479L	↓ actividad de CPT1. Resistencia parcial al malonil-CoA.	Bennett, 2004
Leu <sup>484</sup> (exón 12)	L484P	↓ estabilidad de la proteína .	Brown, 2001
Tyr <sup>498</sup> (exón 13), altamente conservado	Y498C	Residuo del centro catalítico del enzima y de unión del palmitoil-CoA. ↓ estabilidad de la proteína y eficiencia catalítica para ambos sustratos.	Gobin, 2002 Gobin, 2003
Thr <sup>568</sup>	T568A	Presenta un polimorfismo.	Prip-Buus, 2001
Gly <sup>709</sup> (exón 17)	G709E	Afectan al sitio activo y elimina la actividad CPT1. Residuos implicados en la unión de carnitina en CPT2 de rata (Brown, 1994).	Gobin, 2003
Gly <sup>710</sup> (exón 17)	G710E		Prip-Buus, 2001
Tyr <sup>32</sup> (exón 2)	Y32X	Mutación sin sentido, causa una terminación prematura que resulta en una proteína CPT1 inmadura.	Ogawa, 2002
Gln <sup>100</sup> (exón 4)	Q100X	Mutación sin sentido, trunca la proteína a 671 aminoácidos antes del final del TM2 del dominio N-terminal.	Gobin, 2002
Arg <sup>160</sup> (exón 5)	R160X	Mutación sin sentido, produciría una proteína severamente truncada que carece de la mayor parte del centro catalítico y del dominio de unión de la carnitina.	Bennett, 2004
Trp <sup>475</sup> (exón 12)	W475X	Mutación sin sentido, ↓ la actividad CPT1 y no se detecta proteína en el análisis por Western Blot.	Ogawa, 2002
Tyr <sup>498</sup> (exón 13)	Y498X		
1876-2028del (exón 15)		Mutación por <i>splicing</i> , deleciona 51 residuos desde 626 hasta 676. CPT1 es inmadura e inestable.	Gobin, 2002 Ogawa, 2002
2027-2028+2delAAGT (exón 16)		Mutación por <i>splicing</i> , provoca tres transcritos aberrantes:	
• 1876-2028del		Inserción de 6 residuos desde la posición 676 a 677 y resulta en ↓ de actividad CPT.	Ogawa, 2002
• 2027-2028insGTCTCTT			
CCCTTCTTCC			
• 2026-2028del		Delección de 3 nucleótidos delección del E676del.	
Eliminación de 8 kb comprendido entre el intrón 14 hasta el exón 17 del gene. Resulta una proteína truncada desde el residuo 581 hasta 702. La delección provoca un mRNA inestable.			Gobin, 2002
La inserción de 113-bp predice al adición de 8 residuos (FLPYHELIS) que se terminen con un codón de stop, truncando así la proteína por 240 aminoácidos. Se inserta un residuo E525.			

**Tabla 1. Resumen de las mutaciones sin sentido y missense descritas en CPT1A humana relacionadas con la actividad catalítica.** Se indican las características provocadas por cada mutación en la actividad CPT1A.

Exón	Nucleótido <sup>a</sup>	Aminoácido	Referencia
1	109Ins GC		Martin, 2000
	112-113 Ins GC	S38fs <sup>c</sup>	Martin, 2000
	149C>A	P50H <sup>b</sup>	Verdero, 1995
2	216G>C/T	L72F	Ijlst, 1998
3	338C>T	S113L <sup>b</sup>	Taroni, 1993
	IVS3 + 5G>A <sup>d</sup>	Del179_113	Deschauer, 2003
4	359A>G	Y120C	Martin, 1999; 2000
	370C>T	R124X	Yang, 1998
	371G>A	R124Q	Thuillier, 2003
	437A>C	N146T	Thuillier, 2003
	452G>A	R151Q	Yang, 1998
	481C>T	R161W	Thuillier, 2003
	490A>T	K164X	Ijlst, 1998
	520G>A	E174K <sup>b</sup>	Yamamoto, 1996
	533-534insT; 534-558 del	L178F; N179-I186 del	Yang, 1998
	628T>G	Y210D	Ijlst, 1998
	641T>C	M214T	Wieser, 1997
	680C>T	P227L	Taroni, 1994
	821A>T	K274M	Ijlst, 1998
	890C>A/G	Y290X	Ijlst, 1998
	906C>T	R296X	Ijlst, 1998
	907G>A	R296Q	Ijlst, 1998
	907-918ins	L302fs <sup>c</sup>	Gellera, 1994
	983A>G	D328G	Thuillier, 2003
	1145G>A	R382K	Yang, 1997
	1148T>	F383Y <sup>b</sup>	Yamamoto, 1996
	A1238-1239delAG	Q413fs <sup>c</sup>	Taggart, 1999
	1342T>C	F448L	Wieser, 1997
	1436A>T	Y479F	Wieser, 1997
	1459G>A	E487K	Bruno, 2000
	1507C>T	R503C	Taggart, 1999
	1543-1546delGCCT	515del4	Deschauer, 2002
	1646G>A	G549D	Taggart, 1999
5	1649A>G	Q550R	Yang, 1998
	1657G>A	D553N <sup>b</sup>	Verderio, 1995
	1798G>A	G600R	Ijlst, 1998
	1810C>T	P604S	Yang, 1998
	1823G>C	D608H	Thuillier, 2003
	1883A>C	Y628S <sup>b</sup>	Bonnefont, 1996
	1891C>T	R631C <sup>b</sup>	Taroni, 1992

**Tabla 2. Resumen de las mutaciones humanas en CPT2.** Actualización de mutaciones en CPT2 que generan deficiencias descritas en la literatura. a = Nucleótido 1: A del codón ATG; b = Mutaciones expresadas en células COS; c fs = marco de lectura cambiado; d = Intrón 3. La tabla fue tomada de la referencia (Bonnefont, 2004).

## 5. ALINEAMIENTO DE SECUENCIAS CORRESPONDIENTES A CARNITINA/COLINA ACILTRANSFERASAS

Representación de secuencias de aminoácidos de 22 enzimas que catalizan acyl-CoAs de cadena de átomos de carbono corto como sustratos: CrAT (CACP) de levadura, *C. tropicalis*, humano, ratón y paloma; y ChAT (CLAT) de ratón, rata, cerdo, humano, mosca de fruta, y *C. elegans*; y las enzimas que catalizan acyl-CoAs de cadena de átomos de carbono media y larga como sustratos: CPT1A (CPT1) de rata, ratón y humano; CPT1B (CPTM) de rata y ratón; CPT2 (CPT2) de rata, ratón y humano; y COT (OCTC) de humano, rata y bovino; fueron obtenidos del banco de datos SwissProt y alineados utilizando el programa ClustalW. Los residuos han sido coloreados por conservación según el programa Belvu versión 2.8 (disponible en <http://www.sanger.ac.uk/~esr/Belvu.html>).

CPT2_RAT	1	.....	MMPRLLFRWFP	RCPSLVLGAPSRP	24												
CPT2_MOUSE	1	.....	MMPRLLLRDWP	RCPSLVLGAPSRP	24												
CPT2_HUMAN	1	.....	MVPRLLLRWFP	RGPAVGGPAPSRP	24												
CACP_YEAST	1	.....	MRIHSRTLSNLKDLPT	SRRAHSAIVNYS	35												
CACP_CANTR	1	.....	MFNFKLSQQVQKLN	STKS	17												
CACP_HUMAN	1	.....	FAAARTVVKP		10												
CACP_MOUSE	1	.....	MLFAAARTVVKP		12												
CACP_COLLI	1	.....	MDRKQKQAEKARP		13												
CLAT_MOUSE	1	.....			P 1												
CLAT_RAT	1	.....			P 1												
CLAT_PIG	1	.....			P 1												
CLAT_HUMAN	1	MGLR	TAKRGLGGGKWKREGGGR	TRGRRVPAFCFLQSGGRGDPGDVGGPAGNPGCS	PHPRATRPPLPAHTPAHTPEWCGAASAEAEPRRAGPLHCIPAPGLTKTP	110											
CLAT_DROME	1	.....	VASNEASTSAAGSGPESAA	LFSKLRFSFGSGPNSPQRVSVNLRGFLTHR		50											
CLAT_CAEEL	1	.....			MEKEK	5											
CPTM_RAT	1	.....	MAEAHQAVAFQFTVTP	DGVDLRLSREALRHIVL	SGINSWKKRLIRIKNGILRG	53											
CPTM_HUMAN	1	.....	MAEAHQAVAFQFTVTP	DGVDLRLSREALKHVYLSGINSWKKRLIRIKNGILRG		53											
CPT1_RAT	1	.....	MAEAHQAVAFQFTVTP	DGIDLRLSHEALKQICLSGLHSWKKRIRFKNIGIITG		54											
CPT1_MOUSE	1	.....	FQFTVTPDGIDLRLSHEALKQICLSGLHSWKKRIRFKNIGIITG			44											
CPT1_HUMAN	1	.....	MAEAHQAVAFQFTVTP	DGIDLRLSHEALKQIYLSGLHSWKKRIRFKNIGIITG		53											
CPT2_RAT	25	LSAVS	.....	GPDDYLQH	.....	SIVPTMHYQD	.....	47									
CPT2_MOUSE	25	LSAVS	.....	GPAEYLQH	.....	SIVPTMHYQD	.....	47									
CPT2_HUMAN	25	LSAGS	.....	GPQYLQK	.....	SIVPTMHYQD	.....	47									
CACP_YEAST	36	QFPVETNNGEHY	WAE	.....	KPNKFYQNK	.....	RPNFGGITFAKQQ	.....	72								
CACP_CANTR	18	IMPILK	.....	KP	.....	FSTS	.....	HAKGDLFKYQS	.....	40							
CACP_HUMAN	11	LGFLKRF	.....	SLMKASS	.....	RFKAHQD	.....		.....	31							
CACP_MOUSE	13	LGLLKPS	.....	SLMKVSG	.....	RFKAHQD	.....		.....	33							
CACP_COLLI	14	YGLLKPA	.....	ALGKIPG	.....	RFQHQE	.....		.....	34							
CLAT_MOUSE	2	ILEKVF	.....	PKMPVQA	.....	SS	.....	CEEVL	.....	21							
CLAT_RAT	2	ILEKAF	.....	QKMPVKA	.....	SS	.....	WEEL	.....	20							
CLAT_PIG	2	ILEKTF	.....	PKMAKS	.....	PSS	.....	EEEP	.....	21							
CLAT_HUMAN	111	ILEKVF	.....	RKMAAKT	.....	PSS	.....	EES	.....	29							
CLAT_DROME	51	LSNIT	SDTGUKDSILS	.....	IPKKULST	.....	.....	AESVDEFQFP	.....	85							
CLAT_CAEEL	6	VDE	.....	LPP	.....	NDNYET	.....		.....	18							
OCTC_HUMAN	1	.....	.....	MENQLAKS	.....	TEERTFYQD	.....		.....	18							
OCTC_RAT	1	.....	.....	MENQLAKS	.....	IEERTFYQD	.....		.....	18							
OCTC_BOVIN	1	.....	.....	MENQLAKS	.....	TEERTFYQD	.....		.....	18							
CPTM_RAT	54	VYPG	STSMVVMVVMATVGSNYCKVDISMLGVHICIRCLPTRYGSGYTPQTETLLSMVIFSTGWVATGIFLRQTLKLLSYHGUMFEMHS	KTSHATKIWAICVRLSSR	162												
CPTM_HUMAN	54	VYPG	STSMVVMVVMATVGSFCHVDISMLGLVSCIRCLPQGCGPYQPTQRALLSMAIFSTGWVATGIFFRQTLKLLCYHGUMFEMHG	KTNLRIWAMCIRLLSSR	162												
CPT1_RAT	54	VFPAN	SSMLVVMVVMATVGSNYCKVDISMLGVHICIRCLPTRYGSGYTPQTETLLSMVIFSTGWVATGIFLRQTLKLLSYHGUMFEMHS	KMSRSTKIWMVAVKIFSGR	160												
CPT1_MOUSE	45	VFPAS	SSMLVVMVVMATVGSNYCKVDISMLGVHICIRCLPTRYGSGYTPQTETLLSMVIFSTGWVATGIFLRQTLKLLSYHGUMFEMHS	KMSRSTKIWMVAVKIFSGR	151												
CPT1_HUMAN	54	VYPAS	SSMLVVMVVMATVGSNYCKVDISMLGVHICIRCLPTRYGSGYTPQTETLLSMVIFSTGWVATGIFLRQTLKLLSYHGUMFEMHG	KMSRSTKIWMVAVKIFSGR	160												
CPT2_RAT	48	.....	SLPRLPTPKLED	TKRYLNAQKPLLD	.....	SQFRRTTEALCKNF	ETG	.....	VGKELHAHLAQQDKQNKHT	SYISGPFDB	.....	MYLTAR	.....	DSIVLNF	PPMAFNPDP	141	
CPT2_MOUSE	48	.....	SLPRLPTPKLED	TKRYLNAQKPLLD	.....	SQFRKTEVLCKDF	ENG	.....	IGKELHAHLAQQDKQNKHT	SYISGPFDB	.....	MYLTAR	.....	DSIVLNF	PPMAFNPDP	141	
CPT2_HUMAN	48	.....	SLPRLPTPKLED	TKRYLNAQKPLLD	.....	SQFRKTEVCFCKS	ENG	.....	IGKELHEQLVALDQDKQNKHT	SYISGPFDB	.....	MYLTAR	.....	DSIVLNF	PPMAFNPDP	141	
CACP_YEAST	73	.....	DLPSPVPPLEKST	LDKYLQTRPFCNDV	.....	ETTEROQLLCKDF	SEH	.....	MGPILQDRLKEY	.....	ANDKRNMMAKFIDEQ	SYLQYN	.....	DPVYVYFYSHPMLP	166		
CACP_CANTR	41	.....	QLPKLPVPTLEE	TASKYLVTEVFPFLNQ	.....	EQLESTKAKVAE	YRPPGGAGEALQARLNNF	.....	AADKDNMLAEFDDY	.....	AYMSYR	.....	DPVYVYFYSHPMLP	135			
CACP_HUMAN	32	.....	ALPRLPVPPLEKST	LDKYLQTRPFCNDV	.....	EQLESTKAKVAE	YRPPGGAGEALQARLNNF	.....	ARKTENMLSEWJLKT	.....	AYLQYR	.....	DPVYVYFYSHPMLP	125			
CACP_MOUSE	34	.....	ALPRLPVPPLEKST	LDKYLQTRPFCNDV	.....	EQLESTKAKVAE	YRPPGGAGEALQARLNNF	.....	AKKMNEMLSEWJLKT	.....	AYLQYR	.....	DPVYVYFYSHPMLP	128			
CACP_COLLI	35	.....	ALPRLPVPPLEKST	LDKYLQTRPFCNDV	.....	EQLESTKAKVAE	YRPPGGAGEALQARLNNF	.....	AKKDNMLSEWJLKT	.....	AYLEVR	.....	DPVYVYFYSHPMLP	128			
CLAT_MOUSE	22	.....	DLPKLPVPPLEKST	LATYLQCMQHLVPE	.....	EQFRKSQATVRRF	GAPGGLGETLQKLLER	.....	QEKTNAMVSEYULND	.....	MYLNNR	.....	LALPVNSPAPVIFAR	115			
CLAT_RAT	21	.....	DLPKLPVPPLEKST	LATYLQCMQHLVPE	.....	EQFRKSQATVRRF	GAPGGLGETLQKLLER	.....	QEKTNAMVSEYULND	.....	MYLNNR	.....	LALPVNSPAPVIFAR	114			
CLAT_PIG	22	.....	GLPKLPVPPLEKST	LATYLQCMQHLVPE	.....	EQFRKSQATVRRF	GAPGGLGETLQKLLER	.....	QEKTNAMVSEYULND	.....	MYLNNR	.....	LALPVNSPAPVIFAR	115			
CLAT_HUMAN	130	.....	GLPKLPVPPLEKST	LATYLQCMQHLVPE	.....	EQFRKSQATVRRF	GAPGGLGETLQKLLER	.....	QEKTNAMVSEYULND	.....	MYLNNR	.....	LALPVNSPAPVIFAR	223			
CLAT_DROME	86	.....	DTLPKLPVPPLEKST	LATYLQCMQHLVPE	.....	EQFRKSQATVRRF	GAPGGLGETLQKLLER	.....	REARITGPIITGSTR	.....	CTWJFA	.....	FALPINSNPGIVGPA	180			
CLAT_CAEEL	19	.....	ALPKPVPVSL	LEATLDKRYLYAAVAVGQKASL	ATTTHDAHKFYRQ	.....	ATPLQEQLEL	.....	AEKSPNMAIKFALPE	.....	MYMRVR	.....	MPTPVNSNPGYIFPKVK	112			
OCTC_HUMAN	19	.....	SLPSPVPSLEES	KKYLVSVKPFANE	.....	EEKYKTEEVQKQ	QSG	.....	IGKELHQLKLLER	.....	AKGRRNLEEWJLNV	.....	AYLDVR	.....	IPSQNLVNFAGPAAHFE	111	
OCTC_RAT	19	.....	SLPSPVPSLEES	KKYLVSVKPFANE	.....	EEKYKTEEVQKQ	QSG	.....	VGKTLHQLKLLER	.....	AKGRRNLEEWJLNV	.....	AYLDVR	.....	IPSQNLVNFAGPAAHFE	111	
OCTC_BOVIN	19	.....	SLPSPVPSLEES	KKYLVSVKPFANE	.....	EEKYKTEEVQKQ	QSG	.....	IGKELHQLKLLER	.....	AKGRRNLEEWJLNV	.....	AYLDVR	.....	IPSQNLVNFAGPAAHFE	111	
CPTM_RAT	163	.....	RPMLYSFQTS	LPLKLPVPPVAT	THRYLDSVRPLDD	.....	EYFRMESLAK	EFQDK	.....	TAPRLQKYLVLK	.....	SWJATHYVSDWJEEY	.....	YLYRGR	.....	SPMLVNSNYAMDVLI	264
CPTM_HUMAN	163	.....	RPMLYSFQTS	LPLKLPVPPVAT	THRYLDSVRPLDD	.....	EYFRMESLAK	EFQDK	.....	TAPRLQKYLVLK	.....	SWJATHYVSDWJEEY	.....	YLYRGR	.....	SPMLVNSNYAMDVLI	264
CPT1_RAT	161	.....	KPMLYSFQTS	LPLKLPVPPVAT	THRYLDSVRPLDD	.....	EYFRMESLAK	EFQDK	.....	TAPRLQKYLVLK	.....	SWJATHYVSDWJEEY	.....	YLYRGR	.....	SPMLVNSNYAMDVLI	262
CPT1_MOUSE	152	.....	KPMLYSFQTS	LPLKLPVPPVAT	THRYLDSVRPLDD	.....	EYFRMESLAK	EFQDK	.....	TAPRLQKYLVLK	.....	SWJATHYVSDWJEEY	.....	YLYRGR	.....	SPMLVNSNYAMDVLI	253
CPT1_HUMAN	161	.....	KPMLYSFQTS	LPLKLPVPPVAT	THRYLDSVRPLDD	.....	EYFRMESLAK	EFQDK	.....	TAPRLQKYLVLK	.....	SWJATHYVSDWJEEY	.....	YLYRGR	.....	SPMLVNSNYAMDVLI	262

Apéndices

Table with 3 columns: Species, Position, and Sequence. Rows include CPT2\_RAT, CPT2\_MOUSE, CPT2\_HUMAN, CACP\_YEAST, CACP\_CANTR, CACP\_MOUSE, CACP\_COLL1, CLAT\_MOUSE, CLAT\_RAT, CLAT\_PTG, CLAT\_HUMAN, CLAT\_DROME, CLAT\_CAEEL, OCTC\_HUMAN, OCTC\_RAT, OCTC\_BOVIN, CPTM\_MOUSE, CPTM\_HUMAN, CPT1\_RAT, CPT1\_MOUSE, CPT1\_HUMAN.

Table with 3 columns: Species, Position, and Sequence. Rows include CPT2\_RAT, CPT2\_MOUSE, CPT2\_HUMAN, CACP\_YEAST, CACP\_CANTR, CACP\_MOUSE, CACP\_COLL1, CLAT\_MOUSE, CLAT\_RAT, CLAT\_PTG, CLAT\_HUMAN, CLAT\_DROME, CLAT\_CAEEL, OCTC\_HUMAN, OCTC\_RAT, OCTC\_BOVIN, CPTM\_MOUSE, CPTM\_HUMAN, CPT1\_RAT, CPT1\_MOUSE, CPT1\_HUMAN.

Table with 3 columns: Species, Position, and Sequence. Rows include CPT2\_RAT, CPT2\_MOUSE, CPT2\_HUMAN, CACP\_YEAST, CACP\_CANTR, CACP\_MOUSE, CACP\_COLL1, CLAT\_MOUSE, CLAT\_RAT, CLAT\_PTG, CLAT\_HUMAN, CLAT\_DROME, CLAT\_CAEEL, OCTC\_HUMAN, OCTC\_RAT, OCTC\_BOVIN, CPTM\_MOUSE, CPTM\_HUMAN, CPT1\_RAT, CPT1\_MOUSE, CPT1\_HUMAN.

Table with 3 columns: Species, Position, and Sequence. Rows include CPT2\_RAT, CPT2\_MOUSE, CPT2\_HUMAN, CACP\_YEAST, CACP\_CANTR, CACP\_MOUSE, CACP\_COLL1, CLAT\_MOUSE, CLAT\_RAT, CLAT\_PTG, CLAT\_HUMAN, CLAT\_DROME, CLAT\_CAEEL, OCTC\_HUMAN, OCTC\_RAT, OCTC\_BOVIN, CPTM\_MOUSE, CPTM\_HUMAN, CPT1\_RAT, CPT1\_MOUSE, CPT1\_HUMAN.



## Apéndices

CPT2_RAT	518	R	.....	DPSKHSVG.....	ELQHMMAECSKY	GGQLTKEAAMGGFDRHLALRYL	TARGLNL.....	PE	..	LYLDPAYQQMN.....	HNILSTSTLN	593
CPT2_MOUSE	518	R	.....	EPSKHSVG.....	ELQHMMAECSKY	GGQLTKEAAMGGFDRHLALRYL	LAARGVTL.....	PE	..	LYQDPAYQRIN.....	HNILSTSTLS	593
CPT2_HUMAN	518	R	.....	EPSRHSAG.....	ELQQMVECSKY	GGQLTKEAAMGGFDRHLALRYL	RAAKGIIL.....	PE	..	LYLDPAYGQIN.....	HNVLSTSTLS	593
CACP_YEAST	526	NG	.....	DVPIAEK.....	IQALKHBAKEHSTYLNARANGNVD	RHFFLGNMLKSNDDQ.....	IP	..	LFKDFLNFYS.....	TWLSTSTLS	599	
CACP_CANTR	483	IP	.....	NASSADK.....	VATFQAARAKHWAYLSAARADGK	BVDRHLFLGKQMIQGPGE.....	IP	..	IFTDIFFSYBQ.....	TWYISSQV	555	
CACP_HUMAN	482	II	.....	SSVTEHQK.....	VELLRKAVQAHRGYTDRAIRGEAF	GRHLGLKQAIEDLVST.....	PD	..	IFMDSYAIAM.....	HFNLSTSOV	555	
CACP_MOUSE	485	II	.....	STVPEQQK.....	VELLRKAVQAHRGYTDRAIRGEAF	DRHLGLKQAIEDLVSM.....	PD	..	IFMDSYAIAM.....	HFNLSTSOV	558	
CACP_COLLII	485	S	.....	PDKSDQEK.....	ADLLRRATQAKEYTVMATIQGNAI	DRHLGLKQAIEDLVSI.....	PE	..	LFMDTAYAVAM.....	HFNLSTSOV	558	
CLAT_MOUSE	478	HK	.....	AAVLASEK.....	LQLLQRIQAQTEYTMATIGMAID	NHLLALRELARDLCKEP.....	PE	..	MFMDETYLMN.....	RFVLTSOV	553	
CLAT_RAT	477	HK	.....	AAMPASEK.....	LQLLQRIQAQTEYTMATIGMAID	NHLLALRELARDLCKEP.....	PE	..	MFMDETYLMN.....	RFVLTSOV	552	
CLAT_PIG	478	HA	.....	SAMPDSEK.....	LLLLKDIRAQTAYTMATIGMAID	NHLLALRELAREVCKEL.....	PE	..	MFMDETYLMN.....	RFVLTSOV	553	
CLAT_HUMAN	586	HK	.....	AAPVASEK.....	LLLLKDIRAQTAYTMATIGMAID	NHLLALRELARAMCKEL.....	PE	..	MFMDETYLMN.....	RFVLTSOV	561	
CLAT_DROME	561	QGEGANVPLESDREDEEESRKVKF	SIYSKDHLRELFRCAVARQTEVMY	RISWAMASTRCWPARGOYRGHRRDA	.....	RA	..	VQRRVLQQCSQ.....	CNLLSTSOVA	657		
CLAT_CAEEL	484	SK	.....	KESKERK.....	LELFKRVLKVQVTLTENISGYVDN	HALCALFLAREREETTGEDIPS	..	LF	LDPLWSEVM.....	RFPLSTSOV	561	
OCTC_HUMAN	471	IP	.....	SVNLRER.....	QQKMLQFAKHNKMMKDCSAGKGF	DRHLGLLLIAKEEGLPV.....	PE	..	LFDPLFSRGGG.....	GNFVLTSLV	546	
OCTC_RAT	471	IP	.....	SASLLER.....	QQKMLQFAKHNKMMKDCSAGKGF	DRHLGLLLIAKEEGLPV.....	PE	..	LFDPLFSRGGG.....	GNFVLTSLV	546	
OCTC_BOVIN	471	IP	.....	STSLLER.....	KHMLLEFAKHNKMMKDCSTGKGF	DRHLGLLLIAKEEGLPV.....	PE	..	LFDPLFSRGGG.....	GNFVLTSLV	546	
CPTM_RAT	621	TG	.....	SHKKQDL.....	QDLFRKASEKHONMYRLAMT	GAGIDRALFCUYVSKYLVGVS	..	PF	LEVLSERMLSTSQIPQIQCMFDPKQY	703		
CPTM_MOUSE	621	EG	.....	SHTKADL.....	RDLFQKAAKHONMYRLAMT	GAGIDRALFCUYVSKYLVGVS	..	PF	LAEVLSEARMLSTSQIPQSQIRMFDPQHP	703		
CPT1_RAT	621	IP	.....	KSTAEQR.....	LKLFKICEKHONHLYRLAMT	GAGIDRALFCUYVSKYLVAVDS	..	PF	LKEVLSEARMLSTSQTPQQQVQLFDFEKNP	703		
CPT1_MOUSE	612	IP	.....	TTTAEQR.....	LKLFKICEKHONHLYRLAMT	GAGIDRALFCUYVSKYLVAVDS	..	PF	LKEVLSEARMLSTSQTPQQQVQLFDFEKNP	694		
CPT1_HUMAN	621	IP	.....	AQTVEQR.....	LKLFKLESEKHONHMYRLAMT	GAGIDRALFCUYVSKYLVAVES	..	PF	LKEVLSEARMLSTSQTPQQQVQLFDLENN	703		

CPT2_RAT	594	SPAVS...	LGGFAPVVPDGFGLAYAVH	DDWIGCNVSSYSGR...	NAREL	LHCVQKCLEDFDALE	.....	GKAIKT	.....	658
CPT2_MOUSE	594	SPAVS...	LGGFAPVVPDGFGLAYAVH	DDWIGCNVSSYSGR...	NAREL	LHCVQKCLEDFDALE	.....	GKAIKT	.....	658
CPT2_HUMAN	594	SPAVN...	LGGFAPVVPDGFGLAYAVH	DDWIGCNVSSYSGR...	NAREL	LQCEKLEDFDALE	.....	GKSIKS	.....	658
CACP_YEAST	600	SEYFD...	GYGNSQVNDGFGFLAYMLN	NEWLHINTVKNKPSGSAVNR	LHYLLSQADE	FDALEN	.....	ENKRKAKL	.....	670
CACP_CANTR	556	SEFFQ...	SWGNSQVNDGFGFLAYLIN	NDWLHVHTCKGRGN	GLQSDHLKHYLVDSANEMK	DLTKGL	.....	LTDAPKPL	.....	627
CACP_HUMAN	556	AKTDC...	VMFFGPVVPDGYGVCYNPM	EAHINSLSAVNSCAETNAAR	LHAYLEKALLDMRALQSHPR	.....	AKL	.....	624	
CACP_MOUSE	559	AKTDC...	VMFFGPVVPDGYGVCYNPM	EAHINSLSAVNSCAETNAAR	LHAYLEKALLDMRALQSHPR	.....	AKL	.....	627	
CACP_COLLII	559	AKTDC...	VMFFGPVVPDGYGVCYNPM	EAHINSLSAVNSCAETNAAR	LHAYLEKALLDMRALQSHPR	.....	SKL	.....	627	
CLAT_MOUSE	554	TTMEM...	FCCYGPVVPNGYGCYNPH	AEAITFCISSFHCKEISSVE	AEAVGASLVDMRD	CSSROP	..	ADSKPPTAKERARGPSQAKQS	640	
CLAT_RAT	553	TTMEM...	FCCYGPVVPNGYGCYNPH	AEAITFCISSFHCKEISSVE	AEAVGASLVDMRD	CSSROP	..	ADSKPPAPKEKARGPSQAKQS	639	
CLAT_PIG	554	TTMEM...	FCCYGPVVPNGYGCYNPH	AEAITFCISSFHCKEISSVE	AEAVGASLVDMRD	CSSROP	..	GMGKPLATKEKATRPSQVHQP	640	
CLAT_HUMAN	662	TTMEM...	FCCYGPVVPNGYGCYNPH	AEAITFCISSFHCKEISSVE	AEAVGASLVDMRD	CSSROP	..	TESKPLATKEKATRPSQVHQP	748	
CLAT_DROME	658	CSTDS...	FMGYPVTPRGYGCYNPH	PEQIVFCVSAFYSCDTSASR	AKSLQDSLDMRD	LQN	.....	620		
CLAT_CAEEL	562	TSLDIFDCYLTGAVYVADGYGCP	NIQ.PDRVIAPTAFSPDRPDLQ	HKKSLAGMRDKELLSN	.....	627				
OCTC_HUMAN	547	GYLRV...	QGVVPHVHNGYGYFFHIR	DDRFVVTCSVMKSLPE	DAEKLVLQVTFCAFHDH	IQMNSTHL	.....	612		
OCTC_RAT	547	GYLRI...	QGVVPHVHNGYGYFFHIR	DDRFVVTCSVMKSLPE	DAEKLVEIFHAFHDIH	MNTAHL	.....	612		
OCTC_BOVIN	547	GYLRV...	QGVVPHVHNGYGYFFHIR	DDRFVVTCSVMKSLPE	DAEKLVLQVTFCAFHDH	IQMNSTHL	.....	612		
CPTM_RAT	704	NHLGA...	GGGFGPVADHYGYVSI	AGENTIFAHVSSKLSSE	NALRGNHIRQALLD	ADFKIKSTDS	.....	772		
CPTM_MOUSE	704	NHLGA...	GGGFGPVADHYGYVSI	AGENTIFAHVSSKLSSE	NALRGNHIRQALLD	ADFKIKSTDS	.....	772		
CPT1_RAT	704	DYVSC...	GGGFGPVADHYGYVSI	IIVGENFTHHHSKFS	SPEDSHRFGKHLRQAM	ADITFGLTINSKK	.....	773		
CPT1_MOUSE	695	DYVSC...	GGGFGPVADHYGYVSI	IIVGENFTHHHSKFS	SPEDSHRFGKHLRQAM	ADITFGLTANSKK	.....	764		
CPT1_HUMAN	704	EYVSS...	GGGFGPVADHYGYVSI	IIVGENFTHHHSKFS	SPEDSHRFGKHLRQAM	ADITFGLSSNSKK	.....	773		