cDNA from rat cells with reconstitutive galactose-epimerase activity in *E. coli*

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cDNA 47−3 (1373 bp) was isolated from a L6-Myoblast (rat) library by a selective screening procedure using an UDP-Galactose-4-Epimerase deficient *E. coli* strain (DC41−2F'). Expression of this cDNA, leads to reconstitution of epimerase activity in strain DC41/2F' and enables it to grow on medium containing phenylgalactoside. Usually this substrate is lethal for bacteria producing lacZ but lacking galE activity (1). The nucleotide sequence of the isolated cDNA has significant homologies to *E. coli*- (2) and Yeast-Epimerase (3) (GalE and Gal10). Thus, the isolated cDNA should encode an eukaryotic homologue of UDP-Gal-4-Epimerase.

ACKNOWLEDGEMENTS

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5'GAA TTC GGC ACG AGC TCT GCA GGC GCC ATG GAG GAG AAG  39
                                          M   E   E   K
GT GCTC GTC ACG GGC GGG GCT GGC TAC ATC GGT AGC CAC  78
 V   L   V   T   G   G   A   G   Y   I   G   S   H
ACA GTG TTG GAG CTG CTG GAG GCG GGC TAC TCG CCT GTG  117
 T   V   L   E   L   L   E   A   G   Y   S   P   V
GTC ATC GAC AAC TTC CAC AAT TCC ATT CGT GGA GAA GAC  156
 V   I   D   N   F   H   N   S   I   R   G   E   D
TCC ATG CCT GAG AGC CTG CGC CGG GTC CAG GAG CTG ACA  195
 S   M   P   E   S   L   R   R   V   Q   E   L   T
GGC CGC TCT GTG GAG TTT GAG GAG ATG GAC ATC TTG GAC  234
 G   R   S   V   E   F   E   E   M   D   I   L   D
CAG GCA GCC CTA CAG CAC CTC TTT AAG AAG CAC AAT TTT  273
 Q   A   A   L   Q   H   L   F   K   K   H   N   F
AAG GCT GTC ATC CAC TTT GCT GGG CTC AAG GCT GTG GGC  312
 K   A   V   I   H   F   A   G   L   K   A   V   G
GAG TCA GTG CAG AAG CCT CTG GAT TAC TAC AGA GTT AAC  351
 E   S   V   Q   K   P   L   D   Y   Y   R   V   N
CTA ACA GGG ACC ATC CAG CTC CTG GAG ATC ATG AGG GCC  390
 L   T   G   T   I   Q   L   L   E   I   M   R   A
ATG GGG GTG AAG AGT CTG GTC TTC AGC AGC TCA GCC ACC  429
 M   G   V   K   S   L   V   F   S   S   S   A   T
GTG TAT GGG AAA CCC GTA CCT GCC TCT GGA CGA GGC CCA  468
 V   Y   G   K   P   V   P   A   S   G   R   G   P
CCC CAC CGG GGC TGT ACC AAA CCC TAC GGC AAG TCC AAG  507
 P   H   R   G   C   T   K   P   Y   G   K   S   K
TTC TTC ATT GAA GAG ATG ATC CAG GAC CT GTGC CGG GCA  546
 F   F   I   E   E   M   I   Q   D   L   C   R   A
GAC ACG GCC TGG AAC GCT GTG CTG CTT CGG TAC TTC ATC  585
 D   T   A   W   N   A   V   L   L   R   Y   F   I
CCC ATA GGC GCC CAT CGC TCT GCG CGC ATC GGC GAA GAT  624
 P   I   G   A   H   R   S   A   R   I   G   E   D
CCT CAG GGT ATC CCC AAC AAC CTC ATG CCC TAT GTC TCC  663
 P   Q   G   I   P   N   N   L   M   P   Y   V   S
CAG GTG GCA ATC GGG CGA CGA GAG GCC CTG AAT GTC TTT  702
 Q   V   A   I   G   R   R   E   A   L   N   V   F
GGT GAT GAC TAC GCT ACG GAG GAT GGG ACA GGT GTG AGG  741
 G   D   D   Y   A   T   E   D   G   T   G   V   R
GAT TAC ATT CAT GTG GTG GAT CTG GCC AAG GGC CAT ATA  780
 D   Y   I   H   V   V   D   L   A   K   G   H   I
GCA GCC TTG AAG AAG CTG AAG GAG CAG TGT GGT TGC CGG  819
 A   A   L   K   K   L   K   E   Q   C   G   C   R
ATC TAC AAC CTG GGC ACG GGC ACA GGC TAT TCG GTC CTG  858
 I   Y   N   L   G   T   G   T   G   Y   S   V   L
CAG ATG GTC CAA GCC ATG GAG AAG GCC TCA GGG AAG AAG  897
 Q   M   V   Q   A   M   E   K   A   S   G   K   K
ATC CCG TAC AAG GTG GTG GCA CGG CGG GAA GGC GAT GTG  936
 I   P   Y   K   V   V   A   R   R   E   G   D   V
GCG GCC TGT TAT GCC AAC CCC AGC CTG GCC CAT GAG GAG  975
 A   A   C   Y   A   N   P   S   L   A   H   E   E
CTG GGC TGG ACA GCA GCC TTG GGG CTG GAC AGG ATG TGT  1014
 L   G   W   T   A   A   L   G   L   D   R   M   C
GAA GAT CTG TGG CGC TGG CAG AAG CAG AAC CCT TCA GGC  1053
 E   D   L   W   R   W   Q   K   Q   N   P   S   G
CTT GGG GCG CAT GGC TGA GGC TCT CCT TAC CAC GGA CCA  1092
 L   G   A   H   G   *
GAA AAG AGC AGC TAC CTG CTT TGC AGC CGC CAC AGG ACC  1131
CTA CAC CCT CAT GCG CTG AGG CCA CCC TAC CTC AAA GGC  1170
CAG CTG TCT CTC AGC CCT CCC GGC AGG AGA CCT CTG GTT  1209
CTA CTG ACC AGA AAG GAG TCT GGG TCC TTC CAG CCT ATT  1248
TTC CCC AGA GTC CAG CAG CTC ATG TGA TCC CCA GAG CCT  1287
TGT GGA GGC CAG GGG GTC TGG GAC CAA AGC CTC CCT CAG  1326
GCA CTA ACT TAT ACA GCT AAG ATT GAG CTT TCC AAA GTA  1365
TTT AAA ATA AAA ATG TCT TCT TCT CGT GCC GAA TTC 3'  1401
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