

Structure of human muscle ( $\beta$ ) enolase mRNA and protein deduced from a genomic clone

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The human enolase gene family consists of at least three independent members: the general ( $\alpha$ ) and neurone-specific ( $\gamma$ ) gene products have been described previously(1,2). Several lines of evidence(3) establish that the sequences described here, deduced from the 11 coding exons of a genomic clone and corresponding precisely with the exons of the rat  $\gamma$  enolase gene(4), represent human  $\beta$  enolase (ENO 3) mRNA and protein.

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H A H Q K I F A R E I L D S R G N P T V
ATGGCCATCGAAAAATCTTGGCCGGGAAATCTGGACCTCCAGGGGCAACCCACGGTG
    10          20          30          40          50          60

E V D L H T A K G R F R A A V P S G A S
GAGGTGACCTGACACAGGCCAAGGGCCGATCTCCAGCAGCTGTGCCAGTGGGGCTTCC
    70          80          90          100         110         120

T G I Y E A L E L R D G D K G R Y L G K
ACGGTATCTATGAGCTCTGGAACTAAAGACGGGAGACAAAGGCCCTACTGGGGAAA
    130         140         150         160         170         180

G V L K A V E N I N N T L G P A L L Q N
GGATCTCTGAAGCTGTGGAGAACATCAACAATCTGTGGGCCGTCTCTGCTCAAAAAG
    190         200         210         220         230         240

K L S V V D Q E K V D K F M I E L D G T
AAACTAAGCTTGTGTATCAAGAAAAGTTGACAAATTTATGATTGAGCTAGATGGGACC
    250         260         270         280         290         300

E N K S K F G A N A I L G V S L A V C K
GAGAATAAGTCCAAGTTTGGGGCCAAATGCCATCTGGGCCGTCTCTTGGCCGTGTGTAAG
    310         320         330         340         350         360

A G A A E K G V P L Y R H I A D L A G N
GGGGGACCTGAGAAAGGGGTCCTCCCTGTACCCGACACATCCGAGATCTCGCTGGGAAC
    370         380         390         400         410         420

P D L I L P Y P A F N V I N G G S H A G
CCTGACCTCATCTCCGACTCCGCTCAATGTGATGATCAACGGGGCTCCCACTGGTGA
    430         440         450         460         470         480

N N L A M Q E F N I L P V G A S S F K E
AACAACTGGCCATGACAGGATTCATGATTTGGCTGTGGAGCCAGCTCTTCAAGGAA
    490         500         510         520         530         540

A M R I G A E V Y H H L K G V I K A K Y
GCCATGGCATTGGCCCGAGGTCTACCACCACTCAAGGGGTTCATCAAGGCCAAGTAT
    550         560         570         580         590         600

G K D A T N V G D E G G F A P N I L E N
GGGAAGGATGCCCAAAATGTGGGTGATGAAGGTGGCTTCCGACCAACCAATCTGGAGAAC
    610         620         630         640         650         660

N E A L E L L K T A I Q A A G Y P D K V
AATGAGGCCCTGGAGCTGCTGAAGACGGCCATCCAGGCCCTGGTTACCAGACAAAGGTG
    670         680         690         700         710         720
    
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V I G H D V A A S E F Y R N G K Y D L D
CTGATCGGGATGGATGGCAGCATCTGAATTCATCGCAATGGGAAGTACGATCTGGAC
    730          740          750          760          770          780

F K S P D D P A R H I T G E K L G E L Y
TTCAGTGGCTGTATGATCCCGCAGCGCATCACTGGGGAGAAGCTCGGAGAGCTGTAT
    790          800          810          820          830          840

K S F I K N Y P V V S I E D F F D Q D D
AAGAGCTTTATCAAGAACTATCCTGTGTCTCCATCGAAGCCCTTGTACCAGGATGAC
    850          860          870          880          890          900

W A T W T S F L S G V N I Q I V G D D L
TGGGCCATGGACCTCTCTCTCGGGGGTGAACATCCAGATTTGGGGGGTACTTGG
    910          920          930          940          950          960

T V T N P K R I A Q A V E K K A C N C L
ACAGTACCACCCCAAGAGGATTTGCCAGCCGCTTGAGAAGAAGGCCCTGCAACTGTCTG
    970          980          990          1000         1010         1020

L L K V N Q I G S V T E S I Q A C K L A
CTGTGAAGGTCAACCGATCGGCTCGGTGCGCAATGCTCCAGGGCTGCAAACTGGCT
    1030         1040         1050         1060         1070         1080

Q S N G W G V H V S H R S G E T E D T F
CAGTCTAATGGCTGGGGGTGATGGTAGCCACCGCTCAGGGGAGACTGAGGACACTTC
    1090         1100         1110         1120         1130         1140

I A D L V V G L C T G G Q I K T G A P C R
ATTGCTGACTTGTGGGGCTGTGGCAGGACGATCAAGACTGGGCCCTGCGCC
    1150         1160         1170         1180         1190         1200

S E R L A K Y N Q L M R I E E A L G D K
TCGGAGCCTTGGCCAAATCAACCAACTCATGAGGATCGAGAGGCTCTTGGGGACAG
    1210         1220         1230         1240         1250         1260

A I F A G R K K F R N P K A K *
GCAATCTTTGCTGGACCAAGTTTCGTAAACCCGAAGGCCAAGTGAAGAAGTGGAGGCTCC
    1270         1280         1290         1300         1310         1320

AGGACTCCACTGGACAGCCAGGCTTCCAGACCTCTCTGAAATAAACACTGGTGGC
    1330         1340         1350         1360         1370         1380

CAACCAAGAC
    1390
    
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**References**

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