

Sequence of the chicken GABA_A receptor β 3-subunit cDNA

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Complementary DNA cloning has revealed that the GABA_A receptor, which is the major inhibitory neurotransmitter receptor in the vertebrate brain, is a member of the ligand-gated ion channel super-family (1). Such studies have elucidated the sequences of different types of subunit and of different subunit isoforms (2). We screened an embryonic chick whole brain cDNA library in λ gt10 with a linearized plasmid, pbGR β sense, that contains a bovine GABA_A receptor β 1-subunit cDNA (3). A 2.2 kb clone was isolated that encodes a mature polypeptide of 451 amino acids and a signal peptide of 25 amino acids. The mature subunit sequence exhibits 81, 81 and 92% identity to the previously-reported bovine β 1- (3), β 2- and β 3-subunit sequences (4), respectively.

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1          GAATTCCTCACGCGGCAGCCAGGGCAGCCGGATCGCGCGGCAGCAGCTGCTGCTGCTGCTGCTGCGCGGAGGGAGCCCGGGCGGAGGG
-25  M W G F G G G R I F G I F S A P V L V A V V C C A Q S V N D P G N M S F V K E T
92  ATGTGGGGCTTTGGGGGAGGCAGGATCTTCGGGATCTTCTCCGCTCCCGTCTGGTGGCCGTGGTGTGCTGCGCCAGAGCGTGAACGATCCCGGCAACATGTCCTTCGTGAAGGAAACG
16  V D K L L K G Y D I R L R P D F G G P P V C V G M N I D I A S I D M V S E V N M
212 GTGGATAAATGCTGAAGGGCTACGACATCCGCCTCCGCCGGATTTCCGAGGTCCTCCCGTCTGCGTGGGGATGAACATCGACATCGCCAGCAGTCGACATGGTCTCCGAAGTCAACATG
56  D Y T L T M Y F Q Q Y W R D K R L A Y A G I P L N L T L D N R V A A D Q L W V P D
332 GATTACTTTGACTATGTAATTTCAACAGTACTGGAGAGATAAGAGATTGGCATATGCTGGCATACTCTCAACCTGACGCTTGATAATCGAGTGGGAGATCACTCTGGGTGCGCTGAC
96  T Y F L N D K K S I F V H G V T V K N R M I R L H P D G T V L Y G L R I T T T A A
452 ACGTACTTCTAAATGACAAGAAATCATTGTGCATGGCGTTACTGTGAAGAACCAGAAATGATTCGCCTTCAATCCAGATGGAACGGTGCCTTATGGCCTCAGGATCACAACCCAGCAGCT
136  C M M D L R R Y P L D E Q N C T L E I E S Y G Y T T D D I E F Y W R G G D N A V
572 TGTATGATGGACTTGAGAAGATACCCGCTAGATGAGCAGAACTGACTCTCGAAATAGAAAGCTATGGCTACACGACTGATGACATAGAGTTCTACTGGAGAGGTGGAGATAATGCGGTC
176  T G V E R I E L P Q F S I V E Y R L V S K N V V F A T G A Y P R L S L S F R L K
692 ACTGGTGTGGAAAGAAATGAACTTCCCTCAGTTCCTCATTGTGGAATATAGACTGGTTCCTCAAGAAATGTTGTCTTTGCCACAGGTGCCTATCCAAGACTTTCCTAAGCTTCAGGTTGAAA
216  R N I G Y F I L Q T Y M P S I L I T I L S W V S F W I N Y D A S A A R V A L G I
812 AGGAATATGGATACTTTATTCTTCAAACCTACATGCCCTCCACTGATTACCATTTTATCATGGGTGTCATTCTGGATCAATTATGATGCATCAGCAGCAAGAGTTGCCCTTGGAAAT
256  T T V L T M T T I N T H L R E T L P K I P Y V K A I D M Y L M G C F V F V F L A
932 ACAACTGTGCTGACTATGACAACAAATCAACACACATCTGCAGAGACTTTGCCTAAAATTCCTATGTTAAAGCCATTGACATGTATCTTATGGGCTGCTTTGTATTCTGCTTCTTGGCC
296  L L E Y A F V N Y I F F G K G P Q R Q K K L A E K S A K A N N D R S R F E G S R
1052 T T A C T T G A A T A T G C C T T G T C A A C T A C A T T T C T C G G A A A A G C C C T C A A A G G C A G A A A A C T T G C G G A A A A A T C A G C A A A G G C A A A C A C G A T C G C T C A A G G T T T G A A G G C A G C C G G
336  V D T H G N I L L T S L E I H N E V A S N E V T T S V T D A R N S T I S F D N S
1172 GTGGACACCCATGGAAACATCTCTGTAACATCTCTTGAATTCACAACGAGGTGCGAAGCAACGAGGTCAACAACGAGGTTACGGATGCCAGAAAATCAACGATATCCTTTGACAACCTCA
376  G I Q Y R K Q S S H R E S L G R R S S D R T G S H S K R G H L R R R S S Q L K I
1292 GGAATCCAGTACAGAAAACAAGCTCACATCGTGAAGCCCTTGAAGGCGTTTATCAGACAGAACAGGCTCCCACAGCAAGAGGGCCATTACGAAGAAGGCTTTCACAACCTGAAGATA
416  K I P D L T D V N A I D R W S R M V F P F T F S L F N L I Y W L Y Y V N
1412 AAAATTCCTGATCTAACAGATGTGAATGCCATCGACAGATGGTCAAGAAATGGTGTTCCTTCCATTACATTTTCTCTTTTCAACTTAATTTACTGGCTATACTATGTTAACTGAGTGACTGAA
1532 CTTTTTAAAGGACTTCAATTATAACAAGTGAAGTACTACTTGCCTGCAGAGTTTATATATATTTATATGTAATAATATATATATATATATGAACTTTTACAATGTAGAGAACTACTCATG
1652 TATGTGTGGATACGTACAGCGAAGAACTGTGTGTATATATGAGCACACACTGCAGAAACAAAAGTATATGATGTACACATACGTTGACACATTCATTTCTGAGGTTATGGACAATGTAACA
1772 TAGAATGCACCTCCGAGGAACTTTTAAATTTGAAAGTCAGGTGTCGTCCAAAGCAAGCCTTGAGAACGTAAGTGTGTATATATACATTCAAAACCTTTGATGGTCGTAGAAATTTTCAA
1892 ACAGCTGTAATGGTGTATAAAGTCAGTATTTAGTAACATTTGTTGTAATGCTGCCATACACACTAATCATAAAGTGATAGAGTTACACTGGTAAGTTTAAAGTAAGTCGTTTGTATTGC
2012 AGAACCATGAACAACAATTCATCAAGCCAACTTGTCTCTTTGCTAAAATTTCTGGTTTTGTATGACCTAACATATTTTCCCCTCATGAATGGGCATTGTTTTTAAATGGTCTCT
2132 TGCTTCTCTCTCAGTAAGCAAGCTGATCATTGGA

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