

Product datasheet for SC331539

GABA A Receptor alpha 4 (GABRA4) (NM_001204267) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	GABA A Receptor alpha 4 (GABRA4) (NM_001204267) Human Untagged Clone
Tag:	Tag Free
Symbol:	GABA A Receptor alpha 4
Vector:	pCMV6-Entry (PS100001)
Fully Sequenced ORF:	>SC331539 representing NM_001204267. Blue=Insert sequence Red=Cloning site Green=Tag(s)

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ATGTTGCAAAGATGGTTTCTGCCAAGAAGTTAAACGAATCCCCAGGACAGAACCAAAAGGAGGAGAAA
TTGTGCACAGAAAATTTACCCGCATCCTGGACAGTTTGCATCGATGGTTATGACAACAGGCTGCGTCCT
GGATTTGGGGTCTCTGTACAGAAGTAAAAGTACATATATGTCACCAGCTTTGGACCTGTTTCTGAT
GTTGAAATGGAATACACAATGGATGTGTCTTCAGGCAGACATGGATTGACAAAAGATTAATAATGAC
GGCCCCATTGAAATTTGAGATTGAACAATATGATGGTAACGAAAGTGTGGACCCCTGATACTTTCTTC
AGGAATGGAAAGAAATCTGTCTCACATAATATGACAGCTCCAAATAAGCTTTTTAGAAATTATGAGAAAT
GGTACTATTTTATACACAATGAGACTCACCATAAGTGCGGAGTGTCCCATGAGATTGGTGGATTTTCCC
ATGGATGGTCATGCATGCCCTTTGAAATTCGGGAGTTATGCCTATCCAAAGAGTGAGATGATCTATACC
TGGACAAAAGGTCTGAGAAATCAGTTGAAGTCCGAAGGAGTCTCCAGCTTAGTTCAATATGATTTG
ATTGGGCAAACCGTATCAAGTGAACCATCAAATCAATTACGGGAATAACAACGTCTCCTCACCATGACC
ACACTAAGCATCAGTGCACGACATTCTTTGCCAAAGTGTCTATGCTACCGCCATGGACTGGTTCATA
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CAAATGGAAAAAGCCAAAAGGAAGACATCAAAGCCCCCTCAGGAAGTTCCCGCTGCTCCAGTGCAGAGA
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AGGATAAAGACCACAGTTAATACCATAGGGGCTACTGGGAAGTTGTCAGTACTCCTCCTCCATCGGCT
CCACCACCTTCTGGATCTGGCACAAGTAAAATAGACAAATATGCCCGTATTCTCTTTCCAGTCACATTT
GGGGCATTTAACATGGTTTATTGGGTTGTTTATTTATCTAAGGACACTATGGAGAAATCAGAAAGTCTA
ATGTAA
  
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Restriction Sites:	SgfI-MluI
ACCN:	NM_001204267
Insert Size:	1455 bp



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OTI Disclaimer:	Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).
Components:	The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).
Reconstitution Method:	<ol style="list-style-type: none">1. Centrifuge at 5,000xg for 5min.2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.3. Close the tube and incubate for 10 minutes at room temperature.4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.
RefSeq:	NM_001204267.1
RefSeq Size:	10864 bp
RefSeq ORF:	1455 bp
Locus ID:	2557
UniProt ID:	P48169
Cytogenetics:	4p12
Protein Families:	Druggable Genome, Ion Channels: Cys-loop Receptors, Transmembrane
Protein Pathways:	Neuroactive ligand-receptor interaction
MW:	53.9 kDa
Gene Summary:	<p>Gamma-aminobutyric acid (GABA) is the major inhibitory neurotransmitter in the mammalian brain where it acts at GABA-A receptors, which are ligand-gated chloride channels. Chloride conductance of these channels can be modulated by agents such as benzodiazepines that bind to the GABA-A receptor. At least 16 distinct subunits of GABA-A receptors have been identified. This gene encodes subunit alpha-4, which is involved in the etiology of autism and eventually increases autism risk through interaction with another subunit, gamma-aminobutyric acid receptor beta-1 (GABRB1). Alternatively spliced transcript variants encoding different isoforms have been found in this gene.[provided by RefSeq, Feb 2011]</p> <p>Transcript Variant: This variant (3) lacks a segment in the first splice junction, resulting in an upstream AUG start codon, and lacks an in-frame exon in the middle region, as compared to variant 1. The resulting isoform (3) has a shorter and different N-terminus and lacks an internal segment, as compared to isoform 1. Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.</p>