

Product datasheet for **TP724167**

Human ADORA2A Protein, hFc Tag

Product data:

Product Type:	Recombinant Proteins
Description:	Human ADORA2A Protein, hFc Tag
Expression Host:	HEK293
Tag:	C-Human Fc
Predicted MW:	The protein has a predicted molecular mass of 31.7 kDa after removal of the signal peptide. The apparent molecular mass of ADORA2A-hFc is approximately 35-55 kDa due to glycosylation.
Purity:	The purity of the protein is greater than 95% as determined by SDS-PAGE and Coomassie blue staining.
Reconstitution Method:	Lyophilized from sterile PBS, pH 7.4. Normally 5 % - 8% trehalose is added as protectants before lyophilization.
Storage:	Store at -20°C to -80°C for 12 months in lyophilized form. After reconstitution, if not intended for use within a month, aliquot and store at -80°C (Avoid repeated freezing and thawing). Lyophilized proteins are shipped at ambient temperature.
Stability:	12 months from date of despatch
Synonyms:	A2aR, ADORA2, RDC8
Summary:	This gene encodes a member of the guanine nucleotide-binding protein (G protein)-coupled receptor (GPCR) superfamily, which is subdivided into classes and subtypes. The receptors are seven-pass transmembrane proteins that respond to extracellular cues and activate intracellular signal transduction pathways. This protein, an adenosine receptor of A2A subtype, uses adenosine as the preferred endogenous agonist and preferentially interacts with the G(s) and G(olf) family of G proteins to increase intracellular cAMP levels. It plays an important role in many biological functions, such as cardiac rhythm and circulation, cerebral and renal blood flow, immune function, pain regulation, and sleep. It has been implicated in pathophysiological conditions such as inflammatory diseases and neurodegenerative disorders. Alternative splicing results in multiple transcript variants. A read-through transcript composed of the upstream SPECC1L (sperm antigen with calponin homology and coiled-coil domains 1-like) and ADORA2A (adenosine A2a receptor) gene sequence has been identified, but it is thought to be non-coding. [provided by RefSeq, Jun 2013]


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