Division of Signal Tranduction Therapy

Standard Operating Procedure

Preparation of ATP Citrate Lyase [1 - 1101]

Enzyme description:- ATP Citrate Lyase [1 - 1101]

Clone number:- DU 2461

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Calculated molecular mass:-
Monoisotopic 151, 866.59 daltons
Average Mass 151, 964.13 daltons
[cysteines reduced, methionines have not been oxidised

Theoretical pI:- 6.49

Purity:- >80 %

Enzyme storage buffer:-
50 mM Tris-HCl pH 7.5, 270 mM Sucrose, 150 mM NaCl, 0.1 mM EGTA, 0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 1 mM benzamidine, 0.2 mM PMSF

Storage temperature:- -70 °C

Clone Data Sheet

ATP Citrate Lyase [1 - 1101]

Protein	ATP Citrate Lyase [1 - 1101]
Clone number	DU 2461
Species	Human
Accession number	NM_001096.2
Tags	N-terminal GST
Bacterially expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELG LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGA VLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSS KYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGSPGIPGSREATSCWG APDFAGFVGPVEEAPRTDFGRGRAGLSAA**MSAKAISEQTGKELLYKFIC** **TTSAIQNRFKYARVTPDTDWARLLQDHPWLLSQNLVVKPDQLIKRRGKL** **GLVGVNLTLDGVKSWLKPRLGQEATVGKATGFLKNFLIEPFVPHSQAEE** **FYVCIYATREGDYVLFHHEGGVDVGDVDAKAQKLLVGVDEKLNPEDIKK** **HLLVHAPEDKKEILASFISGLFNFYEDLYFTYLEINPLVVTKDGVYVLD** **LAAKVDATADYICKVKWGDIEFPPPFGREAYPEEAYIADLDAKSGASLK** **LTLLNPKGRIWTMVAGGGASVVYSDTICDLGGVNELANYGEYSGAPSEQ** **QTYDYAKTILSLMTREKHPDGKILIIGGSIANFTNVAATFKGIVRAIRD** **YQGPLKEHEVTIFVRRGGPNYQEGLRVMGEVGKTTGIPIHVFGTETHMT** **AIVGMALGHRPIPNQPPTAAHTANFLLNASGSTSTPAPSRTASFSESRA** **DEVAPAKKAKPAMPQDSVPSPRSLQGKSTTLFSRHTKAIVWGMQTRAVQ** **GMLDFDYVCSRDEPSVAAMVYPFTGDHKQKFYWGHKEILIPVFKNMADA** **MRKHPEVDVLINFASLRSAYDSTMETMNYAQIRTIAIIAEGIPEALTRK** **LIKKADQKGVTIIGPATVGGIKPGCFKIGNTGGMLDNILASKLYRPGSV** **AYVSRSGGMSNELNNIISRTTDGVYEGVAIGGDRYPGSTFMDHVLRYQD** **TPGVKMIVVLGEIGGTEEYKICRGIKEGRLTKPIVCWCIGTCATMFSSE** **VQFGHAGACANQASETAVAKNQALKEAGVFVPRSFDELGEIIQSVYEDL** **VANGVIVPAQEVPPPTVPMDYSWARELGLIRKPASFMTSICDERGQELI** **YAGMPITEVFKEEMGIGGVLGLLWFQKRLPKYSCQFIEMCLMVTADHGP** **AVSGAHNTIICARAGKDLVSSLTSGLLTIGDRFGGALDAAAKMFSKAFD** **SGIIPMEFVNKMKKEGKLIMGIGHRVKSINNPDMRVQILKDYVRQHFPA** **TPLLDYALEVEKITTSKKPNLILNVDGLIGVAFVDMLRNCGSFTREEAD** **EYIDIGALNGIFVLGRSMGFIGHYLDQKRLKQGLYRHPWDDISYVLPEH** **MSM**

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Native sequence	Amino acids M1 – M1101 (end) of human ATP Citrate Lyase. Residue M275 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 – 220.
Protease cleavage	PreScission (LEVLFQGP) residues 221 - 228
Cloning sites	*Bam*H1 and *Not*1 of pGEX6P-1

Nucleotide Sequence of Insert:

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