Division of Signal Tranduction Therapy

Standard Operating Procedure

Preparation of ATF2 [19-96]

Protein description:- ATF2 [19-96]

Clone number:- DU 1787

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Expression level:- 10 mg/L

Calculated molecular mass:- 36, 358 daltons

Purity:- > 95 %

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 50 % glycerol, 150 mM NaCl, 0.1 mM EGTA,
0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 0.2 mM PMSF, 1 mM Benzamidine.

Storage temperature:- –20 °C

Assay:- Substrate for JNK1, JNK2 and JNK3

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CLONE DATA SHEET

ATF2 [19-96]

Protein ATF2 [19-96]

Clone number DU 1787

Species Human

Accession number NM_001880

Tags N-terminal GST

Bacterially expressed protein

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFEL
GLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLE
GAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLN
GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKY
LKSSKYIAWPLQGWQATFGGGDHPPKSDLVPRGSIAMDPGLVD**MSDDK
PFLCTAPGCGQRFTNEDHLAVHKHKHEMTLKFGPARNDSVIVADQTPT
PTRFLKNCEEVGLFNELASPFENEF**LEID

Native sequence Amino acids M19 – F96 of human ATF2.
[Full length protein ends at residue S505]
Residue M236 of the fusion protein is equivalent to M19 of the native protein. The GST tag is located at residues 1 – 220. The following sequence is present after the ATF2 sequence, LEID, residues 314 - 317.

Protease cleavage Thrombin (LVPRGS) residues 221 - 226

Cloning sites *Bam*HI and *Eco*RI sites of pGEX-4T-1

Nucleotide sequence of insert

ATGAGTGATGACAAACCCTTTCTATGTACTGCGCCTGGATGTGGCCAG
CGTTTTACCAACGAGGATCATTTGGCTGTCCATAAACATAAACATGAG
ATGACACTGAAATTTGGTCCAGCACGTAATGACAGTGTCATTGTGGCT
GATCAGACCCCAACACCAACAAGATTCTTGAAAAACTGTGAAGAAGTG
GGTTTGTTTAATGAGTTGGCGAGTCCATTTGAGAATGAATTCCTCGAG
ATCGATtag