Division of Signal Tranduction Therapy

Standard Operating Procedure

Preparation of HP1 beta (mouse) [1 – 185]

Enzyme description:- HP1 beta (mouse) [1 – 185]

Clone number:- DU 36262

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Calculated molecular mass:-
Monoisotopic 48, 211.21 daltons
Average Mass 48, 241.94 daltons
[cysteines reduced, methionines have not been oxidised

Theoretical pI:- 5.13

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

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Clone Data Sheet

HP1 beta (mouse) [1 – 185]

Protein	HP1 beta (mouse) [1 – 185]
Clone number	DU 36262
Species	Mouse
Accession number	NM_007622.3
Tags	N-terminal GST
Bacterially expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELG LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGA VLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSS KYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGS**MGKKQNKKKVEEVL** **EEEEEEYVVEKVLDRRVVKGKVEYLLKWKGFSDEDNTWEPEENLDCPDL** **IAEFLQSQKTAHETDKSEGGKRKADSDSEDKGEESKPKKKKEESEKPRG** **FARGLEPERIIGATDSSGELMFLMKWKNSDEADLVPAKEANVKCPQVVI** **SFYEERLTWHSYPSEDDDKKDDKN**
Native sequence	Amino acids M1 – N185 (end) of mouse HP1 beta. Residue M232 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 sites of pGEX6P-1

Nucleotide Sequence of insert

ggatccATGGGGAAAAAGCAAAACAAGAAGAAAGTGGAGGAGGTACTAG
AAGAAGAGGAAGAGGAATATGTGGTGGAAAAAGTTCTTGATCGGCGAGT
TGTCAAGGGCAAGGTGGAATATCTTCTAAAGTGGAAGGGTTTCTCAGAT
GAGGACAACACTTGGGAGCCAGAAGAGAATCTGGATTGCCCTGACCTTA
TTGCTGAGTTTCTACAGTCACAGAAAACAGCTCATGAGACAGATAAGTC
AGAGGGAGGCAAGCGCAAAGCTGATTCTGATTCTGAAGATAAAGGAGAG
GAAAGCAAACCAAAGAAGAAGAAAGAAGAGTCAGAAAAGCCACGAGGCT
TTGCCCGGGGTTTGGAGCCAGAGCGGATTATTGGAGCTACTGACTCCAG
TGGAGAGCTCATGTTCCTGATGAAATGGAAAAACTCTGATGAGGCTGAC
CTGGTCCCTGCCAAGGAAGCCAATGTCAAGTGCCCACAGGTTGTCATAT
CCTTCTATGAGGAAAGGCTAACGTGGCATTCCTACCCCTCAGAGGATGA
TGACAAAAAAGACGACAAGAATtagcggccgc