Division of Signal Tranduction Therapy

Standard Operating Procedure

Preparation of HP1 gamma (mouse) [1 – 183]

Enzyme description:-   HP1 gamma (mouse) [1 – 183]

Clone number:-   DU 36268

Source:-   Recombinant

Expression system:-   *E.coli*

Tag:-   N-terminal GST

Purification method:-   GSH Sepharose

Calculated molecular mass:-
Monoisotopic   47, 604.99 daltons
Average Mass   48, 635.59 daltons
[cysteines reduced, methionines have not been oxidised

Theoretical pI:-   5.47

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

HP1 gamma (mouse) [1 – 183]

Protein	HP1 gamma (mouse) [1 – 183]
Clone number	DU 36268
Species	Mouse
Accession number	NM_007624.3
Tags	N-terminal GST

Bacterially expressed protein

```
MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELG
LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGA
VLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH
VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSS
KYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGSMASNKTTLQKMGKK
QNGKSKKVEEAEPEEFVVEKVLDRRVVNGKVEYFLKWKGFTDADNTWEP
EENLDCPELIEAFLNSQKAGKEKDGTKRKSLSDSESDDSKSKKKRDAAD
KPRGFARGLDPERIIGATDSSGELMFLMKWKDSDEADLVLAKEANMKCP
QIVIAFYEERLTWHSCPEDEAQ
```

Native sequence

Amino acids M1 – Q183 (end) of mouse HP1 gamma.
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

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**Nucleotide
Sequence of insert**

ggatccATGGCCTCCAATAAAACTACATTGCAAAAAATGGGAAAGAAACAAAATGGAAAGAG
TAAAAAAGTTGAAGAGGCAGAGCCTGAAGAATTTGTGGTAGAAAAAGTACTGGACCGTCG
TGTAGTGAATGGGAAGGTGGAGTATTTCCTGAAGTGGAAGGGGTTCACAGATGCTGATAA
TACTTGGGAACCAGAAGAAAATTTAGATTGTCCAGAATTAATTGAAGCATTTCTTAATTCTC
AAAAAGCTGGTAAAGAAAAAGATGGTACAAAAAGGAAATCTTTATCTGACAGTGAATCTGA
TGATAGCAAATCGAAGAAGAAGAGAGATGCTGCTGACAAACCAAGGGGCTTTGCCAGAG
GTCTCGACCCTGAACGAATAATCGGCGCCACAGACAGCAGCGGAGAGTTAATGTTTCTCA
TGAAGTGGAAGGACTCGGACGAGGCCGACTTGGTGCTGGCAAAGGAGGCGAACATGAAG
TGTCCTCAGATTGTCATTGCCTTCTACGAGGAGCGGCTGACTTGGCATTCTTGTCCTGAAG
ATGAAGCACAAtaagcggccgc