Division of Signal Tranduction Therapy

Standard Operating Procedure

Preparation of active BAP1 [1 – 240]

Enzyme description:- BAP1 [1 - 240]

Clone number:- DU 63658

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Calculated molecular mass:-
Monoisotopic 53, 980.44 daltons
Average Mass 54, 015.21 daltons
[cysteines reduced, methionines have not been oxidised

Theoretical pI:- 5.76

Purity:- 80 %

Activation protocol:- Constitutively active

Enzyme storage buffer:-
50 mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT

Storage temperature:- -70 °C

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Clone Data Sheet

BAP1 [1 - 240]

Protein	BAP1 [1 - 240]
Clone number	DU 63658
Species	Human
Accession number	Q92560
Tags	N-terminal GST
Bacterially expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELG LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGA VLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSS KYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGS**MNKGWLELESDPGL FTLLVEDFGVKGVQVEEIYDLQSKCQGPVYGFIFLFKWIEERRSRRKVS TLVDDTSVIDDDIVNNMFFAHQLIPNSCATHALLSVLLNCSSVDLGPTL SRMKDFTKGFSPESKGYAIGNAPELAKAHNSHARPEPRHLPEKQNGLSA VRTMEAFHFVSYVPITGRLFELDGLKVYPIDHGPWGEDEEWTDKARRVI MERIGLATAGEPYHDIRFNLMAVVPDRRIK**
Native sequence	Amino acids M1 – K240 (end residue is Q729) of human BAP1. 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 - 229
Cloning sites	*Bam*H1 and *Not*1 sites of pGEX 6P-1

Nucleotide Sequence

ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCCA
CTCGACTTCTTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTTGTA
TGAGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTGGGT
TTGGAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAATTAA
CACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAACATGTT
GGGTGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAAGGAGCG
GTTTTGGATATTAGATACGGTGTTTCGAGAATTGCATATAGTAAAGACT
TTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAAATGCTGAA
AATGTTCGAAGATCGTTTATGTCATAAAACATATTTAAATGGTGATCAT
GTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTAT
ACATGGACCCAATGTGCCTGGATGCGTTCCCAAAATTAGTTTGTTTTAA
AAAACGTATTGAAGCTATCCCACAAATTGATAAGTACTTGAAATCCAGC
AAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGCCACGTTTGGTGGTG
GCGACCATCCTCCAAAATCGGATCTGGAAGTTCTGTTCCAGGGGCCCCT
GGGATCCATGAATAAGGGCTGGCTGGAGCTGGAGAGCGACCCAGGCCTC
TTCACCCTGCTCGTGGAAGATTTCGGTGTCAAGGGGGTGCAAGTGGAGG
AGATCTACGACCTTCAGAGCAAATGTCAGGGCCCTGTATATGGATTTAT
CTTCCTGTTCAAATGGATCGAAGAGCGCCGGTCCCGGCGAAAGGTCTCT
ACCTTGGTGGATGATACGTCCGTGATTGATGATGATATTGTGAATAACA
TGTTCTTTGCCCACCAGCTGATACCCAACTCTTGTGCAACTCATGCCTT
GCTGAGCGTGCTCCTGAACTGCAGCAGCGTGGACCTGGGACCCACCCTG
AGTCGCATGAAGGACTTCACCAAGGGTTTTAGCCCTGAGAGCAAAGGAT
ATGCGATTGGCAATGCCCCGGAGTTGGCCAAGGCCCATAATAGCCATGC
CAGGCCCGAGCCACGCCACCTCCCTGAGAAGCAGAATGGCCTTAGTGCA
GTGCGGACCATGGAGGCGTTCCACTTTGTCAGCTATGTGCCTATCACAG
GCCGGCTCTTTGAGCTGGATGGGCTGAAGGTCTACCCCATTGACCATGG
GCCCTGGGGGGAGGACGAGGAGTGGACAGACAAGGCCCGGCGGGTCATC
ATGGAGCGTATCGGCCTCGCCACTGCAGGGGAGCCCTACCACGACATCC
GCTTCAACCTGATGGCAGTGGTGCCCGACCGCAGGATCAAGtga