Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-BAP1

Enzyme description:- GST-BAP1

Clone number:- DU12809

Source:- BL21 Recombinant

Tag:- N-terminal GST

Purification method:- GSH sepharose

Expression level:- 2 mg/L

Calculated molecular mass:-

Monoisotopic	107118 Da
Average Mass	107182 Da

[cycsteines reduced, methionines have not been oxidised]

Theoretical pI:- 6.50

Purity:- 70%

Enzyme storage buffer:-

50 mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT

Storage temperature:- -80ºC

Assay:-

Ub-Rho110-Gly cleavage assay monitored by Ex/Em 485/535 nm

Assay buffer:-

40 mM Tris pH 7.5, 100 mM NaCl, 5 mM DTT, 0.01% Triton X-100, 0.005% Ovalbumin, 0.5 μM Ub-Rho110-Gly

Division of Signal Transduction Therapy

Clone Data Sheet

GST-BAP1

Protein	GST-BAP1
Synonyms	hucep-6
Clone Number	DU12809
Species	Human
Accession Number	Protein: Q92560 DNA: AAH01596.1
Tags	N-terminal GST
Amino acid sequence of expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL DIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIA WPLQGWQATFGGGDHPPKSDLEVLFQGPLGS**MNKGWLELESDPGLFTLLV** **EDFGVKGVQVEEIYDLQSKCQGPVYGFIFLFKWIEERRSRRKVSTLVDDT** **SVIDDDIVNNMFFAHQLIPNSCATHALLSVLLNCSSVDLGPTLSRMKDFT** **KGFSPESKGYAIGNAPELAKAHNSHARPEPRHLPEKQNGLSAVRTMEAFH** **FVSYVPITGRLFELDGLKVYPIDHGPWGEDEEWTDKARRVIMERIGLATA** **GEPYHDIRFNLMAVVPDRRIKYEARLHVLKVNRQTVLEALQQLIRVTQPE** **LIQTHKSQESQLPEESKSASNKSPLVLEANRAPAASEGNHTDGAEEAAGS** **CAQAPSHSPPNKPKLVVKPPGSSLNGVHPNPTPIVQRLPAFLDNHNYAKS** **PMQEEEDLAAGVGRSRVPVRPPQQYSDDEDDYEDDEEDDVQNTNSALRYK** **GKGTGKPGALSGSADGQLSVLQPNTINVLAEKLKESQKDLSIPLSIKTSS** **GAGSPAVAVPTHSQPSPTPSNESTDTASEIGSAFNSPLRSPIRSANPTRP** **SSPVTSHISKVLFGEDDSLLRVDCIRYNRAVRDLGPVISTGLLHLAEDGV** **LSPLALTEGGKGSSPSIRPIQGSQGSSSPVEKEVVEATDSREKTGMVRPG** **EPLSGEKYSPKELLALLKCVEAEIANYEACLKEEVEKRKKFKIDDQRRTH** **NYDEFICTFISMLAQEGMLANLVEQNISVRRRQGVSIGRLHKQRKPDRRK** **RSRPYKAKRQ**
Native sequence	in bold
Protease cleavage	Precission site underlined
Cloning sites	BamH1 / Not1

DNA sequence of insert

GGATCCATGAATAAGGGCTGGCTGGAGCTGGAGAGCGACCCAGGCCTCTT
CACCCTGCTCGTGGAAGATTTCGGTGTCAAGGGGGTGCAAGTGGAGGAGA
TCTACGACCTTCAGAGCAAATGTCAGGGCCCTGTATATGGATTTATCTTC
CTGTTCAAATGGATCGAAGAGCGCCGGTCCCGGCGAAAGGTCTCTACCTT
GGTGGATGATACGTCCGTGATTGATGATGATATTGTGAATAACATGTTCT
TTGCCCACCAGCTGATACCCAACTCTTGTGCAACTCATGCCTTGCTGAGC
GTGCTCCTGAACTGCAGCAGCGTGGACCTGGGACCCACCCTGAGTCGCAT
GAAGGACTTCACCAAGGGTTTTAGCCCTGAGAGCAAAGGATATGCGATTG
GCAATGCCCCGGAGTTGGCCAAGGCCCATAATAGCCATGCCAGGCCCGAG
CCACGCCACCTCCCTGAGAAGCAGAATGGCCTTAGTGCAGTGCGGACCAT
GGAGGCGTTCCACTTTGTCAGCTATGTGCCTATCACAGGCCGGCTCTTTG
AGCTGGATGGGCTGAAGGTCTACCCCATTGACCATGGGCCCTGGGGGGAG
GACGAGGAGTGGACAGACAAGGCCCGGCGGGTCATCATGGAGCGTATCGG
CCTCGCCACTGCAGGGGAGCCCTACCACGACATCCGCTTCAACCTGATGG
CAGTGGTGCCCGACCGCAGGATCAAGTATGAGGCCAGGCTGCATGTGCTG
AAGGTGAACCGTCAGACAGTACTAGAGGCTCTGCAGCAGCTGATAAGAGT
AACACAGCCAGAGCTGATTCAGACCCACAAGTCTCAAGAGTCACAGCTGC
CTGAGGAGTCCAAGTCAGCCAGCAACAAGTCCCCGCTGGTGCTGGAAGCA
AACAGGGCCCCTGCAGCCTCTGAGGGCAACCACACAGATGGTGCAGAGGA
GGCGGCTGGTTCATGCGCACAAGCCCCATCCCACAGCCCTCCCAACAAAC
CCAAGCTAGTGGTGAAGCCTCCAGGCAGCAGCCTCAATGGGGTTCACCCC
AACCCCACTCCCATTGTCCAGCGGCTGCCGGCCTTTCTAGACAATCACAA
TTATGCCAAGTCCCCCATGCAGGAGGAAGAAGACCTGGCGGCAGGTGTGG
GCCGCAGCCGAGTTCCAGTCCGCCCACCCCAGCAGTACTCAGATGATGAG
GATGACTATGAGGATGACGAGGAGGATGACGTGCAGAACACCAACTCTGC
CCTTAGGTATAAGGGGAAGGGAACAGGGAAGCCAGGGGCATTGAGCGGTT
CTGCTGATGGGCAACTGTCAGTGCTGCAGCCCAACACCATCAACGTCTTG
GCTGAGAAGCTCAAAGAGTCCCAGAAGGACCTCTCAATTCCTCTGTCCAT
CAAGACTAGCAGCGGGGCTGGGAGTCCGGCTGTGGCAGTGCCCACACACT
CGCAGCCCTCACCCACCCCCAGCAATGAGAGTACAGACACGGCCTCTGAG
ATCGGCAGTGCTTTCAACTCGCCACTGCGCTCGCCTATCCGCTCAGCCAA
CCCGACGCGGCCCTCCAGCCCTGTCACCTCCCACATCTCCAAGGTGCTTT
TTGGAGAGGATGACAGCCTGCTGCGTGTTGACTGCATACGCTACAACCGT
GCTGTCCGTGATCTGGGTCCTGTCATCAGCACAGGCCTGCTGCACCTGGC
TGAGGATGGGGTGCTGAGTCCCCTGGCGCTGACAGAGGGTGGGAAGGGTT
CCTCGCCCTCCATCAGACCAATCCAAGGCAGCCAGGGGTCCAGCAGCCCA
GTGGAGAAGGAGGTCGTGGAAGCCACGGACAGCAGAGAGAAGACGGGGAT
GGTGAGGCCTGGCGAGCCCTTGAGTGGGGAGAAATACTCACCCAAGGAGC
TGCTGGCACTGCTGAAGTGTGTGGAGGCTGAGATTGCAAACTATGAGGCG
TGCCTCAAGGAGGAGGTAGAGAAGAGGAAGAAGTTCAAGATTGATGACCA
GAGAAGGACCCACAACTACGATGAGTTCATCTGCACCTTTATCTCCATGC
TGGCTCAGGAAGGCATGCTGGCCAACCTAGTGGAGCAGAACATCTCCGTG
CGGCGGCGCCAAGGGGTCAGCATCGGCCGGCTCCACAAGCAGCGGAAGCC
TGACCGGCGGAAACGCTCTCGCCCCTACAAGGCCAAGCGCCAGTGAGCGG
CCGC