

## ***MRC PPU REAGENTS***

### **Standard Operating Procedure**

#### **Preparation of BACH1 [1 - 736]**

**Enzyme description:-** BACH1 [1 – 736]

**Clone number:-** DU 29467

**Source:-** Recombinant

**Expression system:-** *E.coli*

**Tag:-** N-terminal GST

**Purification method:-** GSH Sepharose

**Calculated molecular mass:-**

Monoisotopic 108, 712.37 daltons

Average Mass 108, 781.85 daltons

[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 5.07

**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, 0.2 mM PMSF, 1 mM Benzamidine.

**Storage temperature:-** -70 deg C

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## Clone Data Sheet

### BACH1 [1 – 736]

Protein BACH1 [1 – 736]

Clone number DU 29467

Species Human

Accession number O14867

Tags N-terminal GST

Bacterially  
expressed protein

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFEL  
GLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCCKERAETSMLE  
GAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLN  
GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKY  
LKSSKYIAWPLQGWQATFGGGDHPKSDLEVLFGQPLGSM**LSSENSVF**  
**AYESSVHSTNVLLSLNDQRKKDVLCDVTFVVEGQRFRAHRSVLAACSS**  
**YFHSRIVGQADGELNITLPEEVTVKGFELIQFAYTAKLILSKENVDE**  
**VCKCVEFLSVHNI EESCFQFLKFKFLDSTADQQECPKRCFSSHCQKT**  
**DLKLSLLDQRDLETDEVEEFLENKNVQTPQCKLRRYQGNAKASPLQD**  
**SASQTYESMCLEKDAALALPSLCPKYRKFQKAFGTDRTGESSVKDI**  
**HASVQPNERSENECLGGVPECRDLQVMLKCDESKLAMEPEETKDPAS**  
**QCPTEKSEVTPFPHNSSIDPHGLYSLSLLLHTYDQYGDNLNFAQMONTTV**  
**LTEKPLSGTDVQEKTFGESQDLPLKSDLGTREDSSVASSDRSSVEREV**  
**AEHLAKGFWSDICSTDTPCQMQLSPAVAKDGSEQISQKRSECPWLGIR**  
**ISESPEPGQRTFTTLSSVNCPISTLSTEGCSSNLEIGNDDYVSEPQQ**  
**EPCPYACVISLGDDSETDTEGDSESCSAREQECEVKLPFNAQRIISLS**  
**RNDFQSLMKHKLTPQLDCIHDIRRRSKNRIAAQRCRKRKLDICIQNL**  
**ESEIEKLQSEKESLLKERDHILSTLGETKQNLTLGLCQKVCKEAALSQE**  
**QIQILAKYSAADCPLSFLISEKDKSTPDGELALPSIFSLSDRPPAVLP**  
**PCARGNSEPGYARGQESQQMSTATSEQAGPAEQCRQSGGISDFCQOMT**  
**DKCTTDE**

Native sequence Amino acids M1 – E736 (end) of human BACH1.  
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 (LEVLFGQP) residues 221 – 228

Cloning sites BamH1 and Not1 sites of pGEX6P-1

## *MRC PPU REAGENTS*

### Nucleotide Sequence Of Insert

ggatccATGTCTCTGAGTGAGAACTCGGTTTTTGCCTATGAATCTTCTGT  
GCATAGCACCAATGTTTTACTCAGCCTTAATGACCAGCGGAAGAAAGATG  
TGCTGTGCGATGTCACCATCTTTGTGGAGGGACAGCGGTTCCGCGCTCAC  
CGGTCCGTGCTGGCGGCATGCAGCAGTTACTTCCACTCAAGAATCGTAGG  
CCAGGCTGATGGAGAGCTGAACATTACTCTTCCAGAAGAGGTGACAGTTA  
AAGGATTTGAACCTTTAATTCAGTTTGCCTACACTGCTAAACTGATTTTA  
AGTAAAGAGAATGTGGATGAAGTGTGCAAATGTGTGGAGTTTTTAAGTGT  
ACATAATATTGAGGAATCCTGCTTTCAGTTTCTGAAATTTAAGTTTTTGG  
ACTCCACTGCAGACCAGCAAGAATGCCCAAGAAAAAATGCTTTTCATCA  
CACTGTCAGAAAACAGACCTTAAACTTTCACTTTTGGACCAGAGGGATCT  
AGAAACTGATGAAGTGGAGGAATTTCTGGAAAATAAAAATGTTTCAGACTC  
CTCAGTGTAACCTCCGCAGGTATCAAGGAAATGCAAAGCCTCACCTCCT  
CTACAAGACAGTGCCAGTCAGACATATGAGTCCATGTGCTTAGAGAAGGA  
TGCTGCTCTGGCCTTGCCTTCTTTATGCCCAAATACAGAAAATTCCAAA  
AAGCATTTGGAACCTGACAGAGTCCGTACTGGGGAATCTAGTGTCAAAGAC  
ATTCATGCTTCTGTTTCAGCCAAATGAAAGGTCTGAAAATGAATGCCTGGG  
AGGAGTCCCGGAGTGTAGAGATTTGCAGGTGATGTTAAAATGTGACGAAA  
GTAAATTAGCAATGGAACCTGAAGAAACGAAGAAAGATCCTGCTTCTCAG  
TGCCCAACTGAAAAATCAGAAGTGACTCCTTTCCCCACAATTCCTCCAT  
AGACCCTCATGGACTTTTATTCCTTTGTCTCTTTTACACACATATGACCAAT  
ATGGTGACTTGAATTTTGTGCTGGTATGCAAACACAACAGTGTAAACAGAA  
AAGCCTTTGTGTCAGGTACAGACGTCCAAGAAAAAACATTTGGTGAAGTCA  
GGATTTACCTTTGAAATCCGACTTGGGCACCAGGGAAGATAGTAGTGTTG  
CATCTAGTGATAGGAGTAGTGTGGAGCGAGAAGTGGCAGAACACCTAGCA  
AAAGGCTTCTGGAGTGACATTTGCAGCACGGACACTCCTTGCCAAATGCA  
GTTATCACCTGCTGTGGCCAAAGATGGCTCAGAACAGATCTCACAGAAAC  
GGTCTGAGTGTCCGTGGTTAGGTATCAGGATTAGTGAGAGCCCAGAACCA  
GGTCAAAGGACTTTCACAACATTAAGTTCTGTCAACTGCCCTTTTATAAG  
TACTCTGAGTACTGAAGGCTGTTCAAGCAATTTGGAAATTGGAAACGATG  
ATTATGTTTTCAGAACCCAGCAAGAACCTTGCCCATATGCTTGTGTCATT  
AGCTTGGGAGACGACTCTGAGACGGACACCGAAGGAGACAGTGAATCCTG  
TTCAGCCAGAGAACAAGAATGTGAGGTAAAAC TGCCATTCAATGCACAAC  
GGATAATTTCACTGTCTCGAAATGATTTTTCAGTCCTTGTTGAAAATGCAC  
AAGCTTACTCCAGAACAGCTGGATTGTATCCATGATATTCGAAGAAGAAG  
TAAAAACAGAATTGCTGCACAGCGCTGTCGCAAGAGAAAACTTGACTGTA  
TACAGAATCTTGAATCAGAAATTGAGAAGCTGCAAAGTGAAAAGGAGAGC  
TTGTTGAAGGAAAGAGATCACATTTTGTCAACTCTGGGTGAGACAAAGCA  
GAACCTAACTGGACTTTGCCAGAAAGTTTGTAAAGAAGCAGCTCTGAGTC  
AAGAACAAATACAGATACTCGCCAAGTACTCAGCTGCAGATTGCCCACTT  
TCATTTTTAATTTCTGAAAAAGATAAAAAGTACTCCTGATGGTGAACCTGGC  
GTTACCATCAATTTTTCAGTTTATCTGACCGCCTCCAGCAGTGCTGCCTC  
CCTGTGCCAGAGGAAACAGTGAGCCTGGCTACGCGGAGGGCAGGAGTCC  
CAGCAGATGTCCACAGCCACCTCTGAGCAAGCTGGGCCTGCGGAACAGTG  
TCGTCAGAGTGGTGGGATCTCAGATTTCTGTCAGCAGATGACTGATAAAT  
GTACTACTGATGAGtaagcggccgc