Division of Signal Tranduction Therapy

Standard Operating Procedure

Preparation of TAU [1 – 441]

Enzyme description:- TAU [1 - 441]

Clone number:- DU 32246

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Calculated molecular mass:-
Monoisotopic 72, 628.81 daltons
Average Mass 72, 674.07 daltons
[cysteines reduced, methionines have not been oxidised

Theoretical pI:- 6.68

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

TAU [1 - 441]

Protein	TAU [1 - 441]
Clone number	DU 32246
Species	Human
Accession number	NM_005910.5
Tags	N-terminal GST
Bacterially expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELG LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGA VLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSS KYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGS**MAEPRQEFEVMEDH** **AGTYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQTPTEDGSEEPGSET** **SDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTP** **SLEDEAAGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPG** **QKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRS** **RTPSLPTPPTREPKKVAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVKSK** **IGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQI** **VYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSL** **DNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPR** **HLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL**

Native sequence	Amino acids M1 – L441 (end) of human TAU. 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

ggatccATGGCTGAGCCCCGCCAGGAGTTCGAAGTGATGGAAGATCACGC
TGGGACGTACGGGTTGGGGGACAGGAAAGATCAGGGGGGCTACACCATGC
ACCAAGACCAAGAGGGTGACACGGACGCTGGCCTGAAAGAATCTCCCCTG
CAGACCCCCACTGAGGACGGATCTGAGGAACCGGGCTCTGAAACCTCTGA
TGCTAAGAGCACTCCAACAGCGGAAGATGTGACAGCACCCTTAGTGGATG
AGGGAGCTCCCGGCAAGCAGGCTGCCGCGCAGCCCCACACGGAGATCCCA
GAAGGAACCACAGCTGAAGAAGCAGGCATTGGAGACACCCCCAGCCTGGA
AGACGAAGCTGCTGGTCACGTGACCCAAGCTCGCATGGTCAGTAAAAGCA
AAGACGGGACTGGAAGCGATGACAAAAAAGCCAAGGGGGCTGATGGTAAA
ACGAAGATCGCCACACCGCGGGGAGCAGCCCCTCCAGGCCAGAAGGGCCA
GGCCAACGCCACCAGGATTCCAGCAAAAACCCCGCCCGCTCCAAAGACAC
CACCCAGCTCTGGTGAACCTCCAAAATCAGGGGATCGCAGCGGCTACAGC
AGCCCCGGCTCCCCAGGCACTCCCGGCAGCCGCTCCCGCACCCCGTCCCT
TCCAACCCCACCCACCCGGGAGCCCAAGAAGGTGGCAGTGGTCCGTACTC
CACCCAAGTCGCCGTCTTCCGCCAAGAGCCGCCTGCAGACAGCCCCCGTG
CCCATGCCAGACCTGAAGAATGTCAAGTCCAAGATCGGCTCCACTGAGAA
CCTGAAGCACCAGCCGGGAGGCGGGAAGGTGCAGATAATTAATAAGAAGC
TGGATCTTAGCAACGTCCAGTCCAAGTGTGGCTCAAAGGATAATATCAAA
CACGTCCCGGGAGGCGGCAGTGTGCAAATAGTCTACAAACCAGTTGACCT
GAGCAAGGTGACCTCCAAGTGTGGCTCATTAGGCAACATCCATCATAAAC
CAGGAGGTGGCCAGGTGGAAGTAAAATCTGAGAAGCTTGACTTCAAGGAC
AGAGTCCAGTCGAAGATTGGGTCCCTGGACAATATCACCCACGTCCCTGG
CGGAGGAAATAAAAAGATTGAAACCCACAAGCTGACCTTCCGCGAGAACG
CCAAAGCCAAGACAGACCACGGGGCGGAGATCGTGTACAAGTCGCCAGTG
GTGTCTGGGGACACGTCTCCACGGCATCTCAGCAATGTCTCCTCCACCGG
CAGCATCGACATGGTAGACTCGCCCCAGCTCGCCACGCTAGCTGACGAGG
TGTCTGCCTCCCTGGCCAAGCAGGGTTTGtgagcggccgc

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