*MRC PPU Reagents and Services*

# Standard Operating Procedure

# Preparation of TAOK2 [1 - 350]

**Enzyme description:-** TAOK2 [1 - 350]

**Clone number:-** DU 62949

**Source:-** Recombinant

**Expression system:-** Baculovirus expression vector system

**Tag:-** N-terminal GST

**Purification method**:- GSH-Sepharose

**Calculated molecular mass:-**
Monoisotopic 66, 325.61 daltons
Average Mass 66, 368.36 daltons
[cysteines reduced, methionines have not been oxidised

**Theoretical pI:-** 5.83

**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

**Assay Buffer:-**
50 mM Tris-HCl pH 7.5, 0.1mM EGTA, 10 mM DTT, 10 mM MgAc

**Substrate:-**
Myelin Basic protein Final concentration: 1 mg/ml

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# Clone Data Sheet

## TAOK2 [1 - 350]

| | |
|---|---|
| **Protein** | TAOK2 [1 - 350] |
| **Clone number** | DU 62949 |
| **Species** | Human |
| **Accession number** | Q9UL54-1 |
| **Tags** | N-terminal GST |
| **Baculovirus expressed protein** | MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELG<br>LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGA<br>VLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH<br>VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSS<br>KYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGS**MPAGGRAGSLKDPD**<br>**VAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSG**<br>**KQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSA**<br>**SDLLEVHKKPLQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSE**<br>**PGLVKLGDFGSASIMAPANSFVGTPYWMAPEVILAMDEGQYDGKVDVWS**<br>**LGITCIELAERKPPLFNMNAMSALYHIAQNESPVLQSGHWSEYFRNFVD**<br>**SCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDAVRELDNLQ**<br>**YRKMKKILFQEAPNGPGAEAPEEEEEAEPYMHRAGTLTSLES** |
| **Native sequence** | Amino acids M1 – S350 (end residue is R1235) of human TAOK2. 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 pFastBac GST 6P1 |

**Nucleotide Sequence Of Insert**

ggatccATGCCAGCTGGGGGCCGGGCCGGGAGCCTGAAGGACCCAGATG
TGGCTGAGCTCTTCTTCAAGGATGACCCAGAAAAGCTCTTCTCTGACCT
CCGGGAAATTGGCCATGGCAGCTTTGGAGCCGTATACTTTGCCCGGGAT
GTCCGGAATAGTGAGGTGGTGGCCATCAAGAAGATGTCCTACAGTGGGA
AGCAGTCCAATGAGAAATGGCAAGACATCATCAAGGAGGTGCGGTTCTT
ACAGAAGCTCCGGCATCCCAACACCATTCAGTACCGGGGCTGTTACCTG
AGGGAGCACACGGCTTGGCTGGTAATGGAGTATTGCCTGGGCTCAGCTT
CTGACCTTCTAGAAGTGCACAAGAAACCCCTTCAGGAGGTAGAGATCGC
AGCTGTGACCCACGGGGCGCTTCAGGGCCTGGCATATCTGCACTCCCAC
AACATGATCCATAGGGATGTGAAGGCTGGAAACATCCTGCTGTCAGAGC
CAGGGTTAGTGAAGCTAGGGGACTTTGGTTCTGCGTCCATCATGGCACC
TGCCAACTCCTTCGTGGGCACCCCATACTGGATGGCACCCGAGGTGATC
CTGGCCATGGATGAGGGGCAGTACGATGGCAAAGTGGACGTCTGGTCCT
TGGGGATAACCTGCATCGAGCTGGCTGAACGGAAACCACCGCTCTTTAA
CATGAATGCGATGAGTGCCTTATACCACATTGCACAGAACGAATCCCCC
GTGCTCCAGTCAGGACACTGGTCTGAGTACTTCCGGAATTTTGTCGACT
CCTGTCTTCAGAAAATCCCTCAAGACAGACCAACCTCAGAGGTTCTCCT
GAAGCACCGCTTTGTGCTCCGGGAGCGGCCACCCACAGTCATCATGGAC
CTGATCCAGAGGACCAAGGATGCCGTGCGGGAGCTGGACAACCTGCAGT
ACCGCAAGATGAAGAAGATCCTGTTCCAAGAGGCACCCAACGGCCCTGG
TGCCGAGGCCCCAGAGGAGGAAGAGGAGGCCGAGCCCTACATGCACCGG
GCCGGGACTCTGACCAGCCTCGAGAGTtgagcggccgc