*Division of Signal Tranduction Therapy*

# Standard Operating Procedure

# Preparation of PSF [1 – 707]

**Enzyme description:-** PSF [1 - 707]

**Clone number:-** DU 19508

**Source:-** Recombinant

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

**Tag:-** N-terminal GST

**Purification method**:- GSH Sepharose

**Calculated molecular mass:-**
Monoisotopic 103, 615.62 daltons
Average Mass 103, 681.25 daltons
[cysteines reduced, methionines have not been oxidised

**Theoretical pI:-** 8.86

**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

## PSF [1 - 707]

| | |
|---|---|
| **Protein** | PSF [1 - 707] |
| **Clone number** | DU 19508 |
| **Species** | Human |
| **Accession number** | NM_005066.2 |
| **Tags** | N-terminal GST |
| **Bacterially expressed protein** | MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELG<br>LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGA<br>VLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH<br>VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSS<br>KYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGSPNSRVD**MSRDRFRS**<br>**RGGGGGGFHRRGGGGGRGGLHDFRSPPPGMGLNQNRGPMGPGPGQSGPK**<br>**PPIPPPPPHQQQQQPPPQQPPPQQPPPHQPPPHPQPHQQQQPPPPPQDS**<br>**SKPVVAQGPGPAPGVGSTPPASSSAPPATPPTSGAPPGSGPGPTPTPPP**<br>**AVTSAPPGAPPPTPPSSGVPTTPPQAGGPPPPPAAVPGPGPGPKQGPGP**<br>**GGPKGGKMPGGPKPGGGPGLSTPGGHPKPPRRGGGEPRGGRQHHPPYHQ**<br>**QHHQGPPPGGPGGRSEEKISDSEGFKANLSLLRRPGEKTYTQRCRLFVG**<br>**NLPADITEDEFKRLFAKYGEPGEVFINKGKGFGFIKLESRALAEIAKAE**<br>**LDDTPMRGRQLRVRFATHAAALSVRNLSPYVSNELLEEAFSQFGPIERA**<br>**VVIVDDRGRSTGKGIVEFASKPAARKAFERCSEGVFLLTTTPRPVIVEP**<br>**LEQLDDEDGLPEKLAQKNPMYQKERETPTRFAQHGTFEYEYSQRWKSLD**<br>**EMEKQQREQVEKNMKDAKDKLESEMEDAYHEHQANLLRQDLMRRQEELR**<br>**RMEELHNQEMQKRKEMQLRQEEERRRREEEMMIRQREMEDQMRRQREES**<br>**YSRMGYMDPRERDMRMGGGGAMNMGDPYGSGGQKFPPLGGGGGIGYEAN**<br>**PGVPPATMSGSMMGSDMRTERFGQGGAGPVGGQGPRGMGPGTPAGYGRG**<br>**REEYEGPNKKPRF** |
| **Native sequence** | Amino acids M1 – F707 (end) of human PSF.<br>Residue M238 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** | *Sal*1 and *Xho*1 sites into *Sal*1 of pGEX6P-1 |

**Nucleotide Sequence of insert**

gtcgacATGTCTCGGGATCGGTTCCGGAGTCGTGGCGGTGGCGGTGGTGGCTTCCACAGGCGTGGA
GGAGGCGGCGGCCGCGGCGGCCTCCACGACTTCCGTTCTCCGCCGCCCGGCATGGGCCTCAATCAG
AATCGCGGCCCCATGGGTCCTGGCCCGGGCCAGAGCGGCCCTAAGCCTCCGATCCCGCCACCGCCT
CCACACCAACAGCAGCAACAGCCACCACCGCAGCAGCCACCGCCGCAGCAGCCGCCACCGCATCAG
CCGCCGCCGCATCCACAGCCGCATCAGCAGCAGCAGCCGCCGCCACCGCCGCAGGACTCTTCCAAG
CCCGTCGTTGCTCAGGGACCCGGCCCCGCTCCCGGAGTAGGCAGCACACCACCAGCCTCCAGCTCG
GCCCCGCCCGCCACTCCACCAACCTCGGGGGCCCCGCCAGGGTCCGGGCCAGGCCCGACTCCGACC
CCGCCGCCTGCAGTCACCTCGGCCCCTCCCGGGGCGCCGCCACCCACCCCGCCAAGCAGCGGGGTC
CCTACCACACCTCCTCAGGCCGGAGGCCCGCCGCCTCCGCCCGCGGCAGTCCCGGGCCCGGGTCCA
GGGCCTAAGCAGGGCCCAGGTCCGGGTGGTCCCAAAGGCGGCAAAATGCCTGGCGGGCCGAAGCCA
GGTGGCGGCCCGGGCCTAAGTACGCCTGGCGGCCACCCCAAGCCGCCGCGTCGAGGCGGCGGGGAG
CCCCGCGGGGGCCGCCAGCACCACCCGCCCTACCACCAGCAGCATCACCAGGGGCCCCCGCCCGGC
GGGCCCGGCGGCCGCAGCGAGGAGAAGATCTCGGACTCGGAGGGGTTTAAAGCCAATTTGTCTCTC
TTGAGGAGGCCTGGAGAGAAAACTTACACACAGCGATGTCGGTTGTTTGTTGGGAATCTACCTGCT
GATATCACGGAGGATGAATTCAAAAGACTATTTGCTAAATATGGAGAACCAGGAGAAGTTTTTATC
AACAAAGGCAAAGGATTCGGATTTATTAAGCTTGAATCTAGAGCTTTGGCTGAAATTGCCAAAGCC
GAACTGGATGATACACCCATGAGAGGTAGACAGCTTCGAGTTCGCTTTGCCACACATGCTGCTGCC
CTTTCTGTTCGTAATCTTTCACCTTATGTTTCCAATGAACTGTTGGAAGAAGCCTTTAGCCAATTT
GGTCCTATTGAAAGGGCTGTTGTAATAGTGGATGATCGTGGAAGATCTACAGGGAAAGGCATTGTT
GAATTTGCTTCTAAGCCAGCAGCAAGAAAGGCATTTGAACGATGCAGTGAAGGTGTTTTCTTACTG
ACGACAACTCCTCGTCCAGTCATTGTGGAACCACTTGAACAACTAGATGATGAAGATGGTCTTCCT
GAAAAACTTGCCCAGAAGAATCCAATGTATCAAAAGGAGAGAGAAACCCCTACTCGTTTTGCCCAG
CATGGCACGTTTGAGTACGAATATTCTCAGCGATGGAAGTCTTTGGATGAAATGGAAAAACAGCAA
AGGGAACAAGTTGAAAAAAACATGAAAGATGCAAAAGACAAATTGGAAAGTGAAATGGAAGATGCC
TATCATGAACATCAGGCAAATCTTTTGCGCCAAGATCTGATGAGACGACAGGAAGAATTAAGACGC
ATGGAAGAACTTCACAATCAAGAAATGCAGAAACGTAAAGAAATGCAATTGAGGCAAGAGGAGGAA
CGACGTAGAAGAGAGGAAGAGATGATGATTCGTCAACGTGAGATGGAAGACCAAATGAGGCGCCAA
AGAGAGGAAAGTTACAGCCGAATGGGCTACATGGATCCACGGGAAAGAGACATGCGAATGGGTGGC
GGAGGAGCAATGAACATGGGAGATCCCTATGGTTCAGGAGGCCAGAAATTTCCACCTCTAGGAGGT
GGTGGTGGCATAGGTTATGAAGCTAATCCTGGCGTTCCACCAGCAACCATGAGTGGTTCCATGATG
GGAAGTGACATGCGTACTGAGCGCTTTGGGCAGGGAGGTGCGGGGCCTGTGGGTGGACAGGGTCCT
AGAGGAATGGGGCCTGGAACTCCAGCAGGATATGGTAGAGGGAGAGAAGAGTACGAAGGCCCAAAC
AAAAAACCCCGATTTtagctcgag

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