

## *MRC PPU Reagents and Services*

### **Standard Operating Procedure**

#### **Preparation of SRPK1 D497A [2 – 655]**

**Enzyme description:-** SRPK1 D497A [2 - 655]

**Clone number:-** DU 66208

**Source:-** Recombinant

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

**Tag:-** N-terminal GST

**Purification method:-** GSH Sepharose

**Calculated molecular mass:-**

Monoisotopic 100, 909.96 daltons

Average Mass 100, 973.74 daltons

[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 5.83

**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 °C

**Assay:-** Standard filter binding assay

**Assay Buffer:-**

50 mM Tris-HCl pH 7.5, 0.1 % 2 mercaptoethanol, 0.1 mM EGTA, 10 mM MgAc

**Substrate:-**

RSRSRSRSRSRSR residues 204 – 218 of human ASF-1/SF-2

Final concentration: 300  $\mu$ M

*MRC PPU Reagents and Services*

**Clone Data Sheet**

**SRPK1 D497A [2 - 655]**

**Protein** SRPK1 D497A [2 – 655]

**Clone number** DU 66208

**Species** Human

**Accession number** NM\_003137

**Tags** N-terminal GST

**Bacterially expressed protein**

MSPILGYWKIKGLVQPTRLLEYLEEKYEHLIERDEGDKWRNKKFEL  
GLEFPNLPYYIDGDVKLTSMAIIRYIADKHNMLGGCPKERAIEISMLE  
GAVLDIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLN  
GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKY  
LKSSKYIAWPLQGWQATFGGGDHPKSDLEVLFOGPLG**SERKVLALQA**  
**RKKRTKAKDKAQRKSETQHRGSAPHSESDLPEQEEEILGSDDDEQED**  
**PNDYCKGGYHLVKIGDLFNGRYHVIRKLGWGHFSTVWLSWDIQGKKFV**  
**AMKVVKSAEHYTETALDEIRLLKSVRNSDPNDPNREMVVQLLDDFKIS**  
**GVNGTHICMVFEVLGHHLLKWI IKSNYOGLPLPCVKKI IQOVLQGLDY**  
**LHTKCRI IHTDIKPENILLSVNEQYIRRLAAEATEWQORSGAPPPSGSA**  
**VSTAPQPKPADKMSKNKKKKLKKKQKRQAELLEKRMQEI EEMEKESGP**  
**GQKRPNKQEESESPVERPLKENPPNKMTQEKLEESSTIGQDQTLMERD**  
**TEGGAAEINCNGVIEVINYTQNSNETLRHKEDLHNANDCDVQNLNQE**  
**SSFLSSQNGDSSTSQETDSCPTITSEVSDTMVCQSSSTVGQSFSEQHI**  
**SQLOESIRAEIPCEDEQEQHNGPLDNKGKSTAGNFLVNPLEPKNAEK**  
**LKVKIAALGNACWVHKHFTEDIQTRQYRSLEVLIGSGYNTPADIWSTA**  
**CMAFELATGDYLFEPHSGEYTRDEDHIALI IELLGKVPRKLI VAGKY**  
**SKEFFTKKGLKHITKLPWGLFEVLVEKEYEWSQEAAAGFTDFLLPML**  
**ELIPEKRATAAECLRHPWLNS**

**Native sequence** Amino acids E2 – S655 (end) of human SRPK1.  
Residue E2 of the fusion protein is equivalent to E232 of the native enzyme. The GST tag is located at residues 1 – 220.

The enzyme has a D497A mutation. Residue D497A is equivalent to A727 of the fusion protein.

**Protease cleavage** PreScission (LEVLFOG) at residues 221 – 228

**Cloning sites** BamH1 and EcoR1 site of pGEX6P-1

## *MRC PPU Reagents and Services*

### Nucleotide sequence of insert

ggatccGAGCGGAAAGTGCTTGCCTCCAGGCCCGAAAGAAAAGGACC  
AAGGCCAAGAAGGACAAAGCCCAAAGGAAATCTGAAACTCAGCACCGA  
GGCTCTGCTCCCCACTCTGAGAGTGATCTACCAGAGCAGGAAGAGGAG  
ATTCTGGGATCTGATGATGATGAGCAAGAAGATCCTAATGATTATTGT  
AAAGGAGGTTATCATCTTGTGAAAATTGGAGATCTATTCAATGGGAGA  
TACCATGTGATCCGAAAGTTAGGCTGGGGACACTTTTCAACAGTATGG  
TTATCATGGGATATTCAGGGGAAGAAATTTGTGGCAATGAAAGTAGTT  
AAAAGTGCTGAACATTACACTGAAACAGCACTAGATGAAATCCGGTTG  
CTGAAGTCAGTTCGCAATTCAGACCCTAATGATCCAAATAGAGAAATG  
GTTGTTCAACTACTAGATGACTTTAAAATATCAGGAGTTAATGGAACA  
CATATCTGCATGGTATTTGAAGTTTTGGGGCATCATCTGCTCAAGTGG  
ATCATCAAATCCAATTATCAGGGGCTTCCACTGCCTTGTGTCAAAAAA  
ATTATTCAGCAAGTGTTACAGGGTCTTGATTATTTACATACCAAGTGC  
CGTATCATCCACACTGACATTAACCAGAGAACATCTTATTGTCAGTG  
AATGAGCAGTACATTCGGAGGCTGGCTGCAGAAGCAACAGAATGGCAG  
CGATCTGGAGCTCCTCCGCCTTCCGGATCTGCAGTCAGTACTGCTCCC  
CAGCCTAAACCAGCTGACAAAATGTCAAAGAATAAGAAGAAGAAATTG  
AAGAAGAAGCAGAAGCGCCAGGCAGAATTACTAGAGAAGCGAATGCAG  
GAAATTGAGGAAATGGAGAAAGAGTCGGGCCCTGGGCAAAAAGACCA  
ACAAGCAAGAAGAATCAGAGAGTCCTGTTGAAAGACCCTTGAAAGAG  
AACCCACCTAATAAAATGACCCAAGAAAACCTTGAAGAGTCAAGTACC  
ATTGGCCAGGATCAAACGCTTATGGAACGTGATACAGAGGGTGGTGCA  
GCAGAAATTAATTGCAATGGAGTGATTGAAGTCATTAATTATACTCAG  
AACAGTAATAATGAAACATTGAGACATAAAGAGGATCTACATAATGCT  
AATGACTGTGATGTCCAAAATTTGAATCAGGAATCTAGTTTCCTAAGC  
TCCCAAAATGGAGACAGCAGCACATCTCAAGAAACAGACTCTTGTACA  
CCTATAACATCTGAGGTGTCAGACACCATGGTGTGCCAGTCTTCCTCA  
ACTGTAGGTCAGTCATTCAGTGAACAACACATTAGCCAACCTTCAAGAA  
AGCATTTCGGGCAGAGATACCCTGTGAAGATGAACAAGAGCAAGAACAT  
AACGGACCACTGGACAACAAAGGAAAATCCACGGCTGGAAATTTTCTT  
GTTAATCCCCTTGAGCCAAAAATGCAGAAAAGCTCAAGGTGAAGATT  
GCTGCCCTTGGAATGCTTGTGGGTGCACAAACATTTCACTGAAGAT  
ATTCAAACAAGGCAATATCGTTCCTTGGAAGTTCTAATCGGATCTGGC  
TATAATACCCCTGCTGACATTTGGAGCACGGCATGCATGGCCTTTGAA  
CTGGCCACAGGTGACTATTTGTTTGAACCTCATTCAGGGGAAGAGTAC  
ACTCGAGATGAAGATCACATTGCATTGATCATAGAACTTCTGGGGAAG  
GTGCCTCGCAAGCTCATTGTGGCAGGAAAATATTCGAAGGAATTTTTC  
ACCAAAAAGGTGACCTGAAACATATCACGAAGCTGAAACCTTGGGGC  
CTTTTTGAGGTTCTAGTGGAGAAGTATGAGTGGTCTCAGGAAGAGGCA  
GCTGGCTTACAGATTTCTTACTGCCCATGTTGGAGCTGATCCCTGAG  
AAGAGAGCCACTGCCCGGAGTGTCTCCGGCACCTTGGCTtaactcc  
taagaattc