

## *Division of Signal Transduction Therapy*

### **Standard Operating Procedure**

#### **Preparation of active VCPIP1 [25 – 561]**

**Enzyme description:-** VCPIP1 [25 - 561]

**Clone number:-** DU 44386

**Source:-** Recombinant

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

**Tag:-** N-terminal GST

**Purification method:-** GSH Sepharose

**Calculated molecular mass:-**

Monoisotopic 86, 538.24 daltons

Average Mass 86, 594.01 daltons

[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 6.57

**Purity:-** >80 %

**Activation protocol:-** Constitutively active

**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

**Storage temperature:-** -70 °C

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**Clone Data Sheet**

**VCPIP1 [25 - 561]**

**Protein** VCPIP1[25 - 561]

**Clone number** DU 44386

**Species** Human

**Accession number** Q96JH7

**Tags** N-terminal GST

**Bacterially expressed protein**

MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELG  
LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGA  
VLDIRYGVSR IAYS KDFETLKVDFLSKLP EMLKMFEDRLCHKTYLNGDH  
VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS  
KYIAWPLQGWQATFGGGDHPPKSDLEVL FQGPLGSPEFMS **SSLASAAASG**  
**GLLKRRDRRILSGSCPDPKCQARLFFPASGSVSIECTECGORHEQQQLL**  
**GVEEVTDPDVVLHNLRLNALLGVTGAPKNTTELVKVMGLSNYHCKLLSP**  
**ILARYGMDKQTGRAKLLRDMNQGELFDCALLGDRAFLIEPEHVNTVGYG**  
**KDRSGSLLYLHDTLEDIKRANKSQECLIPVHVDGDGHCLVHAVSRALVG**  
**RELFWHALRENLKQHFQQLARYQALFHDFIDAAEWEDIINECDPLFVP**  
**PEGVPLGLRNIIHIFGLANVLRPIILLDSL SGMRSSGDYSATFLPGLIP**  
**AEKCTGKDGHLNKPICIAWSSSSGRNHYIPLVGIKGAALPKLPMNLLPKA**  
**WGVPQDLIKKYIKLEEDGGCVIGGDRSLQDKYLLRLVAAMEEVFMDKHG**  
**IHPSLVADVHQYFYRRTGVIGVQPEEVTAAAKKAVMDNRLHKCLLCGAL**  
**SELHVPPEWLAPGGKLYNLAKSTHGQLRTDKNYSFPLNNLVCSYDSVKD**  
**VLVPDYGMSNLTACNWCHGTSVRKVRGDGSIVYLDGD**

**Native sequence** Amino acids S25 – D561 (end residue is S1222) of human VCPIP1. Residue S236 of the fusion protein is equivalent to S25 of the native enzyme. The GST tag is located at residues 1 – 220.

**Protease cleavage** PreScission (LEVLFQGP) residues 221 - 229

**Cloning sites** *Eco*R1 and *Not*I sites of pGEX 6P-1

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**Nucleotide**  
**Sequence of insert**

gaattcatgTCGTCCTTGGCGTCGGCGGCTGCTTCGGGGGGGCTTTTGA  
AGCGGAGAGACCGGAGAATCCTTTCCGGGAGCTGCCCGGATCCGAAGTG  
TCAGGCGGTCTATTTTTCCCGCCTCCGGTTCGTGTCAGCATCGAGTGT  
ACCGAGTGCGGCCAGCGGCACGAGCAGCAACAGCTGCTGGGGGTTGAGG  
AGGTGACCGACCCGGACGTAGTGCTACACAACCTGCTGCGGAACGCGCT  
GCTCGGGGTTACGGGGGCACCCAAGAAGAACACGGAACCTGGTAAAGGTG  
ATGGGCCTTTCCAACCTATCACTGCAAATTTGTTGTCGCCCATATTAGCTC  
GCTATGGAATGGACAAACAGACAGGCCCGGGCCAAGCTTCTCCGGGACAT  
GAACCAGGGCGAACTGTTTCGATTGCGCCTTACTGGGTGACCGCGCCTTC  
CTCATAGAACCAGAGCATGTTAACACTGTGGGCTATGGCAAGGACCGCT  
CCGGAAGCCTCCTGTATTTGCATGACACTCTGGAGGACATTAAGCGGGC  
CAATAAAAGCCAGGAATGTCTCATTCCAGTGCATGTGGACGGGGATGGA  
CACTGCTTGGTGCATGCTGTGTCTCGGGCTCTAGTAGGCCGAGAGCTCT  
TCTGGCATGCCTTAAGAGAGAATCTTAAACAGCACTTTCAGCAGCACCT  
GGCCCATATCAAGCTCTGTTCCATGACTTCATTGATGCTGCTGAGTGG  
GAGGACATTATCAATGAGTGTGACCCTCTGTTTGTACCACCTGAGGGTG  
TTCCCTTGGGCCTGAGGAATATCCACATATTTGGTCTTGCCAATGTGCT  
ACATCGTCTTATTATTCTGTTAGATTCCCTCAGTGGCATGAGAAGCTCT  
GGTGATTATTCAGCCACCTTTCTACCTGGGCTCATCCCTGCAGAGAAGT  
GCACTGGGAAAGATGGTCATTTGAACAAACCAATCTGTATTGCATGGAG  
CAGCTCCGGTAGAAACCATTATATCCCCTTGGTAGGCATAAAAGGGGCT  
GCTTTGCCCAAACCTGCCTATGAATTTGCTTCCCTAAAGCATGGGGTGTGC  
CTCAGGACCTTATTA AAAAGTACATAAAACTTGAAGAGGATGGTGGTTG  
TGTTATTGGAGGTGACAGAAGTTTGCAAGATAAATACTTACTTAGGCTT  
GTTGCTGCTATGGAAGAAGTCTTTATGGACAAACATGGTATCCATCCTA  
GTTTGGTTGCTGATGTCCATCAGTATTTCTACAGAAGGACTGGAGTGAT  
AGGAGTTCAGCCTGAGGAAGTCACAGCAGCTGCTAAAAAAGCAGTAATG  
GATAATCGCCTTCACAAATGTTTGCTCTGTGGTGCCCTTTCTGAACTTC  
ATGTTCCCTCAGAGTGGTTGGCTCCTGGAGGGAAATTGTATAACCTGGC  
AAAAAGTACTCATGGACAGCTGAGGACTGACAAAAATTACAGCTTTCCC  
TTGAACAATTTGGTTTGCTCATATGATTCAGTGAAAGATGTTCTGGTAC  
CAGACTATGGAATGAGTAACCTAACAGCTTGTAAATGGTGCCATGGCAC  
ATCTGTGCGAAAGGTCAGAGGAGATGGGTCTATTGTGTATTTGGATGGA  
GACtagcggccgc