

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of OSR1 D164A [1 - 477]

<u>Enzyme description:-</u>	OSR1 D164A [1 – 477]
<u>Clone number:-</u>	DU 2961
<u>Source:-</u>	Recombinant
<u>Expression system:-</u>	<i>E.coli</i> expression vector system
<u>Tag:-</u>	N-terminal GST
<u>Purification method:-</u>	GSH Sepharose

Calculated molecular mass:-

Monoisotopic 86, 135.28 daltons
Average Mass 86, 189.88 daltons
[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 5.86

Purity:- >80 %

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 150 mM NaCl, 50 % glycerol, 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, 0.1 mM EGTA, 0.1 % 2-mercaptoethanol, 10 mM MgAc

Division of Signal Transduction Therapy

Clone Data Sheet

OSR1 D164A [1 - 527]

Protein OSR1 D164A [1 - 527]

Clone number DU 2961

Species Human

Accession number NM_005109.2

Tags N-terminal GST + HA

**Bacterially
expressed protein**

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFEL
GLEFPNLPYYIDGDVKLTSMAIIRYIADKHNMLGGCPKERAIEISMLE
GAVLDIRYGVSRIAYS KDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLN
GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKY
LKSSKYIAWPLQGWQATFGGGDHPKSDLEVLFGPPLGSATMYPYDVP
DYAMSEDSSALPWSINRDDYELQEVIGSGATAVVQAAYCAPKKEKVAI
KRINLEKCQTSMDPELLKEIQAMSQCHHPNIVSYYSFVVKDELWLVK
LLSGGSVLDIIKHIVAKGEHKSGVLDESTIATILREVLEGLEYLHKN
QIHRDVKAGNILLGEDGSVQIAAFGVSAFLATGGDITRNKVRKTFVGT
PCWMAPEVMEQVRGYDFKADIWSFGITAEIATGAAPYHKYPPMKVLM
LTLQNDPPSLETGVQDKEMLKKGKSFVKMISLCLQKDPEKRPTAAEL
LRHKFFQKAKNKEFLQEKTLQRAPTISERAKKVRVPGSSGRLHKTED
GGWEWSDEFDEESEEGKAAISQLRSPRVKESISNSELFPTTDPVGT
LQVPEQISAHLPQAGQIATQPTQVSLPPTAEPAKTAQALSSGSGSQE
TKIPIISLVLRLRNSKKELNDRFEFTPGRDTAEGVSQELISAGLVDGR
DLVIVAANLQKIVEEPQSNRSVTFKLAGSVEGSDIPDDGKLIGFAQLS
IS

Native sequence Amino acids M1 – S527 (end) of human OSR1.

Residue M244 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 – 220 and the HA tag (YPYDVPDYA).

The enzyme has a D164A mutation, which produces a kinase dead enzyme. Residue D164A is equivalent to A407 of the fusion protein.

Protease cleavage PreScission site (LEVLFQGP) residues 221 – 228

Division of Signal Transduction Therapy

Cloning sites

*Bam*H1 and *Not*I sites of pGex6P1

Nucleotide sequence of insert

```
ggatccgccaccATGTACCCATACGATGTGCCAGATTACGCCATGTCC
GAAGACTCGAGCGCCCTGCCCTGGTCCATCAACAGGGACGATTACGAG
CTGCAGGAGGTGATCGGGAGTGGAGCAACTGCTGTAGTCCAAGCAGCT
TATTGTGCCCTAAAAAGGAGAAAGTGGCAATCAAACGGATAAACCTT
GAGAAATGTCAAAC TAGCATGGATGAACTCCTGAAAGAAATTCAAGCC
ATGAGTCAATGCCATCATCCTAATATTGTATCTTACTACACATCTTTT
GTGGTAAAAGATGAGCTGTGGCTTGTTCATGAAGCTGCTAAGTGGAGGT
TCTGTTCTGGATATTATTAAGCACATTGTGGCAAAGGGGAACACAAA
AGTGGAGTCCTAGATGAATCTACCATTGCTACGATACTCCGAGAAGTA
CTGGAAGGGCTGGAATATCTGCATAAAAAATGGACAGATCCACAGAGAT
GTGAAAGCTGGAACATTCCTTCTTGGAAGAAGATGGCTCAGTACAGATT
GCAGACTTTGGGGTTAGTGCTTTTTTTAGCAACTGGTGGTGATATTACC
CGAAATAAAGTGAGAAAGACCTTTGTTGGCACCCCTTGTGGATGGCA
CCTGAAGTTATGGAACAGGTCCGTGGTTATGATTTCAAAGCTGATATT
TGGAGTTTGGAAATTACAGCAATTGAATTGGCTACAGGGCGGCTCCT
TATCATAAATATCCACCAATGAAGGTTTTAATGCTGACACTGCAGAAC
GATCCTCCTTCTTTGGAAACTGGTGTTC AAGATAAAGAAATGCTGAAA
AAATATGGAAAATCATTTAGAAAAATGATTTCAATTGTGCCTTCAAAAA
GATCCAGAAAAAAGACCAACAGCAGCAGAACTATTAAGGCACAAATTT
TTCCAGAAAGCAAAGAATAAAGAATTTCTTCAAGAAAAAACATTGCAG
AGAGCACCAACCATTTCTGAAAGAGCAAAAAAGGTTCCGAGGGTACCA
GGTCCAGTGGGCGTCTTCATAAGACAGAGGATGGAGGCTGGGAGTGG
AGTGATGATGAATTTGATGAAGAAAGTGAGGAAGGGAAAGCAGCAATT
TCACAACTCAGGTCTCCCCGAGTGAAAGAATCAATATCAAATTCAGAG
CTCTTTCCAACAAC TGATCCTGTGGGTACTTTGCTCCAAGTTCAGAA
CAGATCTCTGCTCATCTACCTCAGCCAGCTGGGCAGATTGCTACACAG
CCAACTCAAGTCTCTCTCCCACCCACCGCAGAGCCAGCAAAAACAGCT
CAGGCTTTGTCTTCAGGATCAGGTTCAACAAGAAACCAAGATCCCAATC
AGTCTAGTACTAAGATTAAGGAATTCAAAAAAGAACTAAATGATATT
CGATTTGAATTTACTCCTGGGAGAGATACAGCAGAGGGTGTCTCTCAG
GAACTCATTTCTGCTGGCCTGGTCGACGGAAGGGATTTAGTAATAGTG
GCAGCTAATTTGCAGAAAATTGTGGAAGAACCTCAGTCAAATCGATCT
GTCATTTCAAAC TGCGTCTGGTGTCTGAAGGCTCAGATATTCCTGAT
GATGGTAAACTGATAGGATTTGCCAGCTCAGCATCAGCtaagcggcc
gc
```