

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of active VPS34 [2 - 887]

<u>Enzyme description:-</u>	VPS34 [2 - 887]
<u>Clone number:-</u>	DU 3303
<u>Source:-</u>	Recombinant
<u>Expression system:-</u>	Baculovirus expression vector system
<u>Tag:-</u>	N-terminal His(6) and HA
<u>Purification method:-</u>	Ni ²⁺ -NTA agarose
<u>Expression level:-</u>	2 mg/L

Calculated molecular mass:-

Monoisotopic 106, 453.88 daltons
Average Mass 106, 521.77 daltons
[cysteines reduced, methionines have not been oxidised]

<u>Theoretical pI:-</u>	6.05
<u>Purity:-</u>	>80 %
<u>Activation protocol:-</u>	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, 0.2 mM PMSF, 1 mM Benzamidine

<u>Storage temperature:-</u>	-70 °C
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<u>Assay:-</u>	ADP Glo
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Assay buffer:-

20 mM Tris-HCl, 67 mM KCl, 1 mM EDTA, 1 mM DTT, 0.05 mg/ml BSA, 10 mM MgCl₂

Substrate:-

PI Final concentration: 0.04 mM

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Clone Data Sheet

VPS34 [2 – 887]

Protein VPS34 [2 - 887]

Clone number DU 3303

Species Human

Accession number NM_002647

Tags N-terminal His(6) and HA (YPYDVPDYA)

Baculovirus Expressed protein MSYYHHHHHDYDIPTTENLYFQGAMDPEFATMYPYDVPDYA**GEAEK**FH
YIYSCDLINVLKIGSLEGGKREQ**SYKAVLEDPMLKFSGLYQETC**SDL
YVTCQVFAEGKPLALPVRTSYKAFSTRWNWNEWLKL**PKVPDLPRNAQV**
ALTIWDVYGP**GKAVPVGGTTVSLFGKYGMFRQGMHDLKVWPNVEADGSE**
PTKTPGRTS**STLSE**DQMSRLAKLTKAHRQGHMV**KVDWLDRLTFREIEMI**
NESEKRSSNFMYLMVEFRCVKCDDKEYGIVYYEKD**GDESSPILTSFELV**
KVPDPQMSMENLVESKHHKLARSLSG**PSDHDLPNAATR**DQLNIIVSY
PPTKQ**LT**YEEQDLVWKF**RY**YLT**NQEKALTKFLKCVN**WDL**PQ**EAKQALEL
LGKWK**PMDVEDSLELLSSHYTNPTVRRYAVARLRQADDEDLLMYLLQ**LV
QAL**KYENFDDI**KNGLEPT**KKDSQSSVSE**NSVNSGINS**AEIDSSQIITSP**
LPSVSSPP**PASKTKEVPDGENLEQDLCTFLISRACKNSTLAN**YLYWYVI
VE**CE**DQDTQ**Q**RD**PKTHEMYL**NVMRRFSQ**ALLKGD**KSVRVMRS**LLAAQQT**
FV**DRLVHLMKAVQ**RESGNR**KKKNERLQALLGDNEKMNLS**DVELIPLPLE
PQ**VKIRGI**IPETATL**FKSALMPAQLFFK**TEDGGKY**PVIFKHGDDLRQDQ**
LIL**QIISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSV**PVAEVL
DTEGS**IQNF**FRKYAPSENG**PNGISAEVMDTYVKSCAGYCVITYILG**VG**D**
RHL**DNLLLT**KTG**KL**FHIDFGYILGRDPK**PLPPM**KL**NKEMVEGMGGTQS**
EQYQ**EFRKQCYTAF**LHLRRYS**NLILNLFSLMVDANIPDIALEPDKTVKK**
VQDK**FRLDLSDEEAVHYMQSLIDESVHALFAAVVEQIHKFAQYWRK**

Native sequence Amino acids G2 – K887 (end) of human VPS34.
Residue G43 of the fusion protein is equivalent to G2 of the native enzyme. The His(6) tag is located at residues 5 – 10 and the HA tag is located at residues 34 – 42..

Protease cleavage rTEV (ENLYFQG) residues 18 – 24

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Cloning sites

*Eco*R1 of pFastBac HTa

Nucleotide of sequence of insert

gaattcgccaccatgtaccatac gatgtgccagattacgccgggGAAG
CAGAGAAGTTTCACTACATCTATAGTTGTGACCTGGATATCAACGTCCA
GCTTAAGATAGGAAGCTTGGAAAGGGAAGAGAGAACAAAAGAGTTATAAA
GCTGTCCTGGAAGACCCAATGTTGAAGTCTCAGGACTATATCAAGAGA
CATGCTCTGATCTTTATGTTACTTGTCAAGTTTTTGCAGAAGGGAAGCC
TTTGGCCTTGCCAGTGAGAACATCCTACAAAGCATTTAGTACAAGATGG
AACTGGAATGAATGGCTGAAACTACCAGTAAAATACCCTGACCTGCCCA
GGAATGCCCAAGTGGCCCTCACCATATGGGATGTGTATGGTCCCGGAAA
AGCAGTGCCTGTAGGAGGAACAACGGTTTCGCTCTTTGGAAAATACGGC
ATGTTTCGCCAAGGGATGCATGACTTGAAAGTCTGGCCTAATGTAGAAG
CAGATGGATCAGAACCACAAAACTCCTGGCAGAACAAGTAGCACTCT
CTCAGAAGATCAGATGAGCCGTCTTGCCAAGCTCACCAAAGCTCATCGA
CAAGGACACATGGTGAAAGTAGATTGGCTGGATAGATTGACATTTAGAG
AAATAGAAATGATAAATGAGAGTGAAAAACGAAGTTCTAATTTTCATGTA
CCTGATGGTTGAATTTTCGATGTGTCAAGTGTGATGATAAGGAATATGGT
ATTGTTTATTATGAAAAGGACGGTGATGAATCATCTCCAATTTTAAACAA
GTTTTGAATTAGTGAAAGTTCCTGACCCCCAGATGTCTATGGAGAATTT
AGTTGAGAGCAAACACCACAAGCTTGCCCGGAGTTTAAAGAAGTGGACCT
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TCTTGTTTGGAAAGTTTAGATATTATCTTACGAATCAAGAAAAAGCCTTG
ACAAAATTCCTGAAATGTGTTAATTGGGATCTACCTCAAGAGGCCAAAC
AGGCCTTGGAACCTCTGGGAAAATGGAAGCCGATGGATGTAGAGGACTC
CTTGGAGCTGTTATCCTCTCATTACACCAACCCAACTGTGAGGCGTTAT
GCTGTTGCCCGGTTGCGACAGGCCGATGATGAGGATTTGTTGATGTACC
TATTACAATTGGTCCAGGCTCTCAAATATGAAAATTTTGATGATATAAA
GAATGGATTGGAACCTACCAAGAAGGATAGTCAGAGTTCAGTGTGAGAA
AATGTGTCAAATTCCTGGAATAAATTCCTGCAGAAATAGATAGCTCCCAA
TTATAACCAGCCCCCTTCCTTCAGTCTCTTCACCTCCTCCTGCATCAA
AACAAAAGAAGTTCAGATGGCGAAAATCTGGAACAAGATCTCTGTACC
TTCTTGATATCGAGAGCCTGCAAAAACCTCAACACTGGCTAATTATTTAT
ACTGGTATGTGATAGTGGAATGTGAAGATCAAGATACTCAGCAGAGAGA
TCCAAAGACCCATGAGATGTACTTGAACGTAATGAGAAGATTCAGCCAA
GCATTGTTGAAGGGTGATAAGTCTGTGAGAGTTATGCGTTCCTTGCTGG
CTGCACAACAGACATTTGTAGATCGGTTGGTGCATCTAATGAAGGCAGT
ACAACGCGAAAGTGGAATCGTAAGAAAAAGAATGAGAGACTACAGGCA
TTGCTTGGAGATAATGAAAAGATGAATTTGTGAGATGTGGAACCTTATCC
CGTTGCCTTTAGAACCCCAAGTGAAAATTAGAGGAATAATTCGGGAAAC
AGCTACACTGTTTAAAAGTGCCCTTATGCCTGCACAGTTGTTTTTTAAG
ACGGAAGATGGAGGCAAATATCCAGTTATATTTAAGCATGGAGATGATT
TACGTCAAGATCAACTTATTCCTTCAAATCATTTCACTCATGGACAAGCT
GTTACGGAAAGAAAATCTGGACTTGAATTTGACACCTTATAAGGTGTTA
GCCACCAGTACAAAACATGGCTTCATGCAGTTTATCCAGTCAGTTCCTG
TGGCTGAAGTTCTTGATACAGAGGGAAGCATTCAGAACTTTTTTTAGAAA
ATATGCACCAAGTGAGAATGGGCCAAATGGGATTAGTGCTGAGGTCATG
GACACTTACGTTAAAAGCTGTGCTGGATATTGCGTGATCACCTATATAC

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TTGGAGTTGGAGACAGGCACCTGGATAACCTTTTGCTAACAAAAACAGG
CAAACCTCTCCACATAGACTTTGGATATATTTTGGGTCGGGATCCAAAG
CCTCTTCCTCCACCAATGAAGCTGAATAAAGAAATGGTAGAAGGAATGG
GGGACACACAGAGTGAGCAGTACCAAGAGTTCCGTAAACAGTGTTACAC
GGCTTTCTCCACCTGCGAAGGTATTCTAATCTGATTTTGAACCTTGTTT
TCCTTGATGGTTGATGCAAACATTCCAGATATTGCACTTGAACCAGATA
AAACTGTGAAAAAGGTTTCAGGATAAATTCCGCTTAGACCTGTCCGATGA
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