

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of FLAG-Rims1 1-200

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|---|--|
| <u>Enzyme description:-</u> | FLAG-Rims1 aa 1-200 |
| <u>Clone number:-</u> | DU23549 |
| <u>Source:-</u> | BL21 recombinant |
| <u>Tag:-</u> | N-term. FLAG; cleaved from N-terminal GST- |
| <u>Purification method:-</u> | GSH-Sepharose, TEV-protease treatment |
| <u>Expression level:-</u> | 2mg/L |
| <u>Calculated molecular mass:-</u> | |
| Monoisotopic | 23747 Da |
| Average Mass | 23762 Da |
| [cysteines reduced, methionines have not been oxidised] | |
| <u>Theoretical pI:-</u> | 7.09 |
| <u>Purity:-</u> | 90% |
| <u>Enzyme storage buffer:-</u> | |
| 50mM HEPES pH 8.2, 150mM NaCl, 20% glycerol, 1mM TCEP | |
| <u>Storage temperature:-</u> | -80°C |
| <u>Assay:-</u> | |

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Clone Data Sheet

FLAG-Rims1 1-200

Protein FLAG-Rims1 (1-200)

Synonyms CORD7; RAB3IP2; RIM; RIM1

Clone Number DU23549

Species Human

Accession Number Protein: NP_055804 Gene: NM_014989.4

Tags FLAG-tagged, cleaved from N-terminal GST-TEV-

Aminoacid sequence of the expressed protein **MSPILGYWKIKGLVQPTRLLEYLEEKYEELHYERDEGDKWRNKKFELGLEF
PNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRY
GVSRIAYSKDFETLKVDFLSKLP EMLKMFEDRLCHKTYLNGDHVTHPDFMLY
DALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLQGWQA
TFGGGDHPPKSDENLYFQGGSMDYKDDDDKMSAVGPRGPRPPTVPPPMQEL
PDLSHL**TE**EERNI**IM**AVMDR**Q**KEEEKEE**AM**LKCVVRDM**AK**PA**AC**KT**PR**NAE
NQ**PH**Q**S**PR**L**H**Q**Q**F**ESY**K**EQVR**K**IG**E**E**A**RRY**Q**GE**H**K**D**DA**P**TC**G**I**C**HK**T**K**F**AD
GCG**H**LC**S**Y**C**RT**K**F**C**ARC**G**GR**V**SL**R**SN**N**ED**K**V**M**W**V**C**N**LC**R**K**Q**QE**I**LT**K**SG**A**
FFG**S**GP**Q**Q**T**S**D**GT**L**SD**T**AT**G**A**

Native sequence FLAG-Rims1 1-200 in bold

Protease site TEV Protease site underlined

Cloning sites BamH1 / NotI

DNA sequence of cassette ATG**TCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCCACTCGACTT
CTTTTGGAAATATCTTGAAGAAAAATATGAAGAGCATTTGTATGAGCGGATGAAGGT
GATAAATGGCGAAACAAAAAGTTTGAATTGGGTTTGGAGTTTCCCAATCTTCCTTAT
TATATTGATGGTGATGTTAAATTAACACAGTCTATGGCCATCATACGTTATATAGCT
GACAAGCACAACATGTTGGGTGGTTGTCCAAAAAGAGCGTGCAGAGATTTCAATGCCTT
GAAGGAGCGGTTTTGGATATTAGATACGGTGTTCGAGAATTGCATATAGTAAAGAC
TTTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTC
GAAGATCGTTTATGTCATAAAACATATTTAAATGGTGATCATGTAACCCATCCTGAC
TTCATGTTGTATGACGCTCTTGATGTTGTTTTATACATGGACCCAATGTGCCTGGAT
GCGTTCCCAAATTAGTTTGTTTTAAAAAACGTATGAAAGCTATCCACAAATGAT
AAGTACTTGAAATCCAGCAAGTATATAGCATGGCCTTTTCAGGGCTGGCAAGCCACG
TTTGGTGGTGGCGACCATCCTCCAAAATCGGATGAAAACCTGTATTTTCAGGGCGGA
TCCATGGACTACAAGGACGACGATGACAAGATGTCTCGGCCGTGGGGCCCCGCGGT
CCTCGCCCACCCACGGTGCCTCCCCCATGCAAGAGCTGCCCGACCTGAGCCACCTG
ACCGAAGAGGAGAGGAACATTATCAGTCAGTGATGGACCGCAGAAAGGAAGAGGAG
GAAAAAGAAGAAGCCATGCTCAAGTGTGTTGTCAGGGACATGGCGAAGCCTGCTGCC
TGCAAAACACCAAGAAATGCTGAAAACAGCCCCACCAACCTTCACCGAGATTGCAT
CAACAGTTTGAAGCTATAAGGAACAAGTGAAGAAAAATAGGGGAAGAAGCGCGCGT
TACCAGGGCGAGCACAAGACGATGCTCCGACTTGTGGAATCTGTCAATAAAACAAAG
TTTGCTGATGGGTGCGGTCATCTCTGCTCCTATTGTGCGACTAAGTTCTGTGCGCGC
TGCGGAGGCCGCGTGTCTCTACGGTCAAACAACGAGGACAAAGTGGTTATGTGGGTA
TGCAATTTATGTGCGAAAGCAACAAGAAATCTTAACCAAATCTGGGGCATGGTTCTTT
GGAAGTGGCCCTCAGCAGACAAGTCAGGATGGAACCTGAGTGATACAGCTACAGGT
GCTTAGCGGCCGC**