

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of HOIP

<u>Enzyme description:-</u>	GST-HOIP
<u>Clone number:-</u>	DU15972
<u>Source:-</u>	Recombinant
<u>Tag:-</u>	N-terminal GST
<u>Purification method:-</u>	GSH-Sepharose
<u>Expression level:-</u>	1 mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	147360 Da
Average Mass	147449 Da
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	6.40
<u>Purity:-</u>	10 % -30%
<u>Enzyme storage buffer:-</u>	
50 mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT	
<u>Storage temperature:-</u>	-80°C
<u>Assay:-</u>	

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Clone Data Sheet

Protein name HOIP

Protein GST-RNF8 1 - 1072 (full length)
Synonyms RNF31, ZIBRA
Clone Number DU15972
Species Human
Accession Number Protein: Q96EP0 DNA: NM_017999.4
Tags N-terminal GST

Aminoacid sequence
of the expressed
protein

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL
EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL
DIRYGVSR IAYS KDFETLKVDFLSKLP EMLKMFEDRLCHKTYLNGDHVTH
PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA
WPLQGWQATFGGGDHPKSDLEVLFOGPLGSPGIPGSTRAAAMPGEEEEER
AFLVAREELASALRRDSGOAFSLEQLRPLLASSLPLAARYLQLDAARLVR
CNAHGEP RNYLNTLSTALNILEKYGRNLLSPQRPRYWRGVKFNNPVFRST
VDAVQGGRDVLRLYGYTTEEQPDGLSFPEGQEEPDEHQVATVTLEVLLLR
ELSLLLQNTHPRQQALEQLLEDKVEDDMLQLSEFDPLLREIAPGPLTTPS
VPGSTPGPCFLCGSAPGTLHCPSCKQALCPACDHLFHGHPSRAHHLRQTL
PGVLQGTHLSPSLPASAQPRPQSTSLALGDSSLSPNPASAHLPWHCAA
CAMLNEPWAVLCVACDRPRGCKGLGLGTEGPQGTGGLEPDLARGRWACQS
CTFENEAAAVLCSICERPRLAQPPLVVDSRDAGICLQPLQOGDALLASA
QSQVWYCIHCTFCNSSPGWVCVMCNRTSSPIPAQHAPRPYASSLEKGGPK
PGPPRRLSAPLPSSCGDPEKQRQDKMREEGLQLVSMIREGEAAGACPEEI
FSALQYSGTEVPLQWLRSELPHYVLEMVAELAGQODPGLGAFSCQEARRAW
LDRHGND EAVEECVRTRRRKVOELQSLGFGPEEGSLQALFOHGGDVSR
LTELQRORLEPFRQRLWDSGPEPTPSWDGPKQSLVRRLLAVYALPSWGR
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GLAMYLOENGIDCPKCKFSYALARGGCMHFHCTQCRHQFCSGCYNAFYAK
NKCPEPNCRVKKSLHGHHPRDCLFYLRDWTALRLOKLLQDNNVMFNTEPP
AGARAVPGGGCRVIEQKEVPNGLRDEACGKETPAGYAGLCQAHYKEYLVS
LINAHSLDPATLYEVEELETATERYLHVRPQPLAGEDPPAYQARLLQKLT
EEVPLGQSIPRRRK

Native sequence in bold
Protease cleavage Precission site underlined
Cloning sites Not1

DNA sequence of insert

GCGGCCGCGATGCCGGGGGAGGAAGAGGAGCGGGCCTTCCTGGTGGCCCCG
CGAGGAGCTGGCGAGCGCCCTGAGGAGGGATTCCGGGCAGGCGTTTTCCC
TGGAGCAGCTCCGGCCGCTACTAGCCAGCTCTCTGCCGCTAGCCGCCCCG
TACCTGCAGCTGGACGCCGCACGCCTTGTCGCTGCAACGCTCATGGGGA
GCCCCGAAACTACCTCAACACCCTGTCCACGGCTCTGAACATCCTGGAGA
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GTCAAGTTTAATAACCCTGTCTTTCGCAGCACGGTGGATGCTGTGCAGGG
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TGGTGTGCCCAGTGTCTCTTTGGCTTCATATATGAGCGTGAGCAGCTGGA
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AGTGGGAGGAGCAGCACCAGGTCGGAGCTGTGAGGACTTCCAGAAGTGG
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TGCCAGGCACACTACAAAGAGTATCTTGTGAGCCTCATCAATGCCCACTC
GCTGGACCCAGCCACCTTGTATGAGGTGGAAGAGCTGGAGACGGCCACTG
AGCGTACCTGCACGTACGCCCCAGCCTTTGGCTGGAGAGGATCCCCCT
GCTTACCAGGCCCGCTTGTTACAGAAGCTGACAGAAGAGGTACCCTTGGG
ACAGAGTATCCCCGCAGGCGGAAGTAGGCGGCCGC