### **Certificate of Analysis**



## **RBER-IRStide**

### **Recombinant Protein Kinase Substrate**

Product No.: 0863-0000-1

Lot: 033

**Description:** Artificial fusion protein consisting of an N-terminal GST-tag separated by a Thrombin cleavage site from a fragment of the human RB1 protein, amino acids  $S_{773}$ -K<sub>928</sub> (as in <u>NCBI/Protein</u> entry NP\_000312.2) followed by 11 Arg residues (ER) and a peptide sequence (HTDDGYMPMSPGVA, IRStide). Expressed in E.coli.

Theoretical MW<sub>Fusion Protein</sub>: 48,559 Da

Expression host: E.coli

**Purification:** GST-Affinity and ion exchange chromatography

**ATPase activity:** In an ADP-Glo<sup>TM</sup> assay (Promega) with 10 µM ATP or 30 µM ATP, the ATP  $\rightarrow$  ADP conversion within 30 min is approx. 1% at a concentration of 100 µg/ml substrate. Detailed ATPase assay conditions on request

**Storage buffer:** 50 mM HEPES pH 7.5, 100 mM NaCl, 5 mM DTT, 15 mM reduced glutathione, 20 % glycerol

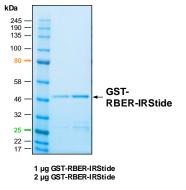
#### Storage temperature: -80°C

For complete recovery, mix well and spin before use. Product must not be stored in diluted solutions, aliquots below 10µl are not advisable. Avoid repeated freeze-thaw cycles!

#### Protein concentration: 0.465 µg/µl

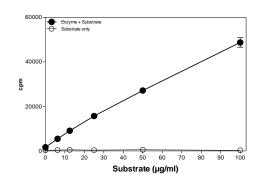
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

#### RBER-IRStide Lot 033: Coomassie stain



# Phosphorylation of RBER-IRStide by p38-gamma

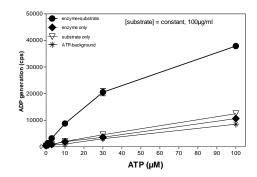
### Radiometric filter binding assay



Assay conditions:

70 mM HEPES-NaOH, pH 7.5 3 mM MgCl<sub>2</sub> 3 mM MnCl<sub>2</sub> 3 µM Na-orthovanadate 1.2 mM DTT 50 µg/ml PEG<sub>20.000</sub> ATP: 1 µM Substrate: variable concentration Kinase: 2 µg/ml MSFC membrane (Millipore)

### ADP-GIo<sup>™</sup> assay (Promega)



70 mM HEPES-NaOH, pH 7.5 3 mM MgCl2 3 mM MnCl2 3 μM Na-orthovanadate 1.2 mM DTT 50 μg/ml PEG20.000 ATP: variable concentration 1 % (v/v) DMSO Substrate (RBER-IRStide): 100 μg/ml Kinase: 2 μg/ml

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# **RBER-IRStide**

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	RBER-IRStide Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60	
61	GDVKLTQSMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120	
121	DFLSKLPEML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180	
181	KRIEAIPQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	<b>LVPRGS</b> PEFS	TRPPTLSPIP	240	
241	HIPRSPYKFP	SSPLRIPGGN	IYISPLKSPY	KISEGLPTPT	KMTPRSRILV	SIGESFGTSE	300	
301	KFQKINQMVC						360	
361	MTSTRTRMQK	QKMNDSMDTS	NKEEKRRRRR	RRRRRR <mark>KKHT</mark>	DDGYMPMSPG	VA	420	
1-218: GST Pink: Thrombin cleavage site Green: R <sub>11</sub> -sequence blue: RB1 fragment						boxed: IRStide sequence		

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