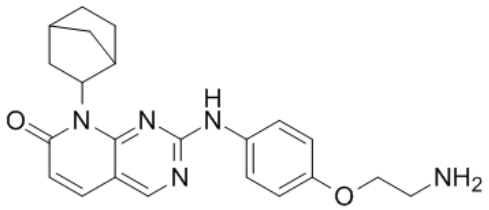
Product Data Sheet

Product Name: VI 16832
Cat. No.: GC32833

Chemical Properties

Cas. No.	1430218-51-1		
SMILES	O=C1C=CC2=CN=C(NC3=CC=C(OCCN)C=C3)N=C2N1C4C(C5)CCC5C4		
Formula	$C_{22}H_{25}N_5O_2$	M.Wt	391.47
Solubility	DMSO : 83.3 mg/mL (212.79 mM)	Storage	Store at -20°C
General tips	For obtaining a higher solubility , please warm the tube at 37 °C and shake it in the ultrasonic bath for a while.Stock solution can be stored below -20°C for several months.		
Shipping Condition	Evaluation sample solution : ship with blue ice All other available size: ship with RT , or blue ice upon request.		

Structure



Protocol

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Kinase experiment: Cells are lysed in a volume of 35 to 40 mL per experiment. The protein amounts of the starting extracts used in the first and second experiments are: 435S, 85 and 120 mg; HCT116, 240 and 175 mg; MV4-11, 180 and 120 mg. Lysates are adjusted to 1 M NaCl prior to loading onto the VI 16832 column at a flow rate of 0.07 mL/min. Subsequent washing and elution steps are performed. Protein-containing elution fractions are lyophilized, resuspended in one tenth of the initial volume, and then desalted by protein precipitation prior to gel electrophoresis[2].

References:

[1]. Kyla. A. L. Collins, et al. Proteomic Analysis Defines Kinase Taxonomies Specific for Subtypes of Breast Cancer. Apr. 1, 2017.
[2]. Felix S. Oppermann, et al. Large-scale Proteomics Analysis of the Human Kinome. Mol Cell Proteomics. 2009 Jul; 8(7): 1751-1764.

Background

VI 16832 is a broad spectrum Type I kinase inhibitor which can be used as an enrichment tool for the comparative expression analysis of protein kinases in different cancer cell lines.

VI 16832 is a broad spectrum Type I kinase inhibitor[1]. Phosphoproteomics analysis of VI 16832-enriched fractions from MV4-11, HCT116, or 435S cells results in more than 8500 phosphopeptide identifications. These translate into almost 1700 distinct phosphopeptide species derived from 212 different members of the protein kinase superfamily. Analysis of VI 16832-retained proteins from the three cancer cell lines considerably increases the overall number of identified phosphorylation sites on protein kinases. Considering the sum of all phosphopeptide intensities as a measure for VI 16832-enriched protein amount, more than 80% is derived from protein kinases[2].

[1]. Kyla. A. L. Collins, et al. Proteomic Analysis Defines Kinase Taxonomies Specific for Subtypes of Breast Cancer. Apr. 1, 2017. [2]. Felix S. Oppermann, et al. Large-scale Proteomics Analysis of the Human Kinome. Mol Cell Proteomics. 2009 Jul; 8(7): 1751-1764.

Caution: Product has not been fully validated for medical applications. For research use only.
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