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Product datasheet for PH311488

KCNIP4 (NM_025221) Human Mass Spec Standard

Product data:

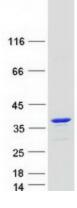
Nescription:KCNIP4 MS Standard C13 and N15-labeled recombinant protein (NP_079497)Species:HumanSpecies:HEK293Expression cDNA ClossRC211488Predicted MW:SA SbaPredicted MW:SRC211488 representing ML_025221 Red=Closing site Green=Tags(s)Protein Sequence:NWRRVESISAQLEEASSTGGFLYAQNSTKRSIKERLMKLLPCSAKTSSPAIQNSVEDELEMATVRHRP Red=Closing site Green=Tags(s)Red=Closing site Green=Tags(s)NWRRVESISAQLEEASSTGGFLYAQNSTKRSIKERLMKLLPCSAKTSSPAIQNSVEDELEMATVRHRP Red=Closing site Green=Tags(s)Tag:CMyc/DDKTag:CMyc/DDKProtein Sequence:Stalledastring VLQCSCTMAGETSERLIMKLPCSAKTSSPAIQNSVEDELEMATVRHRP Red=Closing site Green=Tags(s)Tag:CMyc/DDKTag:CMyc/DDKPartelStalledastring VLQCSCTMAGETSERLIMKLPCSAKTSSPAIQNSVEDELEMATVRHRP EXELLEAQSKTRKKELQILVRGRKMCQCYUPELEQAMDTUNKGCTYPVLKEDAPRQIVE EXELLEAGSKTRKELQILVRGRKMCQCYUPELEQADDTUNKGCTYPVLKEDAPRQIVE EXELLEAGSKTRKELQILVRGRKMCQCYUPELEQADDTUNKGCTYPVLKEDAPRQIVE EXELLEAGSKTRKELQILVRGRKMCQCYUPELEQADDTUNKGCTYPVLKEDAPRQIVE EXELLEAGSKTRKELQILVRGRKMCQCYUPELEQADDTUNKGCTYPVLKEDAPRQIVE EXELLEAGSKTRKELQILVRGRKMCQCYUPELEQADDTUNKGCTYPVLKEDAPRQIVE EXELLEAGSKTRKELQILVRGRKMCQCYUPELEQADDTUNKGCTYPVLKEDAPRQIVE EXELLEAGSKTRKELQILVRGRKMCQCYUPELEQADDTUNKGCTYPVLKEDAPRQUVE EXELLEAGSKTRKELQILVRGRKMCQCYUPELEQADDTUNKGCTYPVLKEDAPRQUVE EXELLEAGSKTRKELQILVRGRKMCQCYUPELEQADDTUNKGCTYPVLKEDAPRQUVE EXELLEAGSKTRKELQILVRGRKMCQCYUPELEQADDTUNKGCTYPVLKEDAPRQUVE EXELLEAGSKTRKELQILVRGRKMCQCYUPELEQADDTUNKGCTYPVLKEDAPRQUVE EXELLEAGSKTRKELQILVRGRKMCQCYUPELEQADDTUNKGCTYPVLKEDAPRQUVE EXELLEAGSKTRKELQILVRGRKMCQCYUPELEQADDTUNKGCTYPVLKEDAPRQUVE EXELLEAGSTRKELQILVRGRKMCQUPACTUNKGCTYPVLKEDAPRQUVE EXELL	Product Type:	Mass Spec Standards
Expression Host:HEK293Expression CDNA CloopRC211488Predicted MW:28.5 kDaProtein Sequence:RC211488 representing NL_025221 Red=Cloning site Green=Tags(s)Protein Sequence:RRC211488 representing NL_025221 Red=Cloning site Green=Tags(s)WWRRVESISADLEEASSTGFLYANPISTKRSIKELHKLLPCSAAKTSSPAIONSVEDELEMATVRHRP EALELEASSET KELLIVEOSAVKETSKELTKELTSSOFFPOGDSTTVAHFLFNAFDTDHNGAV SFEDFIKGLSILLRGSVETKELDUXKORTVPVLKEDAPRQHVE TFFQMMKKDDVVTDEFIESCQKDENIMRSWQLFENVITag:OMVC/DDKPurity:>80% as determined by SDS-PAGE and Coomassie blue stainingConcentration:>0.05 µg/µL as determined by microplate BCA methodIabeling Method:Labeled with [U-13C6, 15N4]-LArginine and [U-13C6, 15N2]-LeysineBuffer:0.05 µg/µL as determined by microplate BCA methodStorage:Stora et -80°C. Avoid repeated freeze-thaw cycles.Storage:Stora et -80°C. Avoid repeated freeze-thaw cycles.FafseqNP 079497Refseq ORF:50Storage:StofStorage:StofStorage:StofStorage:StofStorage:StofStorage:StofStorage:StofStorage:StofStorage:StofStorage:StofStorage:StofStorage:StofStorage:StofStorage:StofStorage:StofStorage:StofStorage:StofStorage:StofStorage:StofStorag	Description:	KCNIP4 MS Standard C13 and N15-labeled recombinant protein (NP_079497)
Presistion cDNA CloneRC211488Predicted MW:28.5 kDaProtein Sequence:RC211488 representing NM_025221 Red=Cloning site Green=Tags(s)Protein Sequence:NVNRRVESISAQLEEASSTGGFLYAQNSTKRSIKERLMKLLPCSAKTSSPAIQNSVEDELEMATVRHRP SEDFITKGLSILLEAQSKTTKKELQILYRGFKNECPSGVNKEETFKEIYSOFFPQGDSTTYAHFLFNAFDTDINGAV SSFPOFTKGLSILLEAQSKTTKKELQILYNGFKNECPSGVNKEETKEIYSOFFPQGDSTTYAHFLFNAFDTDINGAV SSFPOFTKGLSILLEAQSKTTKKELQILYNGFKNECPSGVNKEETKEIYSOFFPQGDSTTYAHFLFNAFDTDINGAV SSFPOFTKGLSILLEAQSKTTKKELDILWKDDDDKVTarrPLEQKLISEEDLAANDILDYKDDDDKVTATRPLEQKLISEEDLAANDILOYKDDDDKVFag:C-Myc/DDKPurity:>80% as determined by SDS-PAGE and Coomassie blue stainingConcentration:>0.05 µg/µL as determined by microplate BCA methodBuffer:>0.05 µg/µL as determined by microplate BCA methodBuffer:>15 mM Tris-HCI, 100 mM glycine, pH 7.3Storage:>15 con Arsoft Avoid repeated freeze-thaw cycles.RefSeq Rize:>156RefSeq ORF:>50Applese>50Ap	Species:	Human
or AA Sequence:Predicted MW:28.5 kDaProtein Sequence:Rc211488 representing NM_025221 Red-Cloning site Green=Tags(s)NVVRRVESISAQLEEASSTGGFLYAQNSTKRSIKERLMKLLPCSAKTSSPAIQNSVEDELEMATVRHRP FALELLEAQSKTYKKL01LYRGFKNECPSGVNWEETFKEIYSOFFPQGDSTTYAHFLFNAFDTDINGAV SFEDFLKGLSILLEAQSKTYKKL01LYNDTMKDGTVRKENLDINKAIYDMMGKCTYPVLKEDAPRQHVE SFEDFLKGLSILLEAQSKTYKKL01LYNDTMKDGTVFUKENLDINKAIYDMMGKCTYPVLKEDAPRQHVE SFEDFLKGLSILLEAQSKTYKKL01LYNDTMKDGTVFUKENLDINKAIYDMMGKCTYPVLKEDAPRQHVE SFEDFLKGLSILLEAQSKTYKKL01LYNDTMKDGTVFUKENLDINKAIYDMMGKCTYPVLKEDAPRQHVE SFEDFLKGLSILLEAQSKTYKKL01LYNDTMKDGTVFUKENLDINKAIYDMMGKCTYPVLKEDAPRQHVE SFEDFLKGLSILLEAQSKTYKKL01LYNDTMKDGTVFUKENLDINKAIYDMMGKCTYPVLKEDAPRQHVE SFEDFLKGLSILLEAQSKTYKKL01LYNDTMKDGTVFUKENLDINKAIYDMMGKCTYPVLKEDAPRQHVE SFEDFLKGLSILLEAQSKTYKKL01LYNDTMKDGTVFUKENLDINKAIYDMMGKCTYPVLKEDAPRQHVE SFEDFLKGLSILLEAQSKTYKKL01LYNDTMKDGTVFUKENLDINKAIYDMMGKCTYPVLKEDAPRQHVE SFEDFLKGLSILLEAQSKTYKKL01LYNDTMKDGTVFUKENLDINKAIYDMMGKCTYPVLKEDAPRQHVE SFEDFLKGLSILLEAQSKTYKKL01LYNDTMKDGTVFUKENLDINKAIYDMMGKCTYPVLKEDAPRQHVE SFEDFLKGLSILLEAQSKTYKKL01LYNDTMKDGTVFUKENLDINKAIYDMMGKCTYPVLKEDAPRQHVE SFEDFLKGLSILLEAQSKTYKKL01LYNDTMKDGTVFUKENLDINKAIYDMMGKCTYPVLKEDAPRQHVE SFEDFLKGLSILLEAQSKTYKKL01LYNDTMKDGTVFUKENLDINKAIYDMMGKCTYPVLKEDAPRQHVE SFEDFLKGLSILLAQSKTYKLGLILTAGTVELNINGAUTON SEDFLSILLAQSKTYKLILTAGTVELNINGAUTON SEDFLSILLAQSKTYKLILTAGTVELNINGAUTON SEDFLSILLAQSKTYKLILTAGTVELNINGAUTON SEDFLSILLAQSKTYPLKENDINGAUTON SEDFLSILLAQSKTYPLKENDINGAUTON SEDFLSILLAQSKTYPLKENDINGAUTON SEDFLSILLAQSKTYPLKENDINGAUTON SEDFLSILLAQSKTYPLKENDINGAUTON SEDFLSILLAQSKTYPLKENDINGAUTON SEDFLSILLAQSKTYPLKENDINGAUTON SEDFLSILLAQSKTYPLKENDINGAUTON SEDFLSILLAQSKTYPLKENDINGAUTON SEDFLSILLAQSKTYPLKENDINGAUTON SEDFLSILLAQSKTYPLKENDINGAUTON SEDFLSILLAQSKTYPLKENDINGAUTON SEDFLSILLAQSKTYPLKENDINGAUTON SEDFLSILLANDSKTYPLKENDINGAUTON <td>Expression Host:</td> <td>HEK293</td>	Expression Host:	HEK293
Protein Sequence:Rc211488 representing NM_025221 Red=Cloning site Green=Tags(s)Red=Cloning site Green=Tags(s)WNVRVESISAQLEEASSTGGFLYAQNSTKRSIKERLMKLLPCSAAKTSSPAIQNSVEDELEMATVRHRP EALELLEAQSKFTKKELQILYRGFKNECPSGVVNEETFKEIYSQFFPQGDSTTYAHFLFNAFDTDHNGAV SFEDFIKGLSILLRGTVQEKLNWAFNLYDINNDGYTIKEEMLDIMKAIYDMMGKCTYPVLKEDAPRQHVE 	•	RC211488
Red=Cloning site Green=Tags(s)MNVRRVESISAQLEEASSTGGFLYAQNSTKRSIKERLMKLLPCSAAKTSSPAIQNSVEDELEMATVRHRP EALELLEAQSKFTKKELQILVRGFKNECPSGVVNEETFKEIVSQFFPQGDSTTYAHFLFNAFDTDHNGAV SFEDFIKGLSILLRGTVQEKLNWAFNLYDINKDGVITKEEMLDIMKAIYDMMGKCTYPVLKEDAPRQHVE TFFQKMDKNKDGVVTIDEFIESCQKDENIMRSMQLFENVITag:C-Myc/DDKPurity:> 80% as determined by SDS-PAGE and Coomassie blue stainingConcentration:> 0.05 µg/µL as determined by microplate BCA methodLabeling Method:Labeled with [U- 13C6, 15N4]-L-Arginine and [U- 13C6, 15N2]-L-LysineBuffer:25 mM Tris-HCl, 100 mM glycine, pH 7.3Storage:Store at -80°C. Avoid repeated freeze-thaw cycles.Stability:Stable for 3 months from receipt of products under proper storage and handling conditions.RefSeq:NP 079497RefSeq ORF:750Synonyms:CALP; KCHIP4Locus ID:80333	Predicted MW:	28.5 kDa
ALELLEAQSKFTKKELQILYRGFKNECPSGVVNEETFKEIYSQFFPQGDSTTYAHFLFNAFDTDHNGAV SFEDFIKGLSILLRGTVQEKLNWAFNLYDINKDGVITKEEMLDIMKAIYDMMGKCTYPVLKEDAPRQHVE TFFQKMDKNKDGVYTIDEFIESCQKDENIMRSMQLFENVITRTRPLEQKLISEEDLAANDILDYKDDDDKVTag:C-Myc/DDKPurity:S80% as determined by SDS-PAGE and Coomassie blue stainingConcentration:>0.05 µg/µL as determined by microplate BCA methodLabeling Method:Labeled with [U-13C6, 15N4]-L-Arginine and [U-13C6, 15N2]-L-LysineBuffer:25 mM Tris-HCl, 100 mM glycine, pH 7.3Storage:Store at -80°C. Avoid repeated freeze-thaw cycles.Stability:Stable for 3 months from receipt of products under proper storage and handling conditions.RefSeq Size:1556RefSeq ORF:750Synonyms:CALP; KCHIP4Locus ID:8033	Protein Sequence:	
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Labeling Method:Labeled with [U-13C6, 15N4]-L-Arginine and [U-13C6, 15N2]-L-LysineBuffer:25 mM Tris-HCl, 100 mM glycine, pH 7.3Storage:Store at -80°C. Avoid repeated freeze-thaw cycles.Stability:Stable for 3 months from receipt of products under proper storage and handling conditions.RefSeq:NP 079497RefSeq Size:1556RefSeq ORF:750Synonyms:CALP; KCHIP4Locus ID:80333	Purity:	> 80% as determined by SDS-PAGE and Coomassie blue staining
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Synonyms: CALP; KCHIP4 Locus ID: 80333	RefSeq Size:	1556
Locus ID: 80333	RefSeq ORF:	750
	Synonyms:	CALP; KCHIP4
UniProt ID: <u>Q6PIL6</u>	Locus ID:	80333
	UniProt ID:	<u>Q6PIL6</u>



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	KCNIP4 (NM_025221) Human Mass Spec Standard – PH311488
Cytogenetics:	4p15.31-p15.2
Summary:	This gene encodes a member of the family of voltage-gated potassium (Kv) channel- interacting proteins (KCNIPs), which belong to the recoverin branch of the EF-hand superfamily. Members of the KCNIP family are small calcium binding proteins. They all have EF-hand-like domains, and differ from each other in the N-terminus. They are integral subunit components of native Kv4 channel complexes. They may regulate A-type currents, and hence neuronal excitability, in response to changes in intracellular calcium. This protein member also interacts with presenilin. Multiple alternatively spliced transcript variants encoding distinct isoforms have been identified for this gene. [provided by RefSeq, Jul 2008]
Protein Families	: Druggable Genome, Ion Channels: Other

Product images:



Coomassie blue staining of purified KCNIP4 protein (Cat# [TP311488]). The protein was produced from HEK293T cells transfected with KCNIP4 cDNA clone (Cat# [RC211488]) using MegaTran 2.0 (Cat# [TT210002]).

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