

Figure S1

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1 50
HIPK1_Hs (1) -----MASQLQVFSP--PSVSSSAFCSAKKLEEPS-GWDVSGQSSND
HIPK1_Mm (1) -----MASQLQVFSP--PSVSSSAFCSAKKLEEPS-GWDVSGQSSND
HIPK1_Gg (1) -----MASQLQVFSP--PSVSSSAFCSAKKLEEPS-VWDVSGQSSSD
HIPK1_Xt (1) -----MASQLQVFSP--SSVSSSAFCSAKKLEEPS-GWDVTGQGSSN
HIPK1_X1 (1) -----MASQLQVFSP--SSVSSSAFYSAKKLEEPS-GWDVTGQGSSS
HIPK2_Hs (1) MAPVYEGMASHVQVFSP--HTLQSSAFCSVKKLEEPSNNDMTGYGSHS
HIPK2_Mm (1) MAPVYEGMASHVQVFSP--HTLQSSAFCSVKKLEEPSNNDMTGYGSHS
HIPK2_Gg (1) -----MASHVQVFSP--HTLQSSAFCSVKKLEEPSNNDMTGYGTHS
HIPK2_Xt (1) -----MASHLQIFSS--HGLPLRTFCKVKKPKLELSPGWDMTGYGCHS
HIPK3_Hs (1) -----MASQVLVYPPYVYQTQSSAFCSVKKLEEPS--SCVFQERNYP
HIPK3_Mm (1) -----MASQVLVYPPYVYQTQSSAFCSVKKLEEPS--GCVFQERTYP
HIPK3_Gg (1) -----MASQVLVYPPYVYQTQSSAFCSVKKLEEPS--SCVYHERAYP
HIPK3_Xt (1) -----MASQVLVYPPYVYQTQSSAFCSIKKLEEPS--SCLYNKRSYQ

51 100
HIPK1_Hs (41) KYYTHSKTLPATQGGQANSSHQ---VANFNIPAYDQGLLLPAPAVEHIVVT
HIPK1_Mm (41) KYYTHSKTLPATQGGQASSHQ---VANFNLPAYDQGLLLPAPAVEHIVVT
HIPK1_Gg (41) KYYTHSKNLPAAQGGQASSHQ---VANFSVPAYDQNLLLPAPSVEHIVVT
HIPK1_Xt (41) KYYTHTKNLPVAQGHASSHQ---VAGFSLPAYEPNLLIPAAAAEHIVVT
HIPK1_X1 (41) KYYTR--NLPVAQGHASSRQ---VVGFSLPAYEPNLLIPAAAAEHIVVT
HIPK2_Hs (49) KVYSQSKNIPLS-QPATTTVSTSLPVPNPSLPYEQTIVFPSTGHIVVTS
HIPK2_Mm (49) KVYSQSKNIPPS-QPASTTVSTSLPIPNSLPYEQTIIFFPGSTGHIVVTS
HIPK2_Gg (42) KVYSQSKSVQSSQAAAAAVNASLQIPNPSIPIYEQTIIFFPASTGHIVVTS
HIPK2_Xt (42) KVVNSGKNSSTS-----GQP-VLSHASLLQSYEQTVIFPSTAGHIVVTS
HIPK3_Hs (42) RTYVNGRNFNGNSHPPTKG-SAFQTKIPFNRPRGHNFSLQTSAVVLKNTAG
HIPK3_Mm (42) QIHVNGRNFNGNSHPSTKG-SAFQTNIPFTKPRGHSFSLQAGAIIVKDTAG
HIPK3_Gg (42) QIYVNGKNFG-ISPFRVS-TFLQTKNPFDRPRGQNVLLQSNVAALKNIAG
HIPK3_Xt (42) RTDLNARSIGFAQPSNKNRAPFQTKNTSDKPRHQAAVSKTSPVTLTNTGT

101 150
HIPK1_Hs (88) AADSSG--SAATSTFQSS-QTLTHRSNVSLLEPYQKCGLKRKSEEVDS-N
HIPK1_Mm (88) AADSSG--SAATATFQSS-QTLTHRSNVSLLEPYQKCGLKRKSEEVES-N
HIPK1_Gg (88) AADSTG--SSATASFQNS-QTLTHRTNLSLLEPYQKCGLKRKSEEVDS-N
HIPK1_Xt (88) AADSTD--SGPTTSFQNS-QILTHRSNVPLLDPYQKCGLKRKSEEVDS-N
HIPK1_X1 (86) AADSTD--SGPTTSFQNS-QILTHRSNVPLLDPYQKCGLKRKSEEVDS-N
HIPK2_Hs (98) ASSTS----VTGQVLGGP-HNLMRRSTVSLLDTYQKCGLKRKSEEIEN-T
HIPK2_Mm (98) ASSTS----VTGQVLGGP-HNLMRRSTVSLLDTYQKCGLKRKSEEIEN-T
HIPK2_Gg (92) ANSTSGVVAVSGQTLGGP-HNLMRRSTVSLLDTYQKCGLKRKSEEIEN-T
HIPK2_Xt (85) SSNGSS--AATGQALGGPQTNLMRRSTVSLLDTYQKCGLKRKCEELEN-N
HIPK3_Hs (91) ATKVIAAQAQQAHVQAPQ--IGAWRNRLHFLEGPQRCGLKRKSEELD NHS
HIPK3_Mm (91) ATKVIAAQAQQAQVEAPR--AVVWRNRLHFLEGPQRCGLKRKSEELENHS
HIPK3_Gg (90) ATKALAAQAQQAQLEAPR--SGTQGSRADILEGPQRCGLKRKSEELD NHS
HIPK3_Xt (92) ASGDLAAQAQQDPKEELT--VGTPESGSDDLDAHQRCGLKRKSKDFENQN

151 200
HIPK1_Hs (134) GSVQIIIEHPPMLQNRVVGAAATTTT VTTK--SSSSSGEGDYQLVQHE
HIPK1_Mm (134) GSVQIIIEHPPMLQNRVVGAAATTTT VTTK--SSSSSGEGDYQLVQHE
HIPK1_Gg (134) GSVQIIIEHPPMLQNRPAVGAATTTT VTTK--SSNSSGEGDYQLVQHE
HIPK1_Xt (134) GSVQIIDERPPLMLQNRVVGAAATTTT VTTK--SSSSNGEGDYQLVQHE
HIPK1_X1 (132) GSVQIIDERPPLMLQNRVVGAAATTTT VTTK--SSSSSGG DYQLVQHE
HIPK2_Hs (142) SSVQIIIEHPPMIQNNASGATVATATTSTATSK-NSGSNSEGDYQLVQHE
HIPK2_Mm (142) SSVQIIIEHPPMIQNNASGATVATATTSTATSK-NSGSNSEGDYQLVQHE
HIPK2_Gg (140) SSVQIIIEHPPMIQNNASGATVATATTSTATSK-NSGSNSEGDYQLVQHE
HIPK2_Xt (132) SSVQIVDEHPPVTQNNASGATAATTSTATSK--NSGSNSEGDYQLVQHE
HIPK3_Hs (139) SAMQIVDELSILPAMLQTNMGNPVTVVTTATTGSKQNC TTGEGDYQLVQHE
HIPK3_Mm (139) GAMQIVDELSILPAMLQTNMGNPVTVVTTATTGSKQNC TTGEGDYQLVQHE
HIPK3_Gg (138) STMQIVDELSILPAMLQTNVGNPVTVVTTAATSKQTGTSGDGDYQLVQHE
HIPK3_Xt (140) GTMQIVDELSILPAML PNNAANQVTVVATTGT SKQSTASGDGDYQLMLHE
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ATP-binding/ Kinase Domain → 250

	201		250
HIPK1_Hs	(182)	ILCSMTNSYEVL EFL GRGTFGQVAKC WKRSTKEIVAIK ILKNHPSYARQG	
HIPK1_Mm	(182)	ILCSMTNSYEVL EFL GRGTFGQVAKC WKRSTKEIVAIK ILKNHPSYARQG	
HIPK1_Gg	(182)	ILCSMTNSYEVL EFL GRGTFGQVAKC WKRSTKEIVAIK ILKNHPSYARQG	
HIPK1_Xt	(182)	ILCSMTNSYEVL EFL GRGTFGQVAKC WKRSTKEIVAIK ILKNHPSYARQG	
HIPK1_X1	(180)	ILCSMTNSYEVLEFLGRGTFGQVAKCWKRSTKEIVAIKILKNHPSYARQG	
HIPK2_Hs	(191)	VLCSMTNTYEVL EFL GRGTFGQVVKC WKRGTNEIVAIK ILKNHPSYARQG	
HIPK2_Mm	(191)	VLCSMTNTYEVL EFL GRGTFGQVVKC WKRGTNEIVAIK ILKNHPSYARQG	
HIPK2_Gg	(189)	VLCSMTNTYEVL EFL GRGTFGQVVKC WKRGTNEIVAIK ILKNHPSYARQG	
HIPK2_Xt	(179)	VLCSMTNTYEVL EFL GRGTFGQVVKC WKRGTNEIVAIK ILKNHPSYARQG	
HIPK3_Hs	(189)	VLCSMKNTYEVL DFL GRGTFGQVVKC WKRGTNEIVAIK ILKNHPSYARQG	
HIPK3_Mm	(189)	VLCSMKNTYEVL DFL GRGTFGQVVKC WKRGTNEIVAIK ILKNHPSYARQG	
HIPK3_Gg	(188)	VLCSVKNTYEVL DFL GRGTFGQVVKC WKRGTNEIVAIK ILKNHPSYARQG	
HIPK3_Xt	(190)	VLCSVKNTYEVL DFL GRGTFGQVVKC WRRGTNEVVAVK ILKNHPSYARQG	

	251		300
HIPK1_Hs	(232)	QIEVSI L SRLSSENADEYNFVRSYECFQHK NHT CLVFEMLEQNL YDFL KQ	
HIPK1_Mm	(232)	QIEVSI L SRLSSENADEYNFVRSYECFQHK NHT CLVFEMLEQNL YDFL KQ	
HIPK1_Gg	(232)	QIEVSI L SRLSSENADEYNFVRSYECFQHK NHT CLVFEMLEQNL YDFL KQ	
HIPK1_Xt	(232)	QIEVSI L SRLSSENADEYNFVRSYECFQHK NHT CLVFEMLEQNL YDFL KQ	
HIPK1_X1	(230)	QIEVSILSRLSSENADEYNFVRSYECFQHKNHTCLVFEMLEQNLYDFLKQ	
HIPK2_Hs	(241)	QIEVSI L ARLSTESAD D YNFVRAYECFQHK NHT CLVFEMLEQNL YDFL KQ	
HIPK2_Mm	(241)	QIEVSI L ARLSTESAD D YNFVRAYECFQHK NHT CLVFEMLEQNL YDFL KQ	
HIPK2_Gg	(239)	QIEVSI L ARLSTESAD D YNFVRAYECFQHK NHT CLVFEMLEQNL YDFL KQ	
HIPK2_Xt	(229)	QIEVSI L ARLSTESAD D YNFVRAYECFQHK NHT CLVFEMLEQNL YDFL KQ	
HIPK3_Hs	(239)	QIEVSI L ARLSTENADEYNFVRAYECFQHR NHT CLVFEMLEQNL YDFL KQ	
HIPK3_Mm	(239)	QIEVSI L ARLSTENADEYNFVRAYECFQHR NHT CLVFEMLEQNL YDFL KQ	
HIPK3_Gg	(238)	QIEVSI L ARLSTENADEFNFVRAYECFQHR NHT CLVFEMLEQNL YDFL KQ	
HIPK3_Xt	(240)	QIE M GILARLSNENADEFNFVRAYECFQHR NHT CLVFEMLEQNL YDFL KQ	

	301		350
HIPK1_Hs	(282)	NKFSPLPLKYIRPILQQVATALMKL K SLGLIHADL K PENIMLVDPVRQPY	
HIPK1_Mm	(282)	NKFSPLPLKYIRPILQQVATALMKL K SLGLIHADL K PENIMLVDPVRQPY	
HIPK1_Gg	(282)	NKFSPLPLKYIRPILQQVATALMKL K SLGLIHADL K PENIMLVDPARQPY	
HIPK1_Xt	(282)	NKFSPLPLKYIRPILQQVATALMKL K SLGLIHADL K PENIMLVDPVRQPY	
HIPK1_X1	(280)	NKFSPLPLKYIRPILQQVATALMKLKSLGLIHADLKPENIMLVDPVRQPY	
HIPK2_Hs	(291)	NKFSPLPLKYIRPVLQQVATALMKL K SLGLIHADL K PENIMLVDP S RQPY	
HIPK2_Mm	(291)	NKFSPLPLKYIRPVLQQVATALMKL K SLGLIHADL K PENIMLVDP S RQPY	
HIPK2_Gg	(289)	NKFSPLPLKYIRPILQQVATALMKL K SLGLIHADL K PENIMLVDP S RQPY	
HIPK2_Xt	(279)	NKFSPLPLKYIRPVLQQVGTALMKL K SLGLIHADL K PENIMLVDP S RQPY	
HIPK3_Hs	(289)	NKFSPLPLKVIRPILQQVATALK K L K SLGLIHADL K PENIMLVDPVRQPY	
HIPK3_Mm	(289)	NKFSPLPLKVIRPVLQQVATALK K L K SLGLIHADL K PENIMLVDPVRQPY	
HIPK3_Gg	(288)	NKFSPLQ L KVIRPILQQVATALK K L K SLGLIHADL K PENIMLVDPVRQPY	
HIPK3_Xt	(290)	NKFSPLPLKVIRAILQQVATALK K L K SLGLIHADL K PENIMLVDPVRQPY	

	351		400
HIPK1_Hs	(332)	RVKVIDFGSASHVSKAVCSTYLQSRYYRAPEIILGLPFCEAIDMWSL G CV	
HIPK1_Mm	(332)	RVKVIDFGSASHVSKAVCSTYLQSRYYRAPEIILGLPFCEAIDMWSL G CV	
HIPK1_Gg	(332)	RVKVIDFGSASHVSKAVCSTYLQSRYYRAPEIILGLPFCEAIDMWSL G CV	
HIPK1_Xt	(332)	RVKVIDFGSASHVSKAVCSTYLQSRYYRAPEIILGLPFCEAIDMWSL G CV	
HIPK1_X1	(330)	RMKVIDFGSASHVSKAVCSTYLQSRYYRAPEIILGLPFCEAIDMWSLGCV	
HIPK2_Hs	(341)	RVKVIDFGSASHVSKAVCSTYLQSRYYRAPEIILGLPFCEAIDMWSL G CV	
HIPK2_Mm	(341)	RVKVIDFGSASHVSKAVCSTYLQSRYYRAPEIILGLPFCEAIDMWSL G CV	
HIPK2_Gg	(339)	RVKVIDFGSASHVSKAVCSTYLQSRYYRAPEIILGLPFCEAIDMWSL G CV	
HIPK2_Xt	(329)	RVKVIDFGSASHVSKAVCSTYLQSRYYRAPEIILGLPFCEAIDMWSL G CV	
HIPK3_Hs	(339)	RVKVIDFGSASHVSKTVCSTYLQSRYYRAPEIILGLPFCEAIDMWSL G CV	
HIPK3_Mm	(339)	RVKVIDFGSASHVSKTVCSTYLQSRYYRAPEIILGLPFCEAIDMWSL G CV	
HIPK3_Gg	(338)	RVKVIDFGSASHVSKTICSTYLQSRYYRAPEIILGLPFCEAIDMWSL G CV	
HIPK3_Xt	(340)	RVKVIDFGSASYVSKTVCSTYLQSRYYRAPEVILGLPFCEAIDMWSL G CV	

401 450
HIPK1_Hs (382) IAELFLGWPLYPGASEYDQIRYISQTQGLPAEYLLSAGTKTTRFFNRDPN
HIPK1_Mm (382) IAELFLGWPLYPGASEYDQIRYISQTQGLPAEYLLSAGTKTTRFFNRDPN
HIPK1_Gg (382) IAELFLGWPLYPGASEYDQIRYISQTQGLPAEYLLSAGTKTSRFFNRDPN
HIPK1_Xt (382) IAELFLGWPLYPGASEYDQIRYISQTQGLPAEYLLSAGTKTSRFFNRDPD
HIPK1_X1 (380) **IAELFLGWPLYPGASEYDQIRYISQTQGLPAEYLLSAGTKTSRFFNRDPD**
HIPK2_Hs (391) IAELFLGWPLYPGASEYDQIRYISQTQGLPAEYLLSAGTKTTRFFNRDTD
HIPK2_Mm (391) IAELFLGWPLYPGASEYDQIRYISQTQGLPAEYLLSAGTKTTRFFNRDTD
HIPK2_Gg (389) IAELFLGWPLYPGASEYDQIRYISQTQGLPAEYLLSAGTKTTRFFNRDTD
HIPK2_Xt (379) IAELFLGWPLYPGASEYDQIRYISQTQGLPAEYLLSSGKTKTTRFFNRDGD
HIPK3_Hs (389) IAELFLGWPLYPGALEYDQIRYISQTQGLPGEQLLNVTGKSTRFFCKETD
HIPK3_Mm (389) IAELFLGWPLYPGALEYDQIRYISQTQGLPGEQLLNVTGKSTRFFCRETD
HIPK3_Gg (388) IAELFLGWPLYPGALEYDQIRYISQTQGLPGEQLLSMGTKTARFFCRETD
HIPK3_Xt (390) IAELFLGWPLYPGAQYDQIRYISQTQGLPGDSLINAGTKTSRFFCREPD

451 500
HIPK1_Hs (432) LGYPLWRLKTPEEHELETGIKSKEARKYIFNCLDDMAQVNMSTDLEGTDM
HIPK1_Mm (432) LGYPLWRLKTPEEHELETGIKSKEARKYIFNCLDDMAQVNMSTDLEGTDM
HIPK1_Gg (432) LGYPLWRLKTPDEHEMETGIKSKEARKYIFNCLDDMAQVNMSTDLEGTDM
HIPK1_Xt (432) LGYPLWRLKAPDEHEMETGIKSKEARKYIFNCLDDMAQVNMSTDLEGTDM
HIPK1_X1 (430) **LGYPWRLKAPDEHEVETGIKSKEARKYIFNCLDDMAQVNMSTDLEGTDM**
HIPK2_Hs (441) SPYPLWRLKTPDDHEAETGIKSKEARKYIFNCLDDMAQVNMSTDLEGSMD
HIPK2_Mm (441) SPYPLWRLKTPDDHEAETGIKSKEARKYIFNCLDDMAQVNMSTDLEGSMD
HIPK2_Gg (439) SPYPLWRLKTPDDHEAETGIKSKEARKYIFNCLDDMAQVNMSTDLEGSMD
HIPK2_Xt (429) SPYPLWRLKTPEDHENETGIKSKEARKYIFNCLDDMAQVNMASDLEGSMD
HIPK3_Hs (439) MSHSGWRLKTL EEHEAETGMKSKEARKYIFNSLDDVAHVNTVM DLEGSDDL
HIPK3_Mm (439) MSHSGWRLKTL EEHEAETGMKSKEARKYIFNSLDDIVHVNTVM DLEGGDDL
HIPK3_Gg (438) APYSSWRLKTL EEHEAETGMKSKEARKYIFNSLDDIVHVNMVM DLEGSDDL
HIPK3_Xt (440) APYPSWRLKTL EEHEAETGIKSKEARKYIFNNLDEIVHVNMV DLDGSDDL

501 ← Kinase Domain 550
HIPK1_Hs (482) LAEKADRREYIDLLKKMLTIDADKRITPLKTLNHQFVTMTHLLDFPHSNH
HIPK1_Mm (482) LAEKADRREYIDLLKKMLTIDADKRITPLKTLNHQFVTMTHLLDFPHSSH
HIPK1_Gg (482) LAEKADRREYIDLLKKMLTIDADKRITPLKTLNHPFVTMTHLLDFPHSNH
HIPK1_Xt (482) LAEKADRREYIDLLKKMLTIDADKRITPLKTLNHPFVTMTHLLDFPHSNH
HIPK1_X1 (480) **LAEKADRREYIDLLKKMLTIDADKRITPLKTLNHPFVTMTHLLDFPHSNH**
HIPK2_Hs (491) LVEKADRREFIDLLKKMLTIDADKRITPIETLNHPFVTMTHLLDFPHSTH
HIPK2_Mm (491) LVEKADRREFIDLLKKMLTIDADKRITPIETLNHPFVTMTHLLDFPHSAH
HIPK2_Gg (489) LVEKADRREFIDLLKKMLTIDADKRITPIETLNHPFVTMTHLLDFPHSTH
HIPK2_Xt (479) LVEKADRREFIDLLKKMLTIDADKRITPIETLNHPFVTMTHLLDFPHSSH
HIPK3_Hs (489) LAEKADRREFVSLKKMLLIDADLRITPAETLNHPFVNMKHLDFPHSNH
HIPK3_Mm (489) LAEKADRREFVNLKKMLLIDADLRITPIETLNHPFVNMKHLDFPHSNH
HIPK3_Gg (488) LAEKADRREFVSLKKMLLIDADLRITPAETLNHSFVTM KHLDFPHSNQ
HIPK3_Xt (490) MAEKADRREFVALLKKMLMIDADKRISPADTLSQSFITM KHLDFPHSNH

551 Homeodomain-Interacting Domain 600
HIPK1_Hs (532) VKSCFQNM EICKRRVHMYDTVSIKSPFTTHVAPNTSTNLTMSFSNQLNT
HIPK1_Mm (532) VKSCFQNM EICKRRVHMYDTVSIKSPFTTHVAPNTSTNLTMSFSNQLNT
HIPK1_Gg (532) VKSCFQNM EICKRRVHMYDTVSIKSPFTTHVAPNTSTNLTMSFNNQLNT
HIPK1_Xt (532) VKSCFQNM EICKRRSVMYDTVSIKSPFTTHVAPNTSTNLTMSFNNQLNS
HIPK1_X1 (530) **VKSCFQNM EICKRRSVMYDTVSIKSPFTTHVAPNTSTNLTMSFNNQLNS**
HIPK2_Hs (541) VKSCFQNM EICKRRVHMYDTVSIKSPFTTHVAPNTSTNLTMTFNNQLTT
HIPK2_Mm (541) VKSCFQNM EICKRRVHMYDTVSIKSPFTTHVAPNTSTNLTMTFNNQLTT
HIPK2_Gg (539) VKSCFQNM EICKRRVHMYDTVSIKSPFTTHVAPNTSTNLTMTFNNQLNT
HIPK2_Xt (529) VKSCFQNM EICKRRVHMYDTVSIKSPFTTHVAPNTSTNLTMTFNNQLNT
HIPK3_Hs (539) VKSCFHIMDICKSHLNSCDTNNHNKTSLLRPVASSSTATLTANFT-KIGT
HIPK3_Mm (539) VKSCFHIMDICKSPS-SCETNNHSMKSLLRPVASNGTAALANFT-KVGT
HIPK3_Gg (538) VKSCFHIMDVCKCRSNLYDLSNRNKTSLMRPVASGSAANLTASFT-KIGT
HIPK3_Xt (540) VKSCFYIMDVCKARPVNGDTANHNKTSIVRPITSTNIGSMSAGFT-KIGT

		601		650
HIPK1_Hs	(582)	VHNQASV	VLASSSTAAAATLSLANS	VDVSLLNYSALY
HIPK1_Mm	(582)	VHNQASV	VLASSSTAAAATLSLANS	VDVSLLNYSALY
HIPK1_Gg	(582)	VHNQASV	VLASN-STAAAATLSLANS	VDVSLLNYSALY
HIPK1_Xt	(582)	VHNQASV	VLASS-STAAAATLSLANS	VDVSLLNYSALY
HIPK1_X1	(580)	VHNQASV	LASS-STAAAATLSLANS	VDVSLLNYSALY
HIPK2_Hs	(591)	VHN	-----	QPSAASMAAVAQRS
HIPK2_Mm	(591)	VHNQAP	---T---TSSATLSLAN	PEVSILNYSALY
HIPK2_Gg	(589)	VHNQTTN	LAPT---SSSATISLAN	PEVSILNYSALY
HIPK2_Xt	(579)	VHS	-----	QPTAASMAAVAQRT
HIPK3_Hs	(588)	LRSQ	-----	ALTTSAHSVHHG
HIPK3_Mm	(587)	LRSQ	-----	ALTTSAHSVHHG
HIPK3_Gg	(587)	LRSQ	-----	ALTASAHSVHQQ
HIPK3_Xt	(589)	IRGQ	-----	ALTTSGHSVHHG

		651		700
HIPK1_Hs	(632)	VSLQPGTT	QICTQTDPFQQT	FIVCPPAFQTG-LQATTKHSGFPVRMDNAV
HIPK1_Mm	(632)	VSLQPGTT	QICTQTDPFQQT	FIVCPPAFQTG-LQATTKHSGFPVRMDNAV
HIPK1_Gg	(631)	VSLQPGTT	QICTQTDPFQQT	FIVCPPAFQTG-LQATTKHSGFPVRMDNAV
HIPK1_Xt	(631)	VSLQPGTT	QLCTQTDPFQQT	FIVCPPAFQAAGLQATTKHSGFPVRMDNSV
HIPK1_X1	(629)	VSLQPGTT	QLCTQTDPFQQT	FIVCPPAFQAAGLQATTKHSGFPVRMDNSV
HIPK2_Hs	(608)	MPLQTGTA	QICARPDFQALIVC	PPGFQGL-QASPSKHAGYSVRMDNAV
HIPK2_Mm	(635)	MPLQTGTA	QICARPDFQALIVC	PPGFQGL-QASPSKHAGYSVRMDNAV
HIPK2_Gg	(637)	MPLQTGTA	QICARPDFQALIVC	PPGFQGL-QASPSKHAGYSVRMDNAV
HIPK2_Xt	(596)	MPLQTGTA	QLCARPDFQALIVC	PPAFQGL-QTSPSKHGGYSVRMDNAV
HIPK3_Hs	(605)	IPLQAGTA	QFGCG-DAFQOTLI	ICPPAIQGI-PATHGKPTSYSIRVDNTV
HIPK3_Mm	(604)	IPLQAGTA	QFGCG-DAFHQTLI	ICPPAIQGI-PAAHGKPTSYSIRVDNTV
HIPK3_Gg	(604)	IPLQAGTA	QFGCS-DIFQOTLI	ICPPTLQGI-TTNHSGKPTSFSLRVDNAV
HIPK3_Xt	(606)	IPLQAGS	APFGCN-DAFQOTLI	LICPPAIQGM-PPNHGKPTSYSVRVDNAV

		701		750
HIPK1_Hs	(681)	PIVPQAPAA	QPLQIQSGVLTQGS	CTPLMVATLHPQVATITPQYAVPFTLS
HIPK1_Mm	(681)	PIVPQAPAA	QPLQIQSGVLTQGS	CTPLMVATLHPQVATITPQYAVPFTLS
HIPK1_Gg	(680)	PIVPQAPAA	QPLQIQSGVLTQGS	CTPLMVATLHPQVATITPQYAVPFTLN
HIPK1_Xt	(681)	PIVPQAPAA	QPLQIQSGVLTQ	-----
HIPK1_X1	(679)	PIVPQAPAA	QPPQIQSGVLTQ	-----
HIPK2_Hs	(657)	PIVTQAPGA	QPLQIQPGLLAQ	-----
HIPK2_Mm	(684)	PIVTQAPGA	QPLQIQPGLLAQ	-----
HIPK2_Gg	(686)	PIVTQAPGA	QPLQIQPGLLAQ	-----
HIPK2_Xt	(645)	PLVTQTAGA	QALQIQPGLLTQ	-----
HIPK3_Hs	(653)	PLVTQAPAV	QPLQIRPGVLS	-----
HIPK3_Mm	(652)	PLVTQAPAV	QPLQIRPGVLSQ	-----
HIPK3_Gg	(652)	PLVTQAHAI	QPLQIRAGILS	-----
HIPK3_Xt	(654)	PLVTQAPAI	QPLQIRAGVLT	-----

		751		800
HIPK1_Hs	(731)	CAAGR	PALVEQTA	AAVLQAWPGGTQQILLPSTWQQLPGVALHNSVQPTAMI
HIPK1_Mm	(731)	CAAGR	PALVEQTA	AAVLQAWPGGTQQILLPSAWQQLPGVALHNSVQPAAVI
HIPK1_Gg	(730)	CAAGR	PALVEQTA	AAVLQAWPGGTQQILLPSTWQQLPGVALHNSVQPAAVI
HIPK1_Xt	(702)	-----	-----	AWPGGTQQILLPSTWQQLPGVALHNSVQPTAMI
HIPK1_X1	(700)	-----	-----	AWPGGTQQILLPSTWQQLPGVALHNSVQPSAMI
HIPK2_Hs	(678)	-----	-----	QAWPSGTQQILLPPAWQQLTGVATHTSVQHATVI
HIPK2_Mm	(705)	-----	-----	QAWPGGAQQILLPPAWQQLTGVATHTSVQHAIVI
HIPK2_Gg	(707)	-----	-----	QAWPSGTQQILLPPAWQQLTGVATHTSVQHATVI
HIPK2_Xt	(666)	-----	-----	QAWPSGTQQILLPPAWQQLAGVAHTSVQHATVI
HIPK3_Hs	(673)	-----	-----	QTWSGRTQQMLVP-AWQQVTPLAPATTTLTSESV
HIPK3_Mm	(673)	-----	-----	QTWSGRTQQMLIP-AWQQVTPMAPAAATLTSEGM
HIPK3_Gg	(672)	-----	-----	QTWSNHTQQILVP-AWQQVAPVAAPATSLASDPV
HIPK3_Xt	(674)	-----	-----	QAWSNGTQPILVP-AWQQMTTIAPTASSLASDTM

← Homeodomain-Interacting Domain

801

850

HIPK1_Hs	(781)	PEAMGSGQQ	LADWR-NAHSHGNQYSTIMQQPSLLTNHVTLATAQPLNVGV
HIPK1_Mm	(781)	PEAMGSSQQ	LADWR-NAHSHGNQYSTIMQQPSLLTNHVTLATAQPLNVGV
HIPK1_Gg	(780)	PETIGSSQQ	LADWR-NAHSHGNQYSTLMQQPSLLTNHVTLATAQPLNVGV
HIPK1_Xt	(735)	PETIGNNQQL	TDWR-NAHSHGNQYSTLMQQPSLLANHVTLAAAQPLNVGV
HIPK1_X1	(733)	PETIGNNQQL	TDWRNAHSHGNQYSTLMQQPSLLANHVTLAAAQPLNVGV
HIPK2_Hs	(712)	PETMAGTQQ	LADWR-NTHAHGSHYNPIMQQPALLTGHVTLPAQAQPLNVGV
HIPK2_Mm	(739)	PETMAGTQQ	LADWR-NTHAHGSHYNPIMQQPALLTGHVTLPAQAQPLNVGV
HIPK2_Gg	(741)	PESMAGTQP	LADWR-NTHAHGSHYNPIMQQPALLASHVTLPAQAQPVNVGV
HIPK2_Xt	(700)	PDGMAGTQQ	LADWR-NTHAHGTHYNPIMQQPALLTGHVTLPSAQAQPLNVGV
HIPK3_Hs	(706)	AGSH----	RLGDWG-KMISCSNHYNVMPQP-LLTNQITLSAPQPVSVGI
HIPK3_Mm	(706)	AGSQ----	RLGDWG-KMIPHSNHYNVMPPP-LLTNQITLSAPQPI SVGI
HIPK3_Gg	(705)	AGPQ----	RLGDWG-KMITQGTHYNVMPQP-LLTHQITFSAPQPI SVGI
HIPK3_Xt	(707)	AGPQ----	RLGDWG-KVIPHGNYNSMIIQP-IITNQMTLSAPQPI SLGI

851 Dsh-Interacting Region →

900

HIPK1_Hs	(830)	AHVVRQQQSSSLPSKKNKQS	-----APV-SSK-
HIPK1_Mm	(830)	AHVVRQQQSSSLPSKKNKQS	-----APV-SSK-
HIPK1_Gg	(829)	AHVVRQQQSSNVPKKNKQP	-----APSTAN--
HIPK1_Xt	(784)	AHVVRQQQNSNTSTKKNKQQ	-----ASQSSSK-
HIPK1_X1	(783)	AHVVRQQQNSNTSTKKNKQQ	-----ASQKSSK-
HIPK2_Hs	(761)	AHVMRQQPTSTTSSRKSQKH	-----QSSVRNVS
HIPK2_Mm	(788)	AHVMRQQPTSTTSSRKSQKH	-----QSSVRNVS
HIPK2_Gg	(790)	AHVMRQPPAAATSTRKSQKH	-----QSAPRNAS
HIPK2_Xt	(749)	AHVMRQQPTSSSSSSR-KKH	-----HSLARNIS
HIPK3_Hs	(750)	AHVVPQPATTKKNKQCQNRGILVKLMEWEPGREEINAFSWSNSLQNTNI	
HIPK3_Mm	(750)	AHVVPQPATTKKNKLCQNR	-----S-NSLQNTNI
HIPK3_Gg	(749)	AHVVPQPAATKRNLKQNR	-----S-NALQNTNI
HIPK3_Xt	(751)	AHVVPQPAANKRNLKQNR	-----I-NAIQDIVV

901

SRS/PEST 950

HIPK1_Hs	(856)	-----SSLDVLP	SQVYSLVGSSPLRTTSS-----YNSL
HIPK1_Mm	(856)	-----SSLEVL	PSQVYSLVGSSPLRTTSS-----YNSL
HIPK1_Gg	(855)	-----STLET	VPTQVYSLIGSSPLRSTSSS-----SNVL
HIPK1_Xt	(811)	----ALSSLD	VIPSPQVYSLVGSSPLQASSS-----YNPL
HIPK1_X1	(810)	----ALSCLDI	IPSQVYSLVGSSPLQASSS-----YNPL
HIPK2_Hs	(789)	TCEVSSSQAISSP	QRSKRVKENTPPRCAMVHSSPACSTSVTCGWGDVASS
HIPK2_Mm	(816)	TCEVTSSQAISSP	QRSKRVKENTPPRCAMVHSSPACSTSVTCGWGDVASS
HIPK2_Gg	(818)	TYEVSSSQSIS	SPQRSKRVKENTPPRCAMVHNSPACSTAVTCGWGDMATS
HIPK2_Xt	(776)	AYEVTSSQSVNS	PQRSKRVKENTPPRCAVPQNTTACVPSITCGWGD SAVG
HIPK3_Hs	(800)	PHSAFISPKI	INGKDVEEVSCIETQDNQNSEGEAR--NCCETSIRQDSDS
HIPK3_Mm	(779)	PHSAFISPKI	ISGKEVEEVSCVDTQDNHTSEGEAR--TCREASVRQDSS-
HIPK3_Gg	(778)	QNSALISPKI	INLKAVKRISCI EAQDNHNSDGQES--NCCEASVRLEPDS
HIPK3_Xt	(780)	HNPVVASPKI	VSENTRAEESALPQDNHEEKEE---EQSSSNNTQGPAP

951

1000

HIPK1_Hs	(884)	VPVQDQHQP	IIIPDTPSPPVSVITIRSDTDEEEDN-----KYKPSSSGLK
HIPK1_Mm	(884)	VPVQDQHQP	IIIPDTPSPPVSVITIRSDTDEEEDN-----KYKPNSSSLK
HIPK1_Gg	(884)	VPVQEQHQ	PVIVIPDTPSPPVSVITIRSDTDEEEDS-----KYKPASLGMK
HIPK1_Xt	(841)	LPLQEQRQ	PVIVIPDTPSPPVSVITIRSDTDEEEDS-----KYKPTNSGMK
HIPK1_X1	(840)	LPLQEQRQ	PVIVIPDTPSPPVSVITIRSDTDEEEDS-----KYKPTNSGME
HIPK2_Hs	(839)	TTTTRERQR	QTIVIPDTPSPTVSVITISSDTDEEEEQ-----KHAPTSTVSK
HIPK2_Mm	(866)	TTTTRERQR	QTIVIPDTPSPTVSVITISSDTDEEEEQ-----KHAPTSTVSK
HIPK2_Gg	(868)	TTTTRERQR	QPIIIPDTPSPAVSVITISSDTDEEEEQ-----KHAPTSTLSK
HIPK2_Xt	(826)	GSHNRQR	QTIVIPDTPSPAVSVITISSDTDEEEEQ-----KHVAPSLP-K
HIPK3_Hs	(848)	SVSDKQR	QTIIADSPSPAVSVITISSDTDEEETSQRHSLRECKGSLDCE
HIPK3_Mm	(826)	-VSDKQR	QTIIADSPSPAVSVITISSDSDDEETS PRPSLRECKGSLDCE
HIPK3_Gg	(826)	SLSNKQR	QAI F IAGSPSPAVSVITISSDTDEDDLQTRSLRECKGSLDCE
HIPK3_Xt	(827)	DTSIQQQ	QAIVIGDSPSPTVSVITINSDTDEDDPAQTL SLRECKRSLDCD

1001

HIPK1_Hs (929) PRSNVISYVTVNDSPDSDSSLSSPYSTDTLSALRGNSGSLVLEGPGRVVAD
HIPK1_Mm (929) ARSNVISYVTVNDSPDSDSSLSPHPTDTLSALRGNSGTLLEGPGRPAAD
HIPK1_Gg (929) QRSNVISYVTVNDSPDSDSSLNSPYATDPLSSLR-STGGALELPSRGAAD
HIPK1_Xt (886) LRSNVISYVTVNDSPDSDSSVSSPYLADRHTSVNGVTGVFDMNSRTHAS
HIPK1_X1 (885) LRSNVISYVTVNDSPDSDSSASSPCLADHSSVNAVTVGFVDISNHRAAHS
HIPK2_Hs (884) QRKNVISCVTVHDSPYSDSSSNTSPYSVQQRAGHNNANAFDTKGSLENHC
HIPK2_Mm (911) QRKNVISCVTVHDSPYSDSSSNTSPYSVQQRAGHNNANAFDTKGSLENHC
HIPK2_Gg (913) QRKNVISCVTVHDSPYSDSSSNTSPYAVQHRAGQNNGNTYDTKGVPEHC
HIPK2_Xt (870) QRRNVISCVTVHDSPI SDSSSNTSPYAASGHRRGNNTSAAESKQGTGNPC
HIPK3_Hs (898) ACQSTLNIDRMCSLSSPDSTLSTSSSGQSSSPCKRPNSMSDDEQESSCD
HIPK3_Mm (875) ACQSTLNIDRMCSLSSPDSTLSTSSSGQSSSPCKRPNSMSDDEQESGCE
HIPK3_Gg (876) ACQNTLNIDRVCSLSSQDSTLSTSSSGQSSSPCKRNSMSDDEQESGCD
HIPK3_Xt (877) TCQSALN---VCSLSSPDSTLSTSSSGQSSSPCKRRNSISDDEPESGCD

1051 1100

HIPK1_Hs (979) GT-----GTRTIIVPPLKTQLGDCTVA
HIPK1_Mm (979) GI-----GTRTIIVPPLKTQLGDCTVA
HIPK1_Gg (978) SS-----NSRTIIVPPLKTQLNDCIVA
HIPK1_Xt (936) QSL-----NSRTIIVPPLKQSOMNDCPLD
HIPK1_X1 (935) QSS-----NSRTIIVPPLKSQINDCSLN
HIPK2_Hs (934) TG-----NPRTIIVPPLKTQASEVLVE
HIPK2_Mm (961) TG-----NPRTIIVPPLKTQASEVLVE
HIPK2_Gg (963) SG-----NPRTIIVPPLKTQASEVLVE
HIPK2_Xt (920) PA-----NPRTIIVPPLKTQPSSEGRLE
HIPK3_Hs (948) TVDGSPTSDSSGHDSPPFAESTFVEDTHELTVSSADTETKPAVCSVVVP
HIPK3_Mm (925) TVDGSPTSDSSGHDSPPFAENFVEDAHQNTLGTGAGPEAKPAVGTAVEP
HIPK3_Gg (926) TVDGSPTSDSSGHDSPPFVEDGFVANTNKNKEARASVNSETKSAVCTVVVP
HIPK3_Xt (924) TVNGSPSSDSSGHDSPPFKN-SFVRDSNQNTESRTPKTDKPAVCTVVVP

1101 1150

HIPK1_Hs (1001) TQASGLLS---NKTTPVASVS-GQSSGCCITPTGYRAQRGGTSAQAQPLN
HIPK1_Mm (1001) TQASGLLS---SKTKPVASVS-GQSSGCCITPTGYRAQRGGASAVQPLN
HIPK1_Gg (1000) TQASGILSN--TSKTKPVASVS-GQSSGCCITPTGYRPHRVVANGVQPLN
HIPK1_Xt (959) TQLTGVLSG--AAKITKCTATNGQSSS-CITQTGCRSHR-MLNGVQPLN
HIPK1_X1 (958) TQLTGVLSS--AAKINKTCTATNGQSSSCTITQTGQRSHR-MLNGVQPLN
HIPK2_Hs (956) CDSLVPVN--TSHHSSSYKSKSSSNTSTSGHSSGSSSGAITRQQRPGP
HIPK2_Mm (983) CDSLGPAIN--ASHHSSSFYKSKSSSTVTSTSGHSSGSSSGAIAYRQQRPGP
HIPK2_Gg (985) CDSLAPGTVTTSHHSSSYKSKSSSTVTSTSGHSSGSSSGAVAYRQQRPGA
HIPK2_Xt (942) CERKQPD---TSHHMYK--AKLLSSVASASHSSASSAGTAYRHSRAPGH
HIPK3_Hs (998) PVELEGNLADEHMAN-TDSICQPLIKGRSAPGRLNQPSAVGTRQOKLTS
HIPK3_Mm (975) PVGRESGLSVGEHMAN-TDSTCQPLRKGQPAPGKLHQPALGARQQKPA
HIPK3_Gg (976) PMSLENRLRLDEQMVNTEDATCQPLKNGRSVLGRKTQSSAVGNRQOKLAS
HIPK3_Xt (973) PIRIEN-RQFNSHRVSNKDTVCYPVIKGRSAPGRINHPNSLGRSQOKLAS

1151 1200

HIPK1_Hs (1046) LSONQQSSAAPTQERSNPAPRR----QQAFVAPLS----QAPYTFQHG
HIPK1_Mm (1046) LSONQQSSASTQERSNPAPRR----QQAFVAPLS----QAPYAFQHG
HIPK1_Gg (1047) LSONQQTTVLAS-QERSGNAVPRR----QQAYVAPLTSTISQAPYTFQHS
HIPK1_Xt (1005) LSON-QQSAMMGTQERSMNPGRSRR----QQAYVAPLP-SISQAPFTFQHS
HIPK1_X1 (1005) LSON-QQSALVGTQERSMNPGRSRR----QQAYVAPIP-SISQAPFTFQHN
HIPK2_Hs (1004) HFQQQQPLNLSQAQQHITTDRTGS----HRRQQAYITPTMAQAPYSFPHN
HIPK2_Mm (1032) HFQQQQPLNLSQAQQHMAADRTGS----HRRQQAYITPTMAQAPYTFPHN
HIPK2_Gg (1035) HFQQQQPLNLSQAQQHITTDRTGS----HRRQQAYITPTIAQAPYSFPHN
HIPK2_Xt (987) SFQQQ-PLNLSQVSQHIISTERTGS----HRRQHAYIAPTIAQAPYSFPHS
HIPK3_Hs (1047) AFQQQH-LNFSQVQHFSGHQEWNGNFGHRRQQAYIPTSVTSNPFTLSHG
HIPK3_Mm (1024) AFPQQH-LNLSQVQHFSGHQEWNGNFGHRRQQAYIPTSVTSNPFTLSHG
HIPK3_Gg (1026) AFHQQH-LNFSQVQHFSGAPQEWNGNYAHRQQAYIPASVASHAFSLPQG
HIPK3_Xt (1022) AFHQHPPLNYSKVQHFSGHQEWNGNYGHMRQQAYMQPTVASHPFTLQHG

		1201	1250
HIPK1_Hs	(1088)	SPLHSTGHPHLAPAPAHLP----	SQAHLYTYAAPTSAALGSTSSIAHLF
HIPK1_Mm	(1088)	SPLHSTGHPHLAPAPAHLP----	SQPHLYTYAAPTSAALGSTSSIAHLF
HIPK1_Gg	(1092)	SPVHP--HLAAATANAHLS----	SQPHMYTYAP-TTAATLGSTTSIAHLF
HIPK1_Xt	(1049)	SPLHSTVHPHLAAAATATS-HLTS	SQPHMYTYAP-TTAASLGSTTSIAHLF
HIPK1_X1	(1049)	SPLHSTVHPHLAAAAASATSHLTS	SQPHMYTYAP-TTAASLGSTTSIAHLF
HIPK2_Hs	(1050)	SPSHGTVHPHLAAAAAAHLP--	TQPHLYTYTA---PAALGSTGTVAHLV
HIPK2_Mm	(1078)	SPSHGTVHPHLAAAA--HLP--	TQPHLYTYTA---PTALGSTGTVAHLV
HIPK2_Gg	(1081)	SPSHGTVHPHLAAAAAA-HLP--	TQPHLYTYTT---PAALGSTGTVAHLV
HIPK2_Xt	(1032)	SPSHGAVHPHLAAAH---LP---	SQPHLYTYTA---PAALGSSGTVAHLV
HIPK3_Hs	(1096)	SPNHTAVHAHLAGNTHLGG----	QPTLLPYPS---SATLSSAAPVAHLL
HIPK3_Mm	(1073)	SPNHTAVHAHLDGSTHLGG----	QPTLLPYPS---SASLSSAAPVAHLL
HIPK3_Gg	(1075)	SPNPTTVHAHLGSGSTHLGG----	QPAILPYPS---SAPLSTAAPVAHLL
HIPK3_Xt	(1072)	SPTHSAHHAHLGAGSTHIGG----	QPAILSYP---SASLSSAAPVAHLL

		1251	Dsh-Interacting Region	1300
HIPK1_Hs	(1134)	SPQGSSR----	HAAAYTTHPSTLVHQVPVSVG	PSLLTSASVAPAQYQHQF
HIPK1_Mm	(1134)	SPQGSSR----	HAAAYTTHPSTLVHQVPVSVG	PSLLTSASVAPAQYQHQF
HIPK1_Gg	(1135)	SPQGSS-----	RHTQYAAHPSTLVHQVPVSVG	PSLLTSANVPPAQYQHQF
HIPK1_Xt	(1097)	SPQGSS-----	RHTTFATHPSTLVHQVPVSVG	PSLLTSANVASAQYPHQF
HIPK1_X1	(1098)	SPQGSS-----	RHTTFSTHPSTLVHQVPVSVG	PSLLTSANVASAQYPHQF
HIPK2_Hs	(1095)	ASQGSAR----	HTVQHTAYPASIVHQVPVSMG	PRVLPSTIHPQSQYPAQF
HIPK2_Mm	(1120)	ASQGSAR----	HTVQHTAYPASIVHQVPVSMG	PRVLPSTIHPQSQYPAQF
HIPK2_Gg	(1125)	ASQGSAR----	HAVQHTTYPASIVHQVPVSMG	PRVLPSTIHPQSQYQAQF
HIPK2_Xt	(1073)	ASQG-----	SARHAAYPASIVPVSMARQLL	LPSPSLHPSQYQAQF
HIPK3_Hs	(1138)	ASPCTSRPMLQHPTYNISHPSG	IVHQVPVGLNPRLLPSPTIHQT	QYKPIF
HIPK3_Mm	(1115)	ASPCTSRPMLQHPTYNISHPSG	IVHQVPVGINPRLLPSPTIHQT	QYKPIF
HIPK3_Gg	(1117)	ASPCTSRPMLQHPTYNISHPSG	IVHQVPVGINPRLLPSPTIHQT	QYKPIF
HIPK3_Xt	(1114)	ASPCTSRPILQHPTYSLSHPSG	IVHQVAVGINPRLLPSPTIHQT	QFKPIF

		1301	1331
HIPK1_Hs	(1180)	ATQSYIGSSRGSTIYTGYP	SPTKISQYSYL
HIPK1_Mm	(1180)	ATQSYIGSSRGSTIYTGYP	SPTKISQYSYL
HIPK1_Gg	(1180)	APQSYIGASRGSAIYTGYP	SPTKINQYSYL
HIPK1_Xt	(1142)	AAQSYIGASRGSAIYTGYP	SPTNINQYSYL
HIPK1_X1	(1143)	ATPSYIGASRGSAIYTGYP	SPTNINQYSYL
HIPK2_Hs	(1141)	AHQTYISASPASTVYTGYP	SPAKVNQYPYI
HIPK2_Mm	(1166)	AHQTYISASPASTVYTGYP	SPAKVNQYPYI
HIPK2_Gg	(1171)	AHQTYISASPASTVYTGYP	SPTKVNQYPYI
HIPK2_Xt	(1112)	AHQTYIPASPTSTVYTGYP	TPPKVNQYPYI
HIPK3_Hs	(1188)	PPhSYIAASP---	AYTGFPLSPTKLSQYPYM
HIPK3_Mm	(1165)	PPhSYIAASP---	AYTGFPLSPTKVSQYPYM
HIPK3_Gg	(1167)	PPhSYIAASP---	AYTGFPLSPTKLSQYPFM
HIPK3_Xt	(1164)	PSHSYITASP---	AYAGFPMSPTKLSQYPYM