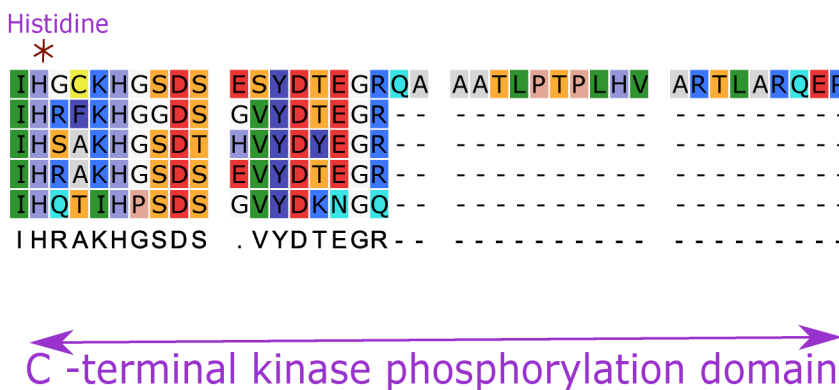
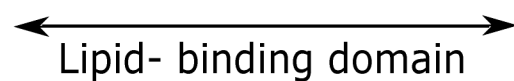
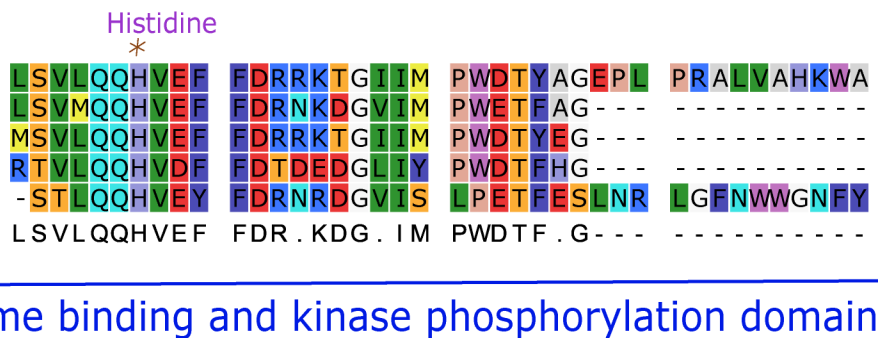


Protein	Sequence	Length
KnCLO2	M-----	9
KnCLO3	MAP-----	13
KnCLO5	MAP-----	11
KnCLO1	MATAFSAPTLGSSKLASLNAHAALGESSQRVSSSRPDCAPLSSARHRSLPKKNNASTCRQLAVTCKASTSPQKSTSKGIA	100
KnCLO4	M-----	17
Consensus	MAP-----	



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KnCLO2	M-----	9
KnCLO3	MAP-----	13
KnCLO5	MAP-----	11
KnCLO1	MATAFSAPTLGSSKLASLNAHAALGESSQRVSSSRPDCAPLSSARHRSLPKKNNASTCRQLAVTCKASTSPQKSTSKGIA	100
KnCLO4	M-----	17
Consensus	MAP-----	-

KnCLO2	-- -- -- PAAP	VT A ERPVPAD	LDQALK - NPG	LPRALVAPS R	ERP DGSRA --	-- -- FHD PKS	LSVLQQHVEF	FDRRK TGIIM	PWDTY AGEPL	PRALVAHKWA	96
KnCLO3	-- -- -- PGAP	VTTRRPAPKR	LEAQLEG NPG	APQAQIAAS R	EQPHGSTD --	-- -- YYD PKG	LSVMQQHVEF	FDRNK DGIVM	PWETF AG---	-----	88
KnCLO5	-- -- -- PAAP	VTY ERVPPTD	LDSKMD - SPS	VPRAQLAATP	EYP QGSAD --	-- -- FKD PKG	MSVLQQHVEF	FDRRK TGIIM	PWDTY EG---	-----	85
KnCLO1	G I V T S L P E A P	FTQ KYAVPED	LDKVIP - KP W	LPRANNTPTL	D Y P S G L A E S D	QM K K F L N G E G	R T V L Q Q H V D F	F D T D E D G L I Y	P W D T F H G ---	-----	186
KnCLO4	- M M L V M P G L -	--- QPTPRV	P D T S Y R A N P -	-----	-----	-----	- S T L Q Q H V E Y	F D R N R D G V I S	L P E T F E S L N R	L G F N W W G N F Y	79
Consensus	-- -- -- P . AP	VT . ERPVP . D	LD . . L . -NPG	LPRAQ . A . . R	EYP . GSAD--	-- -- F . DPKG	LSVLQQHVEF	FDR . KD G . IM	PWDTF . G ---	-----	

KnCLO2	VPHLTRSEEP	LRTASRNRFR	AVGFSMVLSL	VFSALINGSL	SYFSQDSWLP	DPLLISKVRN	IHGCKHGS	ESYDTEGRQA	AATLPTPLHV	ARTLARQERA	196
KnCLO3	- - - - -	- - - - - FR	ALGVNLFSSL	LAPILINGAQ	SYPTQDGWLP	DPLWGIKIKN	IHRFKHGGDS	GVDTEGR - -	- - - - -	- - - - -	148
KnCLO5	- - - - -	- - - - - FR	ALGVNIFFSV	IFTFILNSSL	SYSTQDGWLP	DPLLISKVRN	IHSAKHGSDT	HVYDYEGR - -	- - - - -	- - - - -	145
KnCLO1	- - - - -	- - - - - FR	RLGYNPILICA	LAGLFINSAM	AFPTAPGIL -	DIRLPITYTQR	IHRAKHGSDS	EVDTEGR - -	- - - - -	- - - - -	245
KnCLO4	RAPFINWGLT	MGLYVKG - FP	PLSLS - - SL	ISPAFWNHLL	SF - - - - -	DFQLRPVIQT	IHQTIHPSDS	GVDKNGQ - -	- - - - -	- - - - -	145
Consensus	- - - - -	- - - - - FR	ALG.N.FFSL	. . PA . IN . . L	SYPTQDGWLP	DPLLISK . . N	IHRAKHGSDS	. VYDTEGR - -	- - - - -	- - - - -	

KnCLO2	GVGAEEERRLG	QPRGCLFVPE	KFEEIFSKHD	RSKGSLTFM	EMLALTETNK	NAFDAFGWIA	EKLEWGVTFW	LLA-----DH	RGRVAKHEIR	ECLDGSVFYR	291
KnCLO3	-----	-----FVPE	KFEEIWSKYD	RDNKGALTVS	QLFEMTQGNA	VVYDLFGWLA	EKLEWALTYYW	MLA-----DH	RGLMYKENVR	QCLDGSIFYR	227
KnCLO5	-----	-----FCPE	KFEALFTQFD	HGNKGGLTFE	ELLEMTEKHR	MPYDFFGWMA	EKLEWGLTWW	LLK-----DE	NGLVSKESIR	GSYDGSIIYR	224
KnCLO1	-----	-----FVPQ	KFEEIFTKFD	RDGKGALTWD	ELQGMVAHNR	NLYDFFGRTA	STLEWAVT-W	LLAKEVAPDG	REVMTREAIR	GQYDGSIFYR	328
KnCLO4	-----	-----FNEA	KFERLMS-FD	KAGKGGINRC	EMTRFIKANN	NPPDVPGNIG	SKFEWFNVFE	IL-----HDD	KGVMSREKLL	KMYNGSVFEE	223
Consensus	-----	-----FVPE	KFEEIFSKFD	RDGKG.LTF.	ELLEMTE.NR	NPYDFFGWIA	EKLEW..TFW	LLA-----DH	RG.MSKE.IR	GCYDGS.FYR	

KnCLO2    --- - IEKERQ E-EAHRKQ-- --GRGHAPAS HGHTDAE 319  
 KnCLO3    --- - IEKERQ ELQARRLRVT SCWKKDVEPL YSQLKEE 260  
 KnCLO5    --- - VEAAARK AMK----- -- --KEE 236  
 KnCLO1    KAAEIELAKK KKQTKR----- -GD FEQTLPR 353  
 KnCLO4    IERAV-AAKK GIQTVRTSAM K----- -- --NDA 246  
 Consensus --- - I E . ARK E . Q . R - - - - - - - - - - - QTKEE

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