

N-terminal H caleosin domain

Ca²⁺ binding EF hand motif

Lipid-binding domain

	40	60	80	100	120	140	160	180													
PchCLO1	LCERKP	RIKAAEANN-	ETVIIAEKS	GITSKRLPAV	SLADAIENP-	----GVARAN	AAVSV EKPEG	DLE--WARKC	DGYSPLQQHI	LFWDRDRDGM	IFPWDTYNGF	RELGFNVIFS	IIATFIINVN	FSYPTTHMAYS	WFPDPWFRVH	I					
PruCLO1	LCERKP	RIKAAEANN-	ETVIIAEKS	GITSKRLPAV	SLADAIENP-	----GVARAN	AAVSV EKPEG	DLE--WARKC	DGYSPLQQHI	LFWDRDRDGM	IFPWDTYNGF	RELGFNVIFS	IIATFIINVN	FSYPTTHMAYS	WCPDPWFRVH	I					
PruCLO2	-----	-----	TVIIAEKS	GITSKRLPAV	SLADAIENP-	----GVARAN	AAVSV EKPEG	DLE--WARKC	DGYSPLQQHI	LFWDRDRDGM	IFPWDTYNGF	RELGFNVIFS	IIATFIINVN	FSYPTTHMAYS	WFPDPWFRVH	I					
ParCLO1	FRERKL	NFKTAEENN-	ETVIIAKNS	YITSRRLLAL	SLANDIDNP-	----GVARAN	AAVSV EKPEG	DLE--WARKN	DGYTPLQQHI	LFWDRDGDGM	IFPWDTYNGF	RELGFNVIFS	ILATFIINVN	FSYPTRLAYS	WFPDPYFRVY	L					
PfrCLO1	FRERKP	YIKAAEENN-	ETVIIADQS	YITSERLP	FLANAIENP-	----GVARAN	AAVSV EKPEG	DLE--WARKC	DGYSPLQQHI	LFWDRDGDGM	IYPWNTYNGF	RELGFNLFSS	ILATFIINVN	FSYPTRLAYS	WLPDPWFRVY	I					
PpoCLO1	FRERKP	YIKAAEENN-	ETVIIADQS	YITSERLP	FLANAIENP-	----GVARAN	AAVSV EKPEG	DLE--WARKC	DGYSPLQQHI	LFWDRDGDGM	IYPWNTYNGF	RELGFNLFSS	ILATFIINVN	FSYPTRLAYS	WLPDPWFRVY	I					
PitCLO1	FRERKP	FLKAAQENN-	NTVIIAEKS	YITSERLP	SLANDMENP-	----GVARAN	AAVSVENPEG	DLE--WARKV	DGYSPLQQHI	LFWDRDGDGI	IYPWDTYNGF	RELGFNLFSS	VLATFIINVN	FSYPTRLAYS	WLPDPWFRVY	I					
PanCLO1	FRERKR	YIKAVEENN-	ETVVVAEKS	YITSKRLPAV	SLADAIENP-	----GVARAN	AAVSVEMPEG	DLE--WARKC	DGYTPLQQHI	LFWDRDGDGM	IYPWDTYTGF	RELGFNLFSS	ILATFIINVN	FSYPTRLAYS	WLPDPWFRVY	I					
PisCLO1	QQQIT	DIKNGKKDND	IEIKVVASKA	KVTSQRLPAT	FTDQFIKNP-	----GLARSN	LAVSDKPNG	DLE--WRSRV	KNYTTLQQHI	LFWDSDEDGQ	IFPWDVYNGF	RQLGFNLFSS	IFAVLVININ	FSYPTRLAYS	WFPDPWFRVY	V					
PstCLO1	-----	-----	TQTSD	VDFDISVTKS	IVTQTRVPAI	----SVVRAN	QAVSREHPEG	SRKSGWTEKY	KEYTVMQQHI	LFWDRDMDGH	IWPLDTERGF	RELGFNLFSS	CLAVLIHHLN	FSYPTRLGLT	YFPDPFFRVY	V					
FfuCLO1	K-----	-----	VDPNSI	ITTSI--DVV	PVTVERKP--	----YQPGVDKPR	LAHAGVARAN	LAATHERPEG	TTENDWAQRH	QDQTVLQQHC	DFFDKDHDGV	IWPLDTERGF	YQLGYGIILS	LISVLIHGN	FSYTTQS--S	LLPDPPFRIH	I				
FveCLO1	K-----	-----	VDPNSI	ITTSI--DVV	PVTVERKP--	----YQPGVDKPR	LAHAGVARAN	LAATHERPEG	TTENDWAQRH	QDQTVLQQHC	DFFDKDHDGV	IWPLDTERGF	YQLGYGIILS	LISVLIHGN	FSYTTQS--S	LLPDPPFRIH	I				
FpoCLO1	K-----	-----	VDPNSI	ISTSI--HTV	PVTVERKP--	----YQPGVDKPR	LAHAGVARAN	LAATHERPEG	TTDNDWADRH	RDQTVLQQHC	DFFDKDHDGV	IWPLDTERGF	YQLDYGIILS	LIISVLVIHGN	FSYPTQS--S	LLPDPPFRIY	I				
FoxCLO2	K-----	-----	VDPNSI	ITTSI--DTV	PVTVERKP--	----YQPGVDKPR	LAHAGVARAN	LAATHERPEG	TTDDDWADRH	RDQTVLQQHC	DFFDKDHDGV	IWPLDTERGF	YQLGYGIILS	LISVLIHGN	FSYPTQS--S	LLPDPPFRIH	I				
FprCLO1	K-----	-----	VDPNSI	ITTSI--DAV	PVTVERN--	----YQPGVDKPR	LAHAGVARAN	LAATHERPEG	TTENDWAQRH	QDQTVLQQHC	DFFDKDHDGV	IWPIDTERGF	HQLGYGFILS	LISVLIHGN	FSYPTQS--S	FLPDPPFRIH	I				
FmaCLO1	K-----	-----	VDPNSI	ITTSI--DTV	PVTVERKP--	----YQPGVDKPR	LAHAGVARAN	LAATHERPEG	TTENDWAQRH	QDQT-----	-----	DHDGV	IWPIDTLRGF	YQLGYGIILS	VVSVLVIHGN	FSYPTQS--S	LLPDPPFRIH	I			
FprCLO2	-----	-----	-----	-----	-----	N	KLNNDLTES-	TYVKVCS	SDH	SETQSRQIVT	S-----	KYKD	EKLSP	LQKHV	QFWRDRNDGI	INPWDVYNGF	RELGFGLFFS	I--GSLLIPIF	FSYPTRLGHS	WLPDPLFRIY	V
FfuCLO2	-----	-----	-----	-----	-----	N	KLNNDLTES-	TYVKVCS	SDH	SETQLRQTVT	S-----	KYKG	EKLSP	LQKHV	QFWRDRNDGI	INPWDVYNGF	RELGFGLFFS	T--GSLLIPIF	FSYPTRLGHS	WLPDPLFRIY	V
FmaCLO2	-----	-----	-----	-----	-----	N	KLNDYTES-	TYAKVCS	SDH	NEAQLEPAMT	S-----	KDEN	ERLSP	LQKHV	QFWRDRNDGI	INPWDVYNGF	RELGFGLFFS	I--GSLLIPIF	FSYPTRLGHC	WLPDPLFRIY	V
FoxCLO1	TPAIG	TGVCVSSIRN	KSANVNMVEY	HNDISQSTPN	RLGNDYTKS-	----TFAKVCS	SDH	SETPSAAIVN	S-----	K--D	EKLSP	LQKHV	QFWRDRNDGI	INPWDVYNGF	RELGFGLFFS	T--GSLLIPIF	FSYPTRLGHS	WLPDPLFRIY	V		
FveCLO2	-----	-----	-----	-----	-----	N	KLNDYQAS-	TYAKVCS	SDH	DEKQSKPVVA	S-----	EDEE	KKLSS	LQKHV	QFWRDRNDGI	INPWDVYNGF	RELGFGLFFS	I--GSLLIPIF	FSYPTRLGHS	WLPDPLFRIY	V
FpoCLO2	-----	-----	-----	-----	-----	Y	NTKNLRVTAN	GLNGHCQQR-	----THAQVCGTH	PKQPNCK-PS	DIKDQDQDQD	QDLSP	LQKHV	HFWRDRSDGV	IWPSDVYSGF	RELGFGLFFS	I--GSLLIPIF	FSYPTRLGHS	WIPDPMFRIY	V	
FlaCLO1	-----	-----	-----	-----	-----	D	NTENPHVKAN	GVNGHCRR-	----TYAQICETH	PNAPIYKAPS	T-----	RN	ERLSS	LQKHV	EFWRDRSDGV	IWPLDVYSGF	RELGFGLFFS	I--GSLLIPIF	FSYPTRLGHS	WIPDPMFRIY	I
Consensus	-----	-----	V--NN-	ETVI--DKS	PXTSERLPAX	SLANXIDNP-	---AGVARAN	AAVSV EKPEG	DLE--WARKX	DGYSPLQQHI	LFWDRDHDGV	IWPWDTYNGF	RELGFGLFFS	I	IAXLIINXN	FSYPTRLAYS	WLPDPWFRVY	I			

Heme binding and kinase phosphorylation domain

C-terminal kinase phosphorylation domain

		200		220		240		260	
		↓		↓		↓		↓	
PchCLO1		TSIHKAKHG	SDSGIYDPEG	RFIPQLFEDL	FSKWDKDG	ALTTLRELFQL	MHGHRCAADP	FGWGAAFFEW	GTTWILLI-QK
PruCLO1		TSIHKAKHG	SDSGIYDPEG	RFIPQLFEDL	FSKWDKDG	ALTTLRELFQL	MHGHRCAADP	FGWGAAFFEW	GTTWILLI-QK
PruCLO2		TSIHKAKHG	SDSGIYDPEG	RFIPQLFEDL	FSKWDKDG	ALTTLRELFQL	MHGHRCAADP	FGWGAAFFEW	GTTWILLI-QK
ParCLO1		TSIHKAKHG	SDSGTYDPEG	RFIPQLFENL	FSKWDKDG	ALTTLRELFQL	MHGHRCAADP	FGWSAALFEW	GTTWILLI-QK
PfrCLO1		PSIHKAKHG	SDSGVYDPEG	RFVPQLFENL	FSKWDKDG	ALSLRELFQL	MHGHRCAADP	FGWF AALFEW	GSTWILLI-QK
PpoCLO1		PSIHKAKHG	SDSGVYDPEG	RFVPQLFEDL	FSKWDKDG	ALSLRELFQL	MHGHRCAADP	FGWF AALFEW	GTTWILLI-QK
PitCLO1		PSIHKAKHG	SDSGVYDPEG	RFVPHCFGNL	FSKWDNDNDG	ALTTLRELFQL	MHGNC AADP	FGWF AALFEW	GSTWILLI-QK
PanCLO1		TSIHKAKHG	SDSGVYDPEG	RFVPQLFENL	FSKWDNDNDG	TLTLRELFQL	MHGHRCAADP	FGWF AALFEW	GTTWILLI-QK
PisCLO1		HSVHKAKHG	SDSGTYDPEG	RFVPQGFENI	FSKYDGDSDG	ALTLSSELFKL	MHGHRCAADP	FGWGAAFFEW	GSTWILLI-QK
PstCLO1		FDIHKAKHG	SDSGTYDNEG	RFVPQNFENI	FAKYDSDRD	AITLSDITRL	MKGQRYAADP	FGWGAAFFEW	GTTWILLI-QK
FfuCLO1		DNHKKDKHG	SDTGTYDTEG	RFIPQKFEDI	FSKYAEGRD-	HLTIWDVINL	IKGQRLIADP	IGWGGAFFEW	LATYILLWPD
FveCLO1		DNHKKDKHG	SDTGTYDTEG	RFIPQKFEDI	FSKYAEGRD-	HLTIWDVINL	IKGQRLIADP	IGWGGAFFEW	LATYILLWPD
FpoCLO1		DNHKKDKHG	SDTGTYDTEG	RFIPQKFEDM	FSKYAEDRD-	YLTIWVVISL	MKGQRLIADP	IGWGGAFFEW	LATYILLWPD
FoxCLO2		DNHKKDKHG	SDTGTYDTEG	RFIPQKFEDI	FSKYAEGRD-	YLTIWVVISL	MKGQRLIADP	IGWGGAFFEW	LATYILLWPD
FprCLO1		DNHKKDKHG	SDTGTYDTEG	RFIPQKFEDI	FSKYAEGRD-	YLTIWVVISL	MKGQRLIADP	IGWGGAFFEW	LATYILLWPD
FmaCLO1		DNHKKDKHG	SDTGTYDTEG	RFIPQKFEDM	FSKYTEGRD-	YLTIWVVISL	MKGQRLIADP	IGWGGAFFEW	MATYILLWPD
FprCLO2		NDIHKAKHG	SDTGIFDFDG	NFSPERFEQM	FQRFDTSGDG	GLNADDLWRL	WAKDRCAADP	AGWTF AFMEW	WTTYVLLI-QE
FfuCLO2		NDIHKAKHG	SDTGIFDFDG	NFSPERFEQM	FQRFDTSGDR	GLNADDLWRL	WAKDRCAADP	AGWTF AFMEW	WTTYVLLI-QD
FmaCLO2		NDIHKAKHG	SDTGIFDFDG	NFSHERFEQM	FQRFDTSGDG	GLNYDDLWRL	WAKDRCAADP	AGWTF AFMEW	WTTYVLLI-QE
FoxCLO1		NDIHKAKHG	SDTGIFDFDG	NFSPERFEQM	FQRFDTSGEG	GLTADDLWRL	WAKDRCAADP	AGWTF AFMEW	WTTYVLLI-QE
FveCLO2		NDIHKAKHG	SDTDIFDFDG	NFSPERFEQM	FQRFDTSGDG	ALTADDLWRL	WAKDRCAADP	AGWTF AFMEW	WTTYVLLI-QE
FpoCLO2		KHINKAKHG	SDTGIFYDFDG	NFNHERFEQL	FDRFDSSEEG	GLTADDLLRL	WKKDRCAADP	AGWTF AFMEW	WTTYVLLI-QK
FlaCLO1		KDINKAKHG	SDTGIFYDFDG	NFNHERFEQL	FDRFDSSEEG	ALTADDLLRL	WKKDRCAADP	AGWTF AFMEW	WTTYVLLI-QK
Consensus		DSIHKAKHG	SDTG IYDPEG	RF I PQXFEDL	FSKXDXDGDG	ALTTLRDLFXL	MXGHRCAADP	FGWGAAFFEW	GTTY I LL-QK