

	10	20	30	40	50	60
Sgr_LOC107585029	MELSAAGDRVFAAEAILKRRIRKGRMEYLVKWKGWAIKYSTWEPEENILDERLVAAFEQK					
San_LOC107662367	MELSAAGDRVFAAEAILKRRIRKGRMEYLVKWKGWAIKYSTWEPEENILDERLVAAFEQK					
Srh_LOC107740604	MELSAAGDRVFAAEAILKRRIRKGRMEYLVKWKGWAIKYSTWEPEENILDERLVAAFEQK					
Cau_LOC113046746	MELSAAGDRVFAAEAILKRRIRKGRMEYLVKWKGWAIKYSTWEPEENILDERLVAAFEQK					
Cca_LOC109095357	MELSAAGDRVFAAEAILKRRVRKGRMEYLVKWKGWAIKYSTWEPEENILDERLVAAFEQK					
Cau_LOC113047918	MELSAAGDRVFAAEAILKRRVRKGRMEYLVKWKGWAIKYSTWEPEENILDERLVAAFEQK					
Sgr_LOC107602318	MELSAAGDRVFAAEAIMKRRVRKGRMEYLVKWKGWAIKYSTWEPEENILDERLVAAFEQK					
San_LOC107690738	MELSAAGDRVFAAEAIMKRRVRKGRMEYLVKWKGWAIKYSTWEPEENILDERLVAAFEQK					
Srh_LOC107710048	MELSAAGDRVFAAEAIMKRRIRKGRMEYLVKWKGWAIKYSTWEPEENILDERLVAAFEQK					
Dre_Cbx6b	MELSAAGDRVFAAEAILKRRVRKGRMEYLVKWKGWAIKYSTWEPEENILDERLVAAFEQK					
Ame_cbx6b	MELSAAGDRVFAAEAILKRRVRKGRMEYLVKWKGWAIKYSTWEPEENILDDRDLVAAFEQK					
Pna_LOC108413245	MELSAAGDRVFAAEAILKRRVRKGRMEYLVKWKGWAIKYSTWEPEENILDERLVAAFEQK					
Ipu_LOC108260787	MELSAAGDRVFAAEAILKRRVRKGRMEYLVKWKGWAIKYSTWEPEENILDDRDLVAAFEQK					
Eel_LOC113569862	MELSVAGDRVFAAEAILKRRVRKGRIEYLVKWKGWAIKYSTWEPEENILDDRDLVAAFEQK					
Srh_LOC107720374	MEVSAVGGEQVFPAEAILKSRVRKGRIEYLVKWKGWALKHSTWEPEENILDDRDLITAFEQK					
San_LOC107667890	MEVSTVGEQVFPAEAILKSRVRKGQIEYLVKWKGWALKHSTWEPEENILDDRDLITAFEQK					
Cca_LOC109066300	MEVSAVGGERVFPAAEAILKSRVRKGRIEYLVKWKGWALKHSTWEPEENILDDRDLITAFEKK					
Cau_LOC113065021	MEVSAVGGERVFPAAEAILKSRVRKGRIEYLVKWKGWALKHSTWEPEENILDDRLLAAFEQK					
Sgr_LOC107602676	MELSAVGGERVFAAEAILKSRVRKGRIEYLLKWKGWALKHSTWEPEENILDDRDLITAFEQK					
San_LOC107704552	MELSAVGGERVFAAEAILKSRVRKGRIEYLLKWKGWALKHSTWEPEENILDDRDLITAFEQK					
Srh_LOC107717667	MELSAVGGERVFAAEAILKSRVRKGRIEYLLKWKGWALKHSTWEPEENILDDRDLITAFEKK					
Cca_LOC109066296	MELSAEGERVFAAEAILKSRVRKGRIEYLVKWKGWALKHSTWEPEENILDDRDLITAFEQK					
Cau_LOC113039859	MELSAEGERVFAAEYILKSRVRKGRIEYLVKWKGWALKHSTWEPEENILDDRDLITAFEQK					
Dre_Cbx6a	MELSAAGDRVFAAEAILKSRVKGHIYLVKWKGWALKHSTWEPEENILDDRDLITAFEQK					
Ame_LOC103038090	MELSGMGERVFAAEAILKRRVRKSNIEYLVKWKGWALKHSTWEPEENILDDRDLITAFEKK					
Pna_Cbx6	MELSAMGDRVFAAEAILKRRVRKGSIEYLVKWKGWALKHSTWEPEENILDRGLITAFEQK					
Eel_LOC113585732	MELSAIGDRVFAAEAILKRRVRKGRIEYLVKWKGWALKHSTWEPEENILDDRDLITAFERK					
Ipu_LOC108259424	MELTAIGDRVFAAEAILKRRVRKGNIEYLVKWKGWALKHSTWEPEENILDDRDLITAFERK					
Dcl_LOC114786320	MELSAVGDRVFAAEAILKRRVRKGRIEYLVKWKGWALKYSTWEPEENILDDRDLITGFERK					
Cha_LOC105903838	MELSAVGDRVFAAEAILKRRVRKGQIEYLVKWKGWALKNSTWEPEENILDDRDLITAFEQK					
	: **:*.*.* *:* *: :***:*****:* ***** ***: **:					
Prim.cons.	MELSAAGDRVFAAEAILKRRVRKGRIEYLVKWKGWALKYSTWEPEENILDDRDLVAAFEQK					

	70	80	90	100	110	120
Sgr_LOC107585029	EREQEMYGP-----KKRGPKPKTLLKLSRAQVAETSSRVP-----EFKHTRPQ					
San_LOC107662367	EREQEMYGP-----KKRGPKPKTLLKLSRAQVAETSSRVP-----EFKHTRPQ					
Srh_LOC107740604	EREQEMYGP-----KKRGPKPKTLLKLSRAQVAETSSRVP-----EFKHTRPQ					
Cau_LOC113046746	EREQELYGP-----KKRGPKPKTLLKLSRAQVADTSSRVP-----EFKHTRPQ					
Cca_LOC109095357	EREQEMYGP-----KKRGPKPKTLLKLSRAQVAETSSRVP-----EFKHTRPQ					
Cau_LOC113047918	EREQEMYGP-----KKRGPKPKLTLKLSRAQVAETSSRVP-----EFKHTRPK					
Sgr_LOC107602318	EREQELYGP-----KKRGPKPKTLLKLSRAQVTETSSRVP-----QFKHTRPQ					
San_LOC107690738	EREQEMYGP-----KKRGPKPKLTLKLSRAQVAETSSRVP-----EFKHTRPQ					
Srh_LOC107710048	EREQEMYGP-----KKRGPKPKTLLKLSRAQVAETSSRVP-----ELKHTRPQ					
Dre_Cbx6b	EREQEMYGP-----KKRGPKPKTLLKLSRAQAE--SPRVP-----EFKHSRPQ					
Ame_cbx6b	EREQELYGP-----KKRGPKPKTLLKLSRAQTSDTPHRVP-----EFKHTRPQ					
Pna_LOC108413245	EREQELYGP-----KKRGPKPKTLLKLSRAQASDGTTPRVP-----EFKHTRPQ					
Ipu_LOC108260787	EREQELYGP-----KKRGPKPKTLLKLSRAQAESSPRVL-----EFKPSRPQ					
Eel_LOC113569862	EREQELYGP-----KKRGPKPKTLLKLSRAHAAGESPVP-----EFKHSRPQ					
Srh_LOC107720374	EREQELYGP-----KKRGPKPKNFVLKARAQAGD-RPRSS-----NTRRTPPR					
San_LOC107667890	XRQELYGP-----KKRGPKPKNFVLKARAQAGD-RPRSS-----NTRRTPPR					
Cca_LOC109066300	EREQELYGP-----KKRGPKPKNFVLKARAQAGD-RPRSS-----DTQRTPPQ					
Cau_LOC113065021	ERQELYGP-----KKRGPKPKNFVLKARAHAGD-RPRSSDTQRTPPQISNTQRTPPR					
Sgr_LOC107602676	ERQELYGP-----KKRGPKPKNFVLKARAQAGD-RPRSS-----NTQRTPPR					
San_LOC107704552	ERQELYGP-----KKRGPKPKNFVLKARAQAGD-RPRSS-----NTQRTPPR					
Srh_LOC107717667	EREQELYGP-----KKRGPKPKNFVLKARAQAGD-KPRSS-----NTQRTPPR					
Cca_LOC109066296	EREQELYGP-----KKRGPKPKNFVLKARAQAGD-RPRSS-----NTQRTPPR					
Cau_LOC113039859	EREQELYGP-----KKRGPKPKNFVLKARAQAGD-RPRSS-----NTQRTPPR					
Dre_Cbx6a	EREQELYGPEQELYGPKRGPKPKNFVLKARAQSGD-RPRSS-----YTRRTPPS					
Ame_LOC103038090	EREQELYGP-----KKRGPKPKNLLKARTQP---SPRVS-----KTRNTPPR					
Pna_Cbx6	EREQELYGP-----KKRGPKPKNLLKARAQTGETSSRGS-----SARHTPPH					
Eel_LOC113585732	EREQELYGP-----KKRGPKPKTFVLKARAQAGEPSSRGS-----TTRQAPPR					
Ipu_LOC108259424	ERDQELYGP-----KKRGPKPKNFVLKARAQAGETLSRGS-----STRRAPPC					
Dcl_LOC114786320	EREQELYGP-----KKRGPKPKNFILKARAQAGTSDTSNRFS-----VARQTHNR					
Cha_LOC105903838	ERQELYGP-----KKRGPKPKNFVLKARAHAGETSSRAT-----DPRQLISR					
	::*:* *:*:*:* *:*:*:* *:*:*:* *:*:*:* *:*:*:* *:*:*:*					
Prim.cons.	EREQELYGPEQELYGPKRGPKPKN2LLKARAQAG2TSRVSQTQRTPPQISE2KHTPPQ					

	130	140	150	160	170	180
Sgr_LOC107585029	QHSKLPPPS	-----AAP	-----SYTPTAP	PSNAKLQ	SGTAQP	KLKKDIHRC
San_LOC107662367	QHSKLPPPS	-----AAP	-----SYTPTAP	PSNAKLQ	SGTAQP	KLKKDIHRC
Srh_LOC107740604	QHSKLPPPS	-----AAP	-----SYTPTAP	PSNAKLQ	SGTAQP	KLKKDIHRC
Cau_LOC113046746	QHSKLPPPS	-----ATP	-----SYTPTVP	PSNAKLQ	SGTAQP	KLKKDIHRC
Cca_LOC109095357	QHSKLPPPS	-----AAP	-----SYTPTAP	PSNAKLQ	SGTAQP	KLKKDIHRC
Cau_LOC113047918	QHSKFPPPS	-----AAP	-----SYTPTAP	PSNAKLQ	SGTAQP	KLKKDIHRC
Sgr_LOC107602318	QHSKLPPPS	-----AAP	-----SYTPTT	PSNAKLQ	SGAAQP	KLKKDIHRC
San_LOC107690738	QHSKLPPPS	-----AAP	-----SYTPAA	PSNAKLQ	SGAAQP	KLKKDIHRC
Srh_LOC107710048	QHSKLPPPS	-----AAP	-----SYTPTAP	PSNAKLQ	SGAAQP	KLKKDIHRC
Dre_Cbx6b	PHSKPPPPP	-----PAAP	-----SYTPTAP	PSNAKLQ	SGTAQP	KLKKDIHRC
Ame_cbx6b	PSSKPAPPPL	-----PAP	-----TYTPTC	PSNAKLQ	SGAAQP	KLKKDIHRC
Pna_LOC108413245	PSSKPPPPPL	-----PTP	-----SYPPSC	PSNAKLQ	SGAAQP	KLKKDIHRC
Ipu_LOC108260787	PSSKPPPPPP	-----PAS	-----SYHPSG	PSNAKLQ	SGAAQP	KLKKDIHRC
Eel_LOC113569862	PSSKPPPPPP	-----PLSPP	-----SYPPSG	PSNAKLQ	SGAAQP	KLKKDIHRC
Srh_LOC107720374	TTAKPPAS	-----SSSAS	-----SSSSFST	APTFRVH	SLAAAH	KLKKDIHRC
San_LOC107667890	TTAKPPAS	-----SSSAS	-----SSSSFST	APTFRVH	SLAAAH	KLKKDIHRC
Cca_LOC109066300	IPAKLPAS	-----SSSASSA	--PSQ--PSSSSSL	STPTFRVH	SLAAAH	KLKKDIHRC
Cau_LOC113065021	ITAKLPSS	-----SSSASSA	--PPQ--PSSSSSF	STAPTFRVH	SLAAAH	KLKKDIHRC
Sgr_LOC107602676	TTAKPPAS	-----SSSASAA	--PPP--PSSSSSYN	TAPTFRVH	SLAAAH	KLKKDIHRC
San_LOC107704552	TTAKPPAS	-----SSSASAA	--PPP--PSSSSSYN	TAPTFRVH	SLAAAH	KLKKDIHRC
Srh_LOC107717667	TTAKPPAS	-----SSSASAA	--PPQ--PSSSSSYN	TAPTFRVH	SLAAAH	KLKKDIHRC
Cca_LOC109066296	TTAKPPAS	-----SSASAAA	--PPQ--PSSSSSYN	TAPTFRVH	SLAAAH	KLKKDIHRC
Cau_LOC113039859	TTAKPPAS	-----STSASAA	--PPQ--PSLSSSYN	TAPTFRVH	SLAAAH	KLKKDIHRC
Dre_Cbx6a	TTAKPPTA	-----SSSASAA	--TPQ--PSSSSSH	STAPTFRVH	SLAAAH	KLKKDIHRC
Ame_LOC103038090	SSSSSASS	-----SSSAVPP	VNPNVRSSSSSSSL	LAPTFRVH	SLAASH	KLKKDIHRC
Pna_Cbx6	SSS	-----SAAVTP	--NPP--SSSSSAS	LAPTFRVH	SLAASH	KLKKDIHRC
Eel_LOC113585732	SSS	-----SSVAP	--ANPP--SSSSSSS	LAPTFRVH	SLAASH	KLKKDIHRC
Ipu_LOC108259424	TSS	-----SSVPVP	--NPP--SSSSL	LAPTFRVH	SLAASH	KLKKDIHRC
Dcl_LOC114786320	SAATRPSS	-----SSASSVL	APHT--STSSASSS	LAPTAKLN	SLAATH	KLKKDIRRC
Cha_LOC105903838	SSSRPPSSRP	PTSRPSSSTAL	VSAP--ASSSSSSS	PAPSKLN	SLAATH	KLKKDIRRC
	:		*	*	*****
Prim.cons.	2HSKPPPPSP	PTSRPSSSASP	AL2PP2RSPSSSSP	ST	APT2KL2SLAAQH	KLKKDIHRC

	190	200	210	220	230	240
Sgr_LOC107585029	HRMARPLRP	PD---QTVG	PSPPFSSRP	TVSPFSET	VRILNRKVK	PREVKKGRVILNLK
San_LOC107662367	HRMARPLRP	PD---QTVG	PSPPFSSRP	TVSPFSET	VRILNRKVK	PREVKKGRVILNLK
Srh_LOC107740604	HRMARPLRP	PD---QTVG	PSPPFSSRP	TVSPFSET	VRILNRKVK	PREVKKGRVILNLK
Cau_LOC113046746	HRMARPLRP	PD---QTVG	PSPPFSSRP	TVSPFSET	VRILNRKVK	PREVKKGRVILNLK
Cca_LOC109095357	HRMARPLRP	PD---QTVG	PSPPFSSRP	TVSPFSET	VRILNRKVK	PREVKKGRVILNLK
Cau_LOC113047918	HRMARPLRP	PD---QTVG	PSPPFSSRP	TVSPFSET	VRILNRKVK	PREVKKGRVILNLK
Sgr_LOC107602318	HRMARPLRP	PD---QTVG	PSPPFSSRP	TVSPFSET	VRILNRKVK	PREVKKGRVILNLK
San_LOC107690738	HRMARPLRP	PD---QTVG	PSPPFSSRP	TVSPFSET	VRILNRKVK	PREVKKGRVILNLK
Srh_LOC107710048	HRMARPLRP	PD---QTVG	PSPPFSSRP	TVSPFSET	VRILNRKVK	PREVKKGRVILNLK
Dre_Cbx6b	HRMARPLRP	QD---HTVG	PSPPFSSRP	TVSAFSET	VRILNRKVK	PREVKKGRVILNLK
Ame_cbx6b	HRMSRRPLR	SDPLSQSV	GHS-----L	SPFSET	VRILNRKVK	PREVKKGRVILNLK
Pna_LOC108413245	HRMSRRPLR	PDPLAQSV	GHS-----L	SPFSET	VRILNRKVK	PREVKKGRVILNLK
Ipu_LOC108260787	HRMARPLRP	PDPLAPPI	GSSGPFSSRP	TVSPFCET	VRILNRKVK	PREVKKGRVILNLK
Eel_LOC113569862	HRISRRPLR	LDPLAQV	GSSGPFSSRP	TVSPFSET	VRILNRKVK	PREVKKGRVILNLK
Srh_LOC107720374	HRMSRRPLR	PDPLGDPT	GS--TSSSRPPI	SPFSET	VRILNRKVK	PREVKKGRVILNLK
San_LOC107667890	HRMSRRPLR	PDPLGDPT	GS--TSSSRPPI	SPFSET	VRILNRKVK	PREVKKGRVILNLK
Cca_LOC109066300	HRMSRRPLR	PDPLGEPT	GS--TSSSRPPI	SPFSET	VRILNRKVK	PREVKKGRVILNLK
Cau_LOC113065021	HRMSRRPLR	PDPLGEPT	GS--TSSSRPPI	SPFSET	VRILNRKVK	PREVKKGRVILNLK
Sgr_LOC107602676	HRMSRRPLR	PDPLGDP	MGT--TSLSRPPI	SPFSET	VRILNRKVK	PREVKKGRVILNLK
San_LOC107704552	HRMSRRPLR	PDPLGDPT	GT--TSSSRPPI	SPFSET	VRILNRKVK	PREVKKGRVILNLK
Srh_LOC107717667	HRMSRRPLR	PDPLGDPT	GT--TSSSRPPI	SPFSET	VRILNRKVK	PREVKKGRVILNLK
Cca_LOC109066296	HRMSRRPLR	PDPLGNPR	GS--TSSSRPPI	SPFSET	VRILNRKVK	PREVKKGRVILNLK
Cau_LOC113039859	HRMSRRPLR	PDPLGNPR	GS--TSSSRPPI	SPFSET	VRILNRKVK	PREVKKGRVILNLK
Dre_Cbx6a	HMMSSRRPLR	SDPLANST	G---SSSRPPI	SPFSET	VRILNRKVK	PREVKKGRVILNLK
Ame_LOC103038090	HRMSRRPLR	PRY---DPDGS	--SFSRPPI	SPFSET	VRILNRKVK	PREVKKGRVILNLK
Pna_Cbx6	HRMSRRPLR	PDPLANPD	GS--SFSRLPI	SPFSET	VRILNRKVK	PREVKKGRVILNLK
Eel_LOC113585732	HRMSRRPLR	PDPLANPD	GS--SFSRLPI	SPFSET	VRILNRKVK	PREVKKGRVILNLK
Ipu_LOC108259424	HRMSRRPLR	PDPLANPD	GS--SFSRLPI	SPFSET	VRILNRKVK	PREVKKGRVILNLK
Dcl_LOC114786320	HRMSRRPLR	PDVGP	SNNT--SFSRPPI	SPFSET	VRILNRKVK	PREVKKGRVILNLK
Cha_LOC105903838	HRMSRRPLR	PDPLAPSS	GS-SFPSPRPV	SPFSET	VRILNRKVK	PREVKKGRVILNLK
	* ..:*****	.	.	* ..:*****	* ..:*****	* ..:*****
Prim.cons.	HRMSRRPLR	PDPLGQ	PVGS	SSGPFSSRP	2SPFSET	VRILNR2VKPREVKKGRVILNLK

	250	260	270	280	290	300
Sgr_LOC107585029	-VVDKAGNGG	VANSRRTHVP	STQQSHFGRQK	IPSRNRVIGK	NRRFGEVSYRGIQ	PTIRS
San_LOC107662367	-VVDKAGNG	-GVANSRRTHMP	STQQSHFGRQK	IPSRNRVIGK	NRRFGEVSYRGIQ	PTIRS
Srh_LOC107740604	-VVDKAGNG	-GVANSRRTHVP	STQQSHFGRQK	IPSRNRVIGK	NRRFGEVSYRGIQ	PTIRS
Cau_LOC113046746	-VVDKAGNG	-AVANSRRTHVP	STQQSHFGRQK	IPSRNRVIGK	NRRFGEVSYRGIQ	PTIKS
Cca_LOC109095357	-VVDKAGNG	-TVANSRRTHVP	SAQQSHFGRQK	IPSRNRVIGK	NRRFGELSYRGIQ	PTIRS
Cau_LOC113047918	-VVDKAGHG	-GVPNRRTHVP	SAQQSHFGRQK	IPSRNRVIGK	NRRFGEFSYRGIQ	PTPNRN
Sgr_LOC107602318	-VVDKAGNG	-GVANSRRTHVP	SAQQSHFGRQK	IPSRNRVIGK	NRRFGELSYRGIQ	PTIRS
San_LOC107690738	-VVDKAGNG	-GVANSRRTHVP	SAQQSHFGRQK	IPSRNRVIGK	NRRFGELSYRGIQ	PTIRS
Srh_LOC107710048	-VVDKAGNG	-GVANSRRTHVP	SAQQSHFGRQK	IPSRNRVIGK	NRRFGELSYRGIQ	PTIRS
Dre_Cbx6b	-VLDKAENT	-AVANNKRTHVP	STQQSHFGRQK	IPSRNRVIGK	NRRFGEVSYRGIQ	PPIRG
Ame_cbx6b	-MIDKAGSG	-GSANNKRTQS	-TTHQSHTARQK	VPSRNRVIGK	SRRFGEVSYRGLQL	PVSG
Pna_LOC108413245	-VIDKAGNS	-GVANNRRTPS	-TAHQSYIGRQK	VPSRNRVIGK	SRRFGDVSYRGLPL	PVSG
Ipu_LOC108260787	-VMDKTG---	-PANNKRTQN	-SSHQSHLGRQK	VPSRNRVIGK	SRRFGDVSFRC	LQQPMGG
Eel_LOC113569862	-VIDKPGGG	-GVANNRRTPS	-ATHQPHIGRQK	VPSRNRVIGK	SRRFGDVSYRGLHL	PATA
Srh_LOC107720374	-VIDKSEN---	-SGVTSRRSPQ	-----	SFAGRTKIPSRNRIIGK	--KQGDMPYRPFQ	HPMKM
San_LOC107667890	-VIDKSEN---	-SGVTSRRSPQ	-----	SFAGRAKIPSRNRIIGK	--KQGDMPYRPFQ	HPMKM
Cca_LOC109066300	-VIDKSEN---	-SGVTSRRSPQ	-----	SFAGRAKIPSRNRIIGK	--KQGDMPYRPFQ	HPMKM
Cau_LOC113065021	-VIDKSEN---	-SGVTSRRSPQ	-----	SFAGRAKIPSRNRIIGK	--KQGDMPYRPFQ	HPMKM
Sgr_LOC107602676	-VIDKSQ-----	-----	-----	IPSRNRIIGK	--KHGDMPYRPFQ	HPMKM
San_LOC107704552	-VIDKSQ-----	-----	-----	IPSRNRIIGK	--KHGDMPYRPFQ	HPMKM
Srh_LOC107717667	-VIDKSQ-----	-----	-----	IPSRNRIIGK	--KHGDMPYRPFQ	HPMKM
Cca_LOC109066296	-VIDKSEN---	-SGVASRKTQ	-----	SFMGRAKIPSRNRIIGK	--KHGDMPYRPFQ	HPMKM
Cau_LOC113039859	-VIDKSEN---	-SGVASRRTQ	-----	SFTGRAKIPSRNRIIGK	--KHGDMPYRPFQ	HPMKM
Dre_Cbx6a	-VIDKSEN---	-GGMTSRRTPQ	-----	SFAGRAKIPSRNRIIGK	--KHGDMPYRPFQ	HPMKM
Ame_LOC103038090	-VIDKCG---	-GRAANRGPTQ	-----	SHQGRAQIPSRNRIIGK	--KQGDMPYRPFQ	PPMKM
Pna_Cbx6	-VIDKYG---	-GGATNRRPAQ	-----	TQQGRAQLPSRNRRIIGK	--KQGDMPYRPFQ	PPMKM
Eel_LOC113585732	-VIDKYSGSGGGG	GATHRRPAQ	-----	SHQGRAQIPSRNRIIGK	--RQGELPYRPFQ	PPMKM
Ipu_LOC108259424	-VIDKYG-----	-AGTTK	-----	GHQGRAHIPSRNRIIGK	--RQGEMPYKPFQ	PPMKM
Dcl_LOC114786320	-VIDKPGSGAG	-TSSRKVPT	-----	SHLGRATIPSRNRIIGR	--KCGNMPYRPFQ	PPVKM
Cha_LOC105903838	SCMDKAGGGG	-----PA	-----AR	--RAAIPSRNRIIGK	--RFGDVPYRPFQ	PPMKM
	:**			:**:*:*:*:	:*:.:.:.:	:
Prim.cons.	SVIDKA	GNNGGVANSRRTPQ	STQQSHFGRQK	IPSRNRVIGK	NRRFGDMPYRPFQ	PPMKM

	310	320	330	340	350	360
Sgr_LOC107585029	SGFPVFGKLF	DSHSLNNAENQ	---TQ---	SGESCNNTTNNLSSSQ	---SSKV-DVSKVQ	TTL
San_LOC107662367	SGFPVFGKLYD	SHSLSNAENQ	---TQ---	SGESRNNTTNNLSSSQ	---NSKV-DVSKGQ	TTL
Srh_LOC107740604	SGFPVFGKLF	DSHSLSNAENQ	---TQ---	SGESRNNTTNNLSSSQ	---SSKM-DVSKGQ	TTL
Cau_LOC113046746	SGFPVFGKLF	DSHSLSNAENQ	---TQ---	SGESRNNTTNNLASSQ	---SSKA-DVSKGQ	TTL
Cca_LOC109095357	SGFPVFGKLF	DSHSLNNAENQ	---TQ---	SGESRNMTNTLSSSQ	---CSKL-DASKGQ	TTL
Cau_LOC113047918	SGFPVFGKLF	DSHSLNNAENQ	---TQ---	SGESRDNTAKNLSS	-----	KNQTL
Sgr_LOC107602318	SGFPVFGKLF	FESHSLNNAENQ	---TQ---	SGESRNNTTNNLSSSQ	---SSKV-DASKGQ	TTL
San_LOC107690738	SGFSVFGKLF	DSHSLNNAENQ	---TQ---	SGESRNNTTNDLSSSQ	---SSKV-DASKGQ	TTL
Srh_LOC107710048	SGFPVFGKLF	DSHSLNNAENQ	---TQ---	SGESRNNTTNNLSSSQ	---SSKV-DASKGQ	TTL
Dre_Cbx6b	SGFPVFGKLF	DSHSLKNAE	-----	SGESRNSMTNNLSSSQ	---SSKLLDVSKGQ	NRR
Ame_cbx6b	SGFSMGKTFN	SHPMDSNGQPAVEH	KESGQKSSSKGLSSQSSSQ	---SSKVATSDVPSAL		
Pna_LOC108413245	AGFSVFGKA	FEAHSMDSGQPKLEH	--SGHKPG-KSLSLQSLSQ	---SSKLMSTDVPKAL		
Ipu_LOC108260787	AGFSVFRKPI	EAYPMDPSEKPKAEQ	--SGHKPGTNPS--PSSSQ	---SSKVKNASVPEAL		
Eel_LOC113569862	AGFPVFGKPF	ECHPMEVSEKPKVEQ	--CVPKVACNSSSLPSSSQ	---SPKVMTPDIPKAL		
Srh_LOC107720374	LGFPMYGGP	FGHLPCGSMSSM	-----	ANEESNSGANRRGGN	RGKSCDSHSSANAQKF	
San_LOC107667890	LGFPMYGGP	FGHLPCGSMSSV	-----	ANEESNTGANQRGGN	---CCDSHSSANAQKF	
Cca_LOC109066300	LGFPMYGGP	FGHLPCGSVSSM	-----	ANEESNTGANRRGGN	---CCDSHSSANVQKF	
Cau_LOC113065021	LGFPMYGGP	FGHLPCGSMSSM	-----	ANEESKTGANQRGGN	---CCDSHSSASTQKF	
Sgr_LOC107602676	LGFPMYGGP	FGHLNPGSMSSM	-----	ANEESNTGVNRRGGG	---CCDSHSSANAQKF	
San_LOC107704552	LGFPMYGGP	FGHLNPGSMSSM	-----	ANEESNTGVNRRGGG	---CCDSHSSANARKF	
Srh_LOC107717667	LGLPMYGGP	FGHLNPGSMSSM	-----	ANEESNTGVNRRGGG	---CCDSHSSANAQKF	
Cca_LOC109066296	LGFPMYGGP	FGHLNPGSMSSM	-----	ANDGSNTVVNRQGGG	---CCDSHSSANAQKF	
Cau_LOC113039859	LGFPMYGGP	FGHLNPGSMSSM	-----	ANEESNTGVNRRGGG	---CCDSHSSASTQKF	
Dre_Cbx6a	LGIPLYGGP	FGHLNPGSGASSM	-----	ANEESNTRASHGGGS	---RCGSQSSA--QRF	
Ame_LOC103038090	LGFPMYGGP	FGQLQPFPPVSAQ	-----	PNRRAGSTSGTRGRGG	--GCGPGRPRKATKF	
Pna_Cbx6	LGFPMYGGP	FGQLQPCLPVSVQ	-----	TSKRAGSTPVAKGRG	-----PGRPSKP-KF	
Eel_LOC113585732	PGFPMYGGP	FGQLQPCPMVSVK	-----	TSRSAGPTTSGKGAGR	--NCGPGHSSAE---	
Ipu_LOC108259424	PGFPMYGGP	FGQLQPCPPASAS	-----	AGTRAGSAIGSKTRAH	--S--SADSSRV---	
Dcl_LOC114786320	PGFPMYGGP	FGQLQPMNPVFPQ	-----	THIRFCNTNARGAHS	TASATTGAPQALQ-	
Cha_LOC105903838	TGFPMYGGP	YGMQIRIGSDSFQ	-----	ANAGMASNTEAS	-IGGTSAPASASTPHAVP-	
	*:.:.:	:				
Prim.cons.	LGFPMYGGP	FGHLPCGNASN	QPKVTQKESANESSNNTTNNRGSSQ	TSSSKSHSSSKAQKL		

	370	380	390	400	410	420
Sgr_LOC107585029	DELHP-SNS	SSSEVSDG	EPSPFPQT--	QSQHSSSLPPKAS----	ATKAQDPALHK-----	
San_LOC107662367	DELPP-SNS	SSSEVSDG	EPSPFPQT--	QSQHSSSLPPKAS----	ATKAQDPALHK-----	
Srh_LOC107740604	DELPP-SNS	SSSEVSDG	EPSPFPQT--	QSQHSSSLPPKAS----	ATKAQDPALHK-----	
Cau_LOC113046746	DELPP-SNS	SSSEVSDG	EPSPFPQT--	QSQHSSSLPPKAS----	ATKAQDPALHK-----	
Cca_LOC109095357	DELPP-SNS	SSSEVSDG	EPSPFPQT--	QSQHSSSLQPKSS----	ATKAPDPTLHK-----	
Cau_LOC113047918	DELPP-SNS	SSSEVSDG	EPSPFPQT--	QSQRSSSLQPKSS----	TIKAPDPTLHK-----	
Sgr_LOC107602318	DELPP-SNS	SSSEVSDG	EPSPFPQT--	QSQHSSSLQPKSS----	ATKAPDPTLHK-----	
San_LOC107690738	DELPP-SNS	SSSEVSDG	EPSPFPQT--	QSQHSSSLQPKSS----	ATKAPDPTLHK-----	
Srh_LOC107710048	DELPP-SNS	SSSEVSDG	EPSPFPQT--	QSQHSSSLQPKSS----	ATKAPDPTLHK-----	
Dre_Cbx6b	NEEPPPSNS	SSSEVSDG	EPSPFPQT--	QSQHSSSLQPKASSTKSPSTKAPDPTLHK-----		
Ame_cbx6b	NEPPPS-SAS	SSSEVSDG	ESHTSVAPT	KSHQPLSAHDHK----	SENNNCFKLPSLSLQHN	
Pna_LOC108413245	SEAPP-SAS	SSSEVSDG	ESHLTSSA--	QSHQPSLAHQ-----	SSKVNPAILPP--L---	
Ipu_LOC108260787	VEPPR-SAS	SSSEVSDG	EPHPLPP--	QFHPN-QLPQ-----	SGEANSQISHA-----	
Eel_LOC113569862	SEPPC-SPS	SPFEVSE	GELLFPPT--	HPQPPPSAAQ-----	PCQANLAILPP-----	
Srh_LOC107720374	QYQPPPSPS	SSFSSEN	NSSPS-LQKQ	TQPEAPT-----	SPTKLDSAASSRS-----	
San_LOC107667890	QYQPPPSPS	SSFSSEN	NSSPS-LQKQ	TQPEAPT-----	SPTKLDSAASSRS-----	
Cca_LOC109066300	QYQPPPSPS	SSSGSN	NSSPS-LQKQ	TQPEAPT-----	SPTKLDSAGSSRS-----	
Cau_LOC113065021	QYQHPPSPS	SSSGSN	NSSLS-LQKT	QTLEAPM-----	SPTKLDSASSRS-----	
Sgr_LOC107602676	QYQPPPSPS	SSSGSN	NSSPS-PQKQ	TQPEAP-----	TKLDSAASSRS-----	
San_LOC107704552	QYQPPPSPS	SSSGSN	NSSPS-PQEQT	TQPEAP-----	AKLDSAASSRS-----	
Srh_LOC107717667	QYQPPPSPS	SSSGSN	NSSPS-PQKQ	TQPEAP-----	TKLDSAASSRS-----	
Cca_LOC109066296	QYQPPPSPS	SSSGS	INITPS-LQKQ	TQPEAP-----	TKLDSAASSRS-----	
Cau_LOC113039859	QYQPPPSPS	SSSGSN	NSSPS-PQKQ	TQPEAP-----	TKLDSAASTCS-----	
Dre_Cbx6a	QYQPTPSPS	SSSGSN	SSSPS-TQKQ	TQKEGPT-----	SSAKLTPTESSRS-----	
Ame_LOC103038090	PYQSPPPSPS	SSSGSE	SDASSPPKI	QPGPPQASPS	ETAPSS--PPV-LSPETPSRGSEP--	
Pna_Cbx6	PFQSPPPSPS	SSSGSE	SDAPSPPI	QPGPPQAPP-ETAPSS--	PPV-LSPETPSRCSGV--	
Eel_LOC113585732	QFQSPPPSPS	SSSGSE	SDAPSLPQI	QATPPKAPP-DSAPSS--	PPV-LSPETPSRATDD--	
Ipu_LOC108259424	RIQSPPPSPS	SSSGTE	SDAPSSRQI	HPRRKKAQLAAATSS--	PPLALSTETSSQA-----	
Dcl_LOC114786320	HYQPPPSPS	SSSGSE	SQPPSPSI	QVSAPSAVA---GAPT--	STAKLRSQTQPQ-PGD--	
Cha_LOC105903838	QYMSPPPSPS	SSSGSD	SRPPTPRQ	SKLAAPHPPP---RTRA--	SPPKLRAPAAPQSGST--	
Prim.cons.	QEQPPSPSSSSS	2SDGEPSPFPQT	QPPSP2APLQPKASSSKSSPTKLDS	SPALSRSSGDHN		

	430	440	450	460	470	480
Sgr_LOC107585029	-----LSAQPVASKN-----	SSGPPSAVPS	SPMFSSSSSA---	SSSEDNEHILD--	LSVP	
San_LOC107662367	-----LSAQPVASKN-----	SSGPPSALP	SPMFSSSSSA---	SSSEDNEHILD--	LSVP	
Srh_LOC107740604	-----LSAQPVASKN-----	SSGPPSALP	SPMFSSSSSA---	SSSEDNEHILD--	LSVP	
Cau_LOC113046746	-----LSAQPAASKN-----	SSGPPSALP	SPMFSSSSSA---	SSSEDNEHILD--	LSVP	
Cca_LOC109095357	-----LSGQTVPSKN-----	SLAPSALP	SPMFSSSSSA---	SSSEDNERILD--	LSVP	
Cau_LOC113047918	-----HSAQTVPSKN-----	SLVPTSLP	SPMFSSSSSA---	SSSEDNERILD--	LSVP	
Sgr_LOC107602318	-----LSAQPVPSKN-----	SLGLSALP	SPMFSSSSSA---	SSSEDSERILD--	LSVP	
San_LOC107690738	-----LSAQPVPSKN-----	SLGLSALP	SPMFSSSSSA---	SSSEDSEIRILD--	LSVP	
Srh_LOC107710048	-----LSAQPVPSKN-----	SLGLSALP	SPMFSSSSSA---	SSSEDSEIRILD--	LSVP	
Dre_Cbx6b	-----LGTQPVASKNK-----	DSASSALP	SPMFSSSSSA---	STSEDNEHILD--	LSVP	
Ame_cbx6b	LKDQKQSNQLKDS	QPKKSNPSAAQ	SLLPSPMFSSSSSS---	SSSEDNEHILD--	LSVP	
Pna_LOC108413245	---K-PSNQLTDLKP---	NSSAAKSVLP	SPMFSSSSSS---	SSSEDNEHILD--	LSVP	
Ipu_LOC108260787	---AKSSPQLTDSKA---	KLT--QSAMP	SPMFSSSSSSSLSS---	SSSENEHILD--	LSVP	
Eel_LOC113569862	---AKPNTQLTDCKP---	NSTPAQSTLP	SPMFSSSSSS---	SSSEDSEHILD--	LSVP	
Srh_LOC107720374	---RDASQPPPKSSS-----	APFLLSP	SPSYSSSL-----	SSLEDEDQGSPN-LATS		
San_LOC107667890	---RDASQPPPKSSS-----	APFLLSP	SPSYSSSL-----	SSLEDEDQGSPN-LATS		
Cca_LOC109066300	---QDASQPHPKSSS-----	APFLLSP	SPSYLSSP-----	SFSLDEDQGSPN-LTTS		
Cau_LOC113065021	---QDSSQPHPKSSS-----	APFLLSP	SHSYSSSP-----	SFSLDEDQGSPN-LTTS		
Sgr_LOC107602676	---RDASQPHPKSSS-----	VPFLLSP	SPSYSSS-----	SLGENQGSPN-LVTS		
San_LOC107704552	---QDASQPHPKSSS-----	APFLLSP	SPSYSSS-----	SLGENQGSPN-LVTS		
Srh_LOC107717667	---RDASQPHPKSSS-----	APFLLSP	SPSYSSS-----	SLGENQGSPN-LVTS		
Cca_LOC109066296	---RDASQPHPKSSS-----	APFLLSP	SPSYSSSP-----	SSLEDEDQGSPN-LTTS		
Cau_LOC113039859	---QDASQPHPKSSS-----	APFLLSP	SPSYSTSP-----	SSLEDEDQGSPN-LAIS		
Dre_Cbx6a	---HDTSQPHPKSSS-----	TPFLLSP	SPSYSSSP-----	SSSQEDEDLGLSK-SATS		
Ame_LOC103038090	-PQNHHSSAKPGSASN-----	PTSFLLP	SPSLSSSA-S-----	SSSPDEDEEKAQ-----		
Pna_Cbx6	-PQSRSSGAKPGSASS-----	PTSFLLP	SPSLSS--S-----	SSSPDEDEDERAQK-LPAP		
Eel_LOC113585732	-PQNCPPSSAQPGSVSD-----	PVFFLLP	SPSLSSSS-P-----	SSSPEDDERARN-VPPA		
Ipu_LOC108259424	--HNRSTCTKSGSS-----	APRLP	SPPHSSSSSS--LSSSP	EDKKGRAQN-LPFV		
Dcl_LOC114786320	-PQFQPGSTQASTAP-----	VPFLLP	SPSLSSSQ-----	SSSPFEDDEDEGRGLSTQ		
Cha_LOC105903838	-SQHQPTAAQSAAVPE-----	SAAFLP	CPSPSLSS-----	SSSLEDEEGEDAANLSAS		
Prim.cons.	LPQ2DLSQQPPKSKKSNSS2	GASFLPSSPSFSSSSSSASSSSSSSEDEE2	ILDN2LSVP			

	490	500	510	520	530	540
Sgr_LOC107585029	-HEMDRRLRRHHPFSG-----			RHPLKVPEVPVSEEE----	PSEEEEDFDW	
San_LOC107662367	-HEMDRRLRRHHPFSG-----			RHPLKVPEVPVSEEE----	PSEEEEDLDW	
Srh_LOC107740604	-HEMDRRLRRHHPFSG-----			RHPLKVPEVPVSEEE----	PSEEEEDLDW	
Cau_LOC113046746	-HEMDRRLRRHHPFSG-----			RHPLKVPEVPVSEEE----	PSEEEEDLDW	
Cca_LOC109095357	-HEMDRRLRRHHPFSG-----			RHPLKVPEVPVSEEE----	PSEEEEDLDW	
Cau_LOC113047918	-HEMDKRLRRHHPFSG-----			RHPLKVPEVPVSEEE----	PSEEEEDLDW	
Sgr_LOC107602318	-HEMDRRLRRHHPFSG-----			RHPLKVPEVPVSEEE----	PSEEEEDLDW	
San_LOC107690738	-HEMDRRLRRHHPFSG-----			RHPLKVPEVPVSEEE----	PSEEEEDLDW	
Srh_LOC107710048	-HEMDRRLRRHHPFSG-----			RHPLKVPEVPVSEEE----	PSEEEEDVDW	
Dre_Cbx6b	-HEMDRRLRRHHPFSG-----			RHPLKVPEVPVSEEE----	PSEEEEDLDW	
Ame_cbx6b	-HGSDRRGKRHYHFCR-----			HRQPKLPEIPISEEE----	ASEEEEE-LDW	
Pna_LOC108413245	-HGSDRRAKRHHHFCR-----			HQQPKLPEIPMSEEE----	ASEEEEEELDW	
Ipu_LOC108260787	-HGTDRRARQQRHFRG-----			RRQPKVPEIPISEEE----	ASEEDQDLDW	
Eel_LOC113569862	-HSTERRCRRNSFGP-----			RRPAEFPENPLPHK----	VSEEDLDLDW	
Srh_LOC107720374	-RGRKRKLRRHTQVGQ---AS-----			VCQVSDRTTTPHPEEN---	REPKEGDPDW	
San_LOC107667890	-RGRKRKLRRHTQVGR---AS-----			VCQVSDRTTTPHPEEN---	REPKEGDPDW	
Cca_LOC109066300	-RGRKRKLRRHTQVGR---AS-----			LCQVSDRTTTPLPVET---	REPKEGDPDW	
Cau_LOC113065021	-RGRKRKLQHRHTQVGR---AS-----			VCQVSDCTTTPLEET---	REPKEGNPDW	
Sgr_LOC107602676	-QGGRKLRRHTQVGR---AS-----			VCQVSDRNTAPLPEEN---	RVPKEGDPDW	
San_LOC107704552	-RGGRKLRRHTQVGR---AS-----			VCQVSDRNTAPLPEEN---	RVPKEGDPDW	
Srh_LOC107717667	-RGGRKLRRHTQVGR---AS-----			VCQVSDRNTAPLPEEN---	RVPKEGDPDW	
Cca_LOC109066296	-RGGRKLRRHTQVGR---AS-----			VCQVSDRTTAPLPEEN---	RVPKEGDPDW	
Cau_LOC113039859	-RGGRKLRRHTQVGR---AS-----			VCQVSDCTTTPLEEN---	RVPKEGDPDW	
Dre_Cbx6a	-RGRKQELRHQTQVGR---AS-----			VCQVSNQTTASFPEKN---	RVPKEGDPDW	
Ame_LOC103038090	--GGKRKPCRIRAS-----			EAATSHPAAEKRAERRALKKADPDW		
Pna_Cbx6	PKGGRKPCRFRAS-----			EGANSRPTAEK----	KALKRGNPDW	
Eel_LOC113585732	PKDGKWKPRRRTRASV---S-----			KSARQGDNSRPLAEK----	SAPERGDPDW	
Ipu_LOC108259424	ARGRKRKARRRFQTS-----			NPSSGDGTEK----	TAPKPGDPDW	
Dcl_LOC114786320	SKGRRRGRHCHHHQSSDCHATLVIANASQPLTQAIDRNAYQPS			TEQA---	RAPVEGDPDW	
Cha_LOC105903838	QKVKRSLRRRSQAS----			QP-TSASDNNTVSSPAEDATSAAL	GET---	RAPVEGDPDW
	:			:	:	**
Prim.cons.	PHGM2RRLRRHQFS2DCHASL22A22222VRQP2KVPEVP2SEENAERRS2EEGDPDW					

	550	560	570	580	590	600
Sgr_LOC107585029	HPDMTSQCANVVVDITANLLTVTIK-EFCHPPS-----			ATPPPCYPKNISAQHDT		
San_LOC107662367	RPDMTSQCANVVVDITANLLTVTIK-EFCHPPS-----			ATPPPCYPKNISAQHDT		
Srh_LOC107740604	HPDMTSQCANVVVDITANLLTVTIK-EFCHPPS-----			ATPPPCYPKNISAQHDT		
Cau_LOC113046746	HPDMTSRCANVVVDITANLLTVTIK-EFCHPPS-----			ATPPPCYPKNISQHDT		
Cca_LOC109095357	HPDMTSQCANVVVDITANLLTVRSRSSVIHPPLPLL-----			PATPKIYQLKMTQNSQS		
Cau_LOC113047918	RPDMTSKCANVVVDITANLLTVTIK-EFCHPPS-----			VNPPPCYPKNILAQHDT		
Sgr_LOC107602318	HPDMTSQCANVVVDITANLLTVTIK-EFCHPPS-----			ATPPPCYPKNISAQHDT		
San_LOC107690738	HPDMTSQCANVVVDITANLLTVTIK-EFCHPPS-----			ATPPPCYPKNISAQHDT		
Srh_LOC107710048	HPDMTSQCANVVVDITANLLTVTIK-EFCHPPS-----			ATPPPCYPKNISAQHDT		
Dre_Cbx6b	RPDMTSRCANVVVDITANLLTVTIK-EFCHPPS-----			ASSPFCYSKNVSTQNNT		
Ame_cbx6b	HPDMAAQCANVVVDVTTNLLTVTIK-EFCHPHGLPP-----			SSSSPC-----		
Pna_LOC108413245	HPDMAAQCANVVVDVTTNLLTVTIK-EFCHPHGLPP-----			SASSPCYANHFSASNKT		
Ipu_LOC108260787	HPDMAAQCANVVIDVTTNLLTVTIK-EFCHPHGLPA-----			VASSPCCANNLPSKKKT		
Eel_LOC113569862	RPDMAARCANVVVDVTTNLLTVTIK-EFCHPHGLPP-----			PVSSACFSNHLASANKT		
Srh_LOC107720374	NPEMAPSCTNVVVVDVTTNLLTVTIK-EFCHSGA-GS-----			EPSSPCQADNPPCPTTA		
San_LOC107667890	NPEMAPSCTNVVVVDVTTNLLTVTIK-EFCHSGA-GS-----			EPSSPCLADNPPCPTTA		
Cca_LOC109066300	HPQMTSCTNVVVVDVTTNLLTVTIK-EFCHSGA-GS-----			ETSSPCQADNPPCPTTA		
Cau_LOC113065021	HPEMTSCTNVVVVDVTTNLLTVTIK-EFCQSGA-GS-----			KPSSPCQADNPP-----		
Sgr_LOC107602676	HPEMAPSSANVVVDVTTNLLTVTIK-EFCHSGA-GS-----			EPSSPCQADKPPCPTTV		
San_LOC107704552	HPEMAPSCANVVVDVTTNLLTVTIK-EFCHSGA-GS-----			EPSSPCQADKPPCPTTA		
Srh_LOC107717667	HPEMAPSCANVVVDVTTNLLTVTIK-EFCHSGA-GS-----			EPSSPCQADKPPCPTTA		
Cca_LOC109066296	HPEMAPSCTNVVVVDVTTNLLTVTIK-EFCHSGA-GS-----			EPSSPCQADNPPCPTTA		
Cau_LOC113039859	HPEMAPSCANVVVDVTTNLLTVTIK-EFCQSGA-GS-----			EPSSPCQADKPPCPTTA		
Dre_Cbx6a	HPEMAPSSANVVVDVTTNLLTVTIK-EFCNSGA-GS-----			DPSSPCQADNPNSPTTT		
Ame_LOC103038090	RPERSPGCINVVVDVATNHQTVTIK-EFCKPGA-GSKGSTGSSPPSPSQAKNPGSSAPA					
Pna_Cbx6	RPERAPSCANVVVDVATNQLTVTIK-EFCKPGA-SS---			TDSTPPSPSQAKSPSFTLS		
Eel_LOC113585732	RPERAPSCANVVVDVATNHLTVTIK-EFCQPGA-GSAGSVASAPASPSHSENLTSTFTS					
Ipu_LOC108259424	HPKRTPTCANVVVDVATNHLTVTIK-EFCQSGA-AS-----			GPSPSHSENAKSSTTT		
Dcl_LOC114786320	RPDMAPCCANVVVDVTTNLLTVTIK-EFCQPTETGS-----			MPSPSPIN-STPPSVST		
Cha_LOC105903838	RPDMAPRCANVVVDVTTNLLTVTIK-EFCQPAEAGS-----			GPSPSATSSSPPPPSQ		
	*****:			*****:		
Prim.cons.	HPEMAPSCANVVVDVTTNLLTVTIKSEFCHP2ALGS2GST3SAPSSPC2AKNPPAPT					

	610	620	630	640
Sgr_LOC107585029	KQPKQHPNKT	-----	-----	-----
San_LOC107662367	KQPKQHPNKT	-----	-----	-----
Srh_LOC107740604	KQPKQHPNKT	-----	-----	-----
Cau_LOC113046746	KQPKDHPNKA	-----	-----	-----
Cca_LOC109095357	NTPTKHECRHRYALLQPSEGILEGLLVVCLQFQLPGAHVSLC	-----	-----	-----
Cau_LOC113047918	KQPKQHPNKT	-----	-----	-----
Sgr_LOC107602318	KQPKHHPNKT	-----	-----	-----
San_LOC107690738	KQPKHHPNKT	-----	-----	-----
Srh_LOC107710048	KQPKHHPKKT	-----	-----	-----
Dre_Cbx6b	QQPKQNPKNKT	-----	-----	-----
Ame_cbx6b	-----	-----	-----	-----
Pna_LOC108413245	KQPQ	-----	-----	-----
Ipu_LOC108260787	NP	-----	-----	-----
Eel_LOC113569862	NTRP	-----	-----	-----
Srh_LOC107720374	AS	-----	-----	-----
San_LOC107667890	AS	-----	-----	-----
Cca_LOC109066300	AS	-----	-----	-----
Cau_LOC113065021	-----	-----	-----	-----
Sgr_LOC107602676	AS	-----	-----	-----
San_LOC107704552	AS	-----	-----	-----
Srh_LOC107717667	AS	-----	-----	-----
Cca_LOC109066296	AS	-----	-----	-----
Cau_LOC113039859	AS	-----	-----	-----
Dre_Cbx6a	AYK	-----	-----	-----
Ame_LOC103038090	AT	-----	-----	-----
Pna_Cbx6	GT	-----	-----	-----
Eel_LOC113585732	SA	-----	-----	-----
Ipu_LOC108259424	-----	-----	-----	-----
Dcl_LOC114786320	TSVATESKP	-----	-----	-----
Cha_LOC105903838	AELPSLPLPATSVAP	-----	-----	-----
Prim.cons.	A2PKQHPNKT222A22QPSEGILEGLLVVCLQFQLPGAHVSLC	-----	-----	-----

Supplementary Figure S2. Sequence alignment for Cbx6 proteins from Ostariophysi including zebrafish (Dre, *Danio rerio*), goldfish (Cau, *Carassius auratus*), common carp (Cca, *Cyprinus carpio*), three Chinese barbels (San, *Sinocyclocheilus anshuiensis*; Sgr, *Sinocyclocheilus grahami* and Srh, *Sinocyclocheilus rhinoceros*), cave fish (Ame, *Astyanax mexicanus*), red-bellied piranha (Pna, *Pygocentrus nattereri*), channel catfish (Ipu, *Ictalurus punctatus*), electric eel (Eel, *Electrophorus electricus*) and Clupeomorpha including denticle and atlantic herrings (Dcl, *Denticeps clupeoides*; Cha, *Clupea harengus*). The alignment was performed with the CLUSTALW multiple alignment tool. Sequences of the chromodomain are highlighted in bleu, of the ATHL motif in grey, of the Cx6.1 motif in light green, of the Cx6.2 motif in dark green and of the Pc-box in violet.