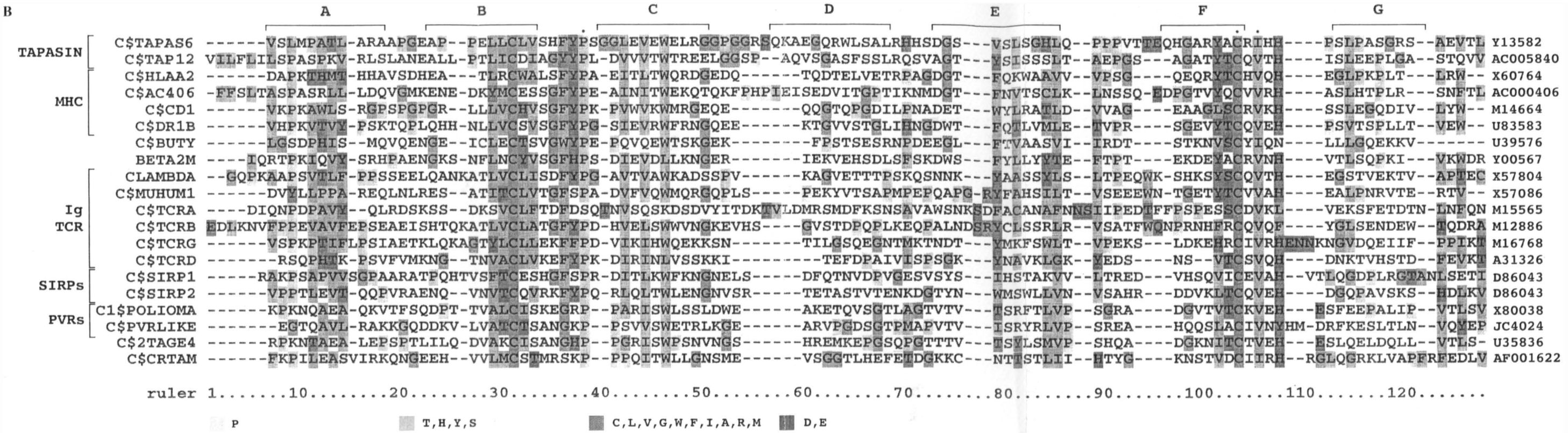


		A	B	C	C'	C''	D	E	F	G																																																			
Inv.	V\$GEODIA	---	LIVEVDSSGLV	REGSEVIVLTCEVYGY	---	PRDSSPPMWS	SPGRNL	---	ESGRFNITPRYTGTLSN	---	GSVSSSDKV	---	ALSQLTIFNITVA	DEGEYKCSVDGE	---	SASFRVDL	---	X77528																																											
	V\$AMA	---	VISQISKDVVAS	SDSVEFNCTVEEV	---	GQLSVSWAKR	RPSES	---	DTNSVVL	SMRNL	SLPD	---	KRYNVTVTEGPKTG	SAINTFRIQNIEVS	---	DMGPEYECQVLVS	---	ATEKVTK	---	KESLQ	---	M23561																																							
	V\$FREP2	---	SWLNFTG	NSETIRELIQPLKLTCTFOISKND	---	DND	SQVLFMS	TIYHETKR	---	VIASISKQPVATSLYPSVTKVQGH	IYHSNES	---	KDSYLQV	TWTHPKLS	---	ESGKYFCLAHAW	---	NSTSQN	---	SV	---	U82479																																							
	V\$FASCICLI	---	QVNVEP	TALLNRGDRTELLCRYGRS	---	INVCRIE	IPGEQ	---	KVLNLSPEWSKTPGF	---	TYFGAGLTA	---	GQCGVSI	IERVKAS	---	NNGQVKCSLGE	---	GEELSGT	---	IDLVV	---	M27813																																							
Ig-TCR	V\$KAPPA	---	EIVLTQ	SPSFLSAFV-GDRITITTCR-ASQ	---	GISSY	---	LAWYQKPGK	---	APKLLIYDASTLQRGVP	---	SRFSGRRSG	---	TDFTLT	ISSLQPE	---	IVGTYYCQKYKS	---	VP-LTF	---	GGGTKLEIKRAA	---	X97553																																						
	V\$LAMBDA	---	LTQ-PRSVSGSP	-GQSDTISCTGTSS	---	DVGGYNFVSWY	QQHPGK	---	APKLMIYDATKRPSGVP	---	DRFSGSKSG	---	NTASLT	ISLQAE	---	DEADYYC	SSQYAGD	---	YTPGVVF	---	GGGTLTVLV	---	X98219																																						
	VH\$HUM	---	QTQLVQSGAEVRKPGASVRVSK-ASG	---	YTFIDS	YTHWIR	QAPGH	---	GLEWGW	WINPN	NSGGT	---	NYAPR	FOGRVT	---	MTTRDAS	---	FSTAYMD	LRSLRSD	---	DSAVFYCAKSDPF	---	WSSYTLDVWGQGT	---	TVTVS	---	X97553																																		
	V\$TCRA	---	QQVRQSPQSLTWEGETA	ILNCSYENS	---	AFDYF	PWYQ	QFPGE	---	GPALLISILSVSDKED	---	GRFTIF	FNKRE	---	KKLSLH	ADSQPG	---	DSATY	PCAA	---	NGRALIF	---	GTGTTV	---	VSVP	---	M17660																																		
Ig-TCR like	VTCRB	---	DAGVIQSPRHEVTEM	-GQEVTLRCKPISG	---	HDYLF	FWYRQ	TMMR	---	G-LELLIYFN	NNVPID	---	DDSGMPE	---	DRFS	AKMPN	---	ASFSL	KIQP	---	SEPR	---	DSAVFYCAKSDPF	---	WSSYTLDVWGQGT	---	TVTVS	---	X97553																																
	V\$TCRG	---	SNLEGR	TKSVTRPTGSSAVITCDLPVE	---	NAVYTHWY	LHQEGK	---	APQRLIY	DSYNSR	VLVES	---	GISREKYHT	YATSG	---	KSLK	FILENLIER	---	DSGVY	YCATWKD	---	YKKLF	---	SGGTL	---	TVVTD	---	M30894																																	
	V\$TCRD	---	GIAQKITQ	TQPGMFVQEK	EAVTLDCTYDTS	---	DPSYGL	FWYKQ	PSSG	---	EMIFLI	YQGSYD	---	QONAT	---	E-	GRYSLN	FQKAR	---	KSANL	VISASQLG	---	DSAMY	FCAMRAVY	---	TDKLIF	---	GKGT	---	RVTVPEP	---	M21624																													
	V\$NAR	---	ARVDQTPQ	ITTKETGESL	TINCVLRNS	---	ACALST	TYWYR	KKSSAS	---	TNE	ESISKG	---	RYVET	VNSGS	---	KSF	SLRINDL	---	TVE	---	DSGT	---	YRCM	---	VLRCASWY	---	LLDDVY	---	CGGT	---	TVTVNP	---	U87261																											
CTX-like	V\$HFTCR	---	VLIQQT	PASISHP-GSPVRIE	CIYTEA	---	TASSV	NWYR	WHLDR	---	EPENHF	YS	PAGTIT	PSGEV	---	DGFT	ARPN-N	---	SHEF	LESSSLQVN	---	QSAVY	YCAWNQDR	---	NAGEAYF	---	GDGT	---	TKLV	---	VLG	---	U09531																												
	V\$SN193	---	VTQDPR	FMTATVGD	TVTLRCFCGED	---	SVTFF	SWYQ	QLLGG	---	KPVIL	SSRL	RHNT	TEATY	---	PQF	GRFEV	---	ESKE	---	KVNHL	TISD	---	VLPS	---	DSATY	---	YCGI	---	LEFN	---	SLEF	---	GEGTL	---	LQVRM	---	U22678																							
	V\$CRTAM	---	QEASLT	NHTETITVEEG	QTLTKCVLSL	---	KNSSL	QWL	TPSGFT	---	IFLNE	Y	PALKNSK	---	YQLL	HHSAN	---	QLSIT	VPNV	---	TLQ	---	DEGVY	---	KCHL	---	YS	---	SVST	---	KEVK	---	IVL	---	AF001622																										
	V\$CTX	---	VQVTI	QNP	IIINTSGQNTATLYCTMILNN	---	QNKNN	LVI	QWNIF	QAKS	---	QNQET	VFFY	QNGQ	SLSGPSY-K	---	NRVTA	AMSP	---	GNATIT	ISNMQSQ	---	DTGI	---	YTC	---	EVNLN	---	PESS	---	GQ	---	KILL	---	TVL	---	U43330																								
Tapasin-PVR	V\$CHT1	---	VVTVPE	KTVN	VKTG	GATLLCTYTSS	---	QPLGNFF	IOWS	FYSAKE	---	SQLHTI	Y	YSEG	QSYSGF-K	---	DRIT	AA	---	GNASIT	ISNMQPS	---	DTGS	---	YTC	---	EVFSP	---	QDDA	---	GQ	---	SQ	---	SVI	---	VNL	---	AF061023																						
	V\$CTH	---	VEVKVP	TEPL	STPLG	KTAELTCTYSTS	---	VGDTF	FALE	WSFVQ	PGKPI	---	SESHPT	ILYFT	NGHLYPT	SGK-S	---	KRVSL	LQNP	---	PTV	---	GLAT	---	KL	---	DLRPS	---	DTGT	---	YL	---	CNNVP	---	PDFYTN	---	GL	---	GLIN	---	TVL	---	AF061022																		
	V\$CTM	---	GLAVE	VTVP	TEPLS	VPKGKTAELSCSYKTS	---	VGDNF	FALE	WSFVQ	PGKPI	---	SASVP	VL	YFTNGH	LYPTGSK-A	---	DRAILL	HDP	---	PTG	---	GLAT	---	KL	---	DLRPS	---	DTGT	---	YL	---	CNNVP	---	PDFYTN	---	GL	---	GLIN	---	TVL	---	AF061024																		
	VCTHUMX	---	VQVTI	PDGF	VNVTV	GSNVTLICITTTT	---	ASREQL	SI	QWSFFHKE	---	MESIS	I	YSEG	QSYSGF-K	---	DRIT	GSNDP	---	GNASIT	ISNMQPA	---	DSGI	---	Y	---	ICD	---	VNNP	---	PDFL	---	QNGQ	---	GILN	---	YS	---	HS889N15																						
	V\$A33	---	TSVET	PQD	VLRA	SQKSVTLPCYHTS	---	TSSRE	GLI	QWDK	LLTH	---	T-ERV	V	WFFSN	KNYIHG	ELYK	---	NRV	SISN	---	NAEQ	---	SDASIT	---	ITD	---	Q	---	MA	---	DN	---	GT	---	YCS	---	SVSLM	---	SDLEGN	---	TKSR	---	VRL	---	LV	---	Q99795													
	V\$HCAR	---	SITTP	PEEMIE	KAKGETA	YLPCKFTLSP	---	EDQGL	DIE	WLIS	PADNQ	---	KVDQ	V	ILYSG	DKIYDDYYP	---	DLKGR	VHFT	---	SNDLKS	---	GDASIN	---	VTN	---	LQLS	---	DIGT	---	Y	---	QCK	---	VKKA	---	PGVANKKI	---	-HL	---	VVL	---	E28408																		
	V\$EVA	---	A	VEIYTS	RVLEA	VNGTDARLCTESSFA	---	PVGDAL	T	YWNFR	PLDG	---	GPEQ	F	YHYHID	PFQPM	SRFK	---	DRV	SWDGN	---	PER	---	YDAS	---	ILL	---	WK	---	LQ	---	D	---	NGT	---	Y	---	QV	---	KNP	---	PDV	---	DGV	---	IG	---	EIRL	---	SVVHTV	---	AF030455									
	VP0	---	VVYTD	REVH	GAVG	SRVTLHCSFWSSE	---	WVSD	D	ISFTW	RYQPEG	---	RD	AIS	I	FHYAKG	QPYIDEV	---	TEK	RIQW	---	VGD	---	P	---	RW	---	KDGS	---	Y	---	IV	---	HN	---	LD	---	Q	---	TS	---	VDV	---	G	---	KT	---	SV	---	YV	---	Q15109									
	VRAGE	---	GAVV	G	AQNTAR	IGEPLVLKCKGAPK	---	KPPQ	R	LEWKL	NTGRT	---	EAWK	V	LPQGGG	---	WDS	VARVLPN	---	G-SL	---	FLPA	---	VGIQ	---	DEGI	---	FR	---	CAMR	---	NR	---	KN	---	SVR	---	RV	---	VQI	---	Q15109																			
	VAVB\$HS1235	---	GDGQ	NLFT	KDVT	IEGEVATISQVKNKS	---	DDSVI	L	LNPN	RQT	---	YFRD	R	VDD	DEMP	---	QHAVL	SGP	---	NLF	---	FINN	---	LKNT	---	NGT	---	Y	---	CE	---	ASNI	---	---	---	VG	---	KAH	---	SD	---	YML	---	YVG	---	AC001235														
	VBASIGIN	---	PPRIK	V	GKKSEH	SEGE	LAKLVCKSDAS	---	YPPIT	D	WFWFK	TS	---	TGEE	E	AITNSTEAN	---	GKYV	V	---	VSTF	---	EKSQ	---	L	---	TIS	---	LDVN	---	VD	---	PGT	---	Y	---	VC	---	NATNA	---	QCT	---	TRET	---	-IS	---	LR	---	V	---	X64369										
	V\$CD83	---	APAT	FEV	KVAC	SEDVDLPCTAPWDP	---	QVPT	V	SWVK	LLEGE	---	ERMET	P	QEDH	IRGQHYH	QKQ	---	GSF	D	---	APNER	---	PYSI	---	K	---	IRNT	---	TSC	---	NS	---	GT	---	YR	---	CT	---	LQDP	---	DQ	---	RNL	---	SG	---	KV	---	IL	---	RV	---	T	---	Q01151					
	V\$STAGE4	AGG	ETAVQ	VLSN	STGFL-GGSVTLHCSLASKD	---	NVTIT	Q	L	WNR	KRBDG	---	SHPS	V	AFHP	PKKGPS	SIDPE-R	---	VKFL	VAKV	---	YEDL	---	RNAS	---	L	---	AI	---	SNLRVE	---	DEGI	---	Y	---	EQ	---	IATF	---	PT	---	DS	---	KSAN	---	-VWL	---	KVFA	---	U35836											
	V\$PVR	---	VVVQ	APTQ	V	PGFL-GDSVTLPCLYQVP	---	NMEV	TH	VSQ	L	TWARHC	---	ESQ	S	MAVPH	Q	TQGPS	YSESK-R	---	LEF	V	---	AARL	---	G	---	AEL	---	RNAS	---	L	---	RM	---	FL	---	GRVE	---	DEGN	---	Y	---	TC	---	LF	---	VTF	---	PO	---	CS	---	RSVD	---	-IWL	---	RVL	---	M24406	
	V1335	---	AGQ	E	VQ	TENVTVACGGVAEITCR	LHQY	---	DGSI	V	VTQ	NPARQT	---	LF	FN	T	RALKDER	---	FQ	LEEF	---	SPR	---	RVR	---	I	---	R	---	L	---	DARLE	---	DEGGY	---	PC	---	QLYTE	---	DT	---	HHQIA	---	-TL	---	TVL	---	V	---	AC005525											
	V\$TAPAS12	---	FOVMT	Q	TQSL	SFLGSSASLDCGFSMAP	---	GLDL	I	SV	WRLQHKGR	---	QOLV	S	WTAG	QQA	AVRKG	---	RD	ASLT	---	L	---	PLG	---	---	---	DEG	---	T	---	Y	---	Q	---	ITTS	---	---	---	LYRAQ	---	QI	---	Q	---	LN	---	Q	---	AC005840											
V\$TAPASCH	---	VALAV	L	THPT	TLRARV	GSPITHLHCAFAAP	---	PSSF	V	LEWR	HQNRGA	---	GRVLL	A	YDSS	TARAPRAH	PG-AELL	---	L	---	L	---	GTRD	---	GDV	---	TAV	---	L	---	R	---	L	---	ARE	---	SPG	---	DEGT	---	Y	---	IC	---	SV	---	FLPHG	---	HTQ	---	TV	---	LQ	---	HLV	---	FEPP	---	KVTL	---	AL023516
	V\$TAPAS6	---	VVL	T	VL	THTPAPRVRLQDALLDLS	FAYMPTTSEA	---	ASSL	A	PGPPF	GLEWRR	QH	LK	---	GHL	L	AAT	P	GLNG	---	QMPAAQ	---	E	---	GAFA																																			



**Fig. 11. A** Alignment of V domain sequences found in invertebrates and vertebrates molecules. The sequences have been grouped in function of the criteria described in Fig. 6 and according to the families defined *at left*. Otherwise the molecules are listed in alphabetical order with their accession number. The CTXhumx V tapasin 12 V2320 vhs159 v1235 v1335 are reconstructed and presented here for the first time. **B** Alignment of the constant C1 domain sequences. Sequences have been grouped according to the families defined *at left*. In both panels the strand composition is drawn *above the sequence*. Various shades of gray, the most conserved amino acids. The color code for the amino acids for which there is a consensus which is indicated *at the bottom*. *Right*, Accession numbers  
Please refer to text, p. 180