

	(1)	1	10	20	30	40	50	60	70	83						
Ab PB 53-197 aa	(1)	GSALSPATPPPSLNL	SHQQQQHQ	QH	YALKW	NDFQSS	ILSSFRHLRDEED	FVDVTLACDE	RSFTA	HKVVL	SACSPYFRRLLKA					
GAF PC 1-131 aa	(1)	-----	MSL	PMNSL	YSLT	WGDYGT	SLVSAIQLLRCHGDLVD	CTLAAGG	RSFPA	HKIVL	CAASPFLLDLLKN					
CP190 PA 1-131 aa	(1)	-----	MGEVK	SVKVD	NWGVFFL	QKLQNF	FNKTDYCDL	TLQFRD	NSQLKV	HRLVL	SACTDYFN	VLEQT				
Psq/BTB V 1-141 aa	(1)	-----	MAAV	VRGH	QYFSL	LRWNNYQNTMT	SVFQQ	LREDLS	FVDVTL	SCFH	GLKA	HKVVL	SACSTYFQKLLLE			
Mod(mdg4) 1-131 aa	(1)	-----	MADDE	QFSL	LCWNN	FNTNLS	SAGFHES	LCRGDLVD	VSLAAEG	QIVKA	HRLVL	SVCS	PFRRKMFTQ			
Bab2 PA 194-313 aa	(1)	-----	EG	QQF	CLR	WNNYQSNL	TNVFDELL	QSES	FVDVTL	SC	EGHS	IKAH	KMVL	SACSPYFQALFYD		
BtbVII PA 1-119 aa	(1)	-----	MSV	QQF	CLR	WNNHQ	PNFISV	CSSLHNGT	LV	DVTLAAEG	RQLQA	HKIVL	SACSSYFQALFTT			
Lola PA 1-120 aa	(1)	-----	MDDD	QQF	CLR	WNNHQ	STLISV	FDTLLENET	LV	DCTLA	AEGKFL	KA	HKVVL	SACSPYFATLLQE		
Ttk 1-131 aa	(1)	-----	MKMAS	QR	FCLR	WNNHQ	SLLSV	FDQLLHAET	FTD	VTLAVEG	QHLKA	HKMVL	SACSPYFNTL	FVS		
Lolal 1-127 aa	(1)	-----	M	SSD	QQF	FLK	WND	FQTNM	VTSFRHLRDEK	SFTD	VTLACEG	QTC	KA	HKMVL	SACSPYFKALL	EE

	(84)	84	90	100	110	120	130	140	158										
Ab PB 53-197 aa	(83)	NPC	-EHP	IVILRDV	RCD	DVENL	LSFMY	NGEVN	VSHEQLP	DFLKT	AHL	LQIRGL	ADV	NGGYPYSK	-----				
GAF PC 1-131 aa	(66)	TPC	-KHP	VMLAG	VNAN	DLEA	LEFVY	RGEV	SVDHA	QLPS	LLQAA	QCIN	IQGLA	PQTVTKDDY	TTHS	-----			
CP190 PA 1-131 aa	(63)	CEI	VDDAL	IMPNE	FQADV	VVP	IVNFM	YTG	TEFEL	KMYGK	LLRTA	KEMN	MTVL	LKLL	LEA	HRR	TMENVNR	-----	
Psq/BTB V 1-141 aa	(67)	NPC	KHPT	IILP	ADIIFT	DLKTI	IDFVY	RGEI	DVTE	SELQ	GLLRTA	EQLK	IKGL	CE	TAEN	ADDL	NDAATATITVSE		
Mod(mdg4) 1-131 aa	(64)	MPS	NTHA	IVFL	NNVSH	SALKD	LIQF	MYCGE	VNVKQ	DALPA	FISTA	ESLQ	IKGL	TD	NDP	PAPQPPQ	ESSP	-----	
Bab2 PA 194-313 aa	(62)	NPC	-QH	PII	MRDVS	WS	DLKAL	VEFMY	KGEI	NVCQD	QINP	LLKVA	ETLK	IRGL	AEV	SAGR	-----		
BtbVII PA 1-119 aa	(63)	NPC	-QH	PIV	ILKDV	QYD	DLKTM	VDFMY	YGEV	NVSQE	QLPH	ILKTA	EMLK	IKGL	AE	MP	-----		
Lola PA 1-120 aa	(64)	QYD	-KH	PIF	ILKDV	KYQ	ELRAM	MDYMY	RGEV	NISQD	QLAAL	LKAA	ESLQ	IKGL	SD	NRT	-----		
Ttk 1-131 aa	(65)	HPE	-KH	PIV	ILKDV	PYS	DMKSL	LD	FMYR	GEV	SVDQ	ERLTA	FLRVA	ESLR	IKGL	TEV	NDDK	PSPAAAAA	-----
Lolal 1-127 aa	(65)	NPS	-KH	PII	ILKDV	SYI	HLQA	ILEF	MYA	GEV	NVSQE	QLPA	FLKTA	DR	LKVK	GLAE	TPSS	IKREG	-----

CP190 BTB alignment with BTB domains of Ttk-group members

		1	10	20	30	40	50	60	70	81	Section 1																																																					
Ab PB 53-197 aa	(1)	GSALSPATPPPSLNL	SHQQQH	QH	YALKW	NDFQSSIL	SFRHLR	DEEDFV	DVTLA	CDERSFT	AHKVVL	SACSPYFRRLLK																																																				
CG41099 PB 33-164 aa	(1)	-----	-----	SE	NEESGLSS	FLSRLS	SLTVAS	LF	DKN	TYADIY	IRSQTR	VFP	AHKIVL	HARSEK	WGNDLL																																																	
GAF PC 1-131 aa	(1)	-----	-----	MS	LPMN	SLY	SLTW	G	Y	GTSLV	SAIQ	LLRCHG	DL	VD	CTLAAGGRSFP	AHKIVL	CAAS	PFLLDLLK																																														
Lolal 1-127 aa	(1)	-----	-----	MM	SSD	QQF	FLK	W	NDF	Q	T	N	M	V	S	F	R	L	R	D	E	K	S	F	T	D	V	T	L	A	C	E	G	Q	T	C	K	A	H	K	M	V	L	S	A	C	S	P	Y	F	K	A	L	L	E									
Bab2 PA 194-313 aa	(1)	-----	-----	EG	Q	F	C	L	R	W	N	Y	Q	S	N	L	T	N	V	F	D	E	L	L	Q	S	E	S	F	V	D	V	T	L	S	C	E	G	H	S	I	K	A	H	K	M	V	L	S	A	C	S	P	Y	F	Q	A	L	F	Y				
Psq/BTB V 1-141 aa	(1)	-----	-----	MAA	V	R	G	H	Q	Y	F	S	L	R	W	N	Y	Q	N	T	M	T	S	V	F	Q	Q	L	R	E	D	L	S	F	V	D	V	T	L	S	C	E	H	G	S	L	K	A	H	K	V	V	L	S	A	C	S	T	Y	F	Q	K	L	L
Mod(mdg4) 1-131 aa	(1)	-----	-----	MAD	D	E	Q	F	S	L	C	W	N	N	F	N	T	N	L	S	A	G	F	H	E	S	L	C	R	G	D	L	V	D	V	S	L	A	A	E	G	Q	I	V	K	A	H	R	L	V	L	S	V	C	S	P	F	F	R	K	M	F	T	
BtbVII PA 1-119 aa	(1)	-----	-----	MSV	Q	F	C	L	R	W	N	N	H	Q	P	N	F	I	S	V	C	S	S	L	L	H	N	G	T	L	V	D	V	T	L	A	A	E	G	R	L	Q	A	H	K	I	V	L	S	A	C	S	S	Y	F	Q	A	L	F	T				
Lola PA 1-120 aa	(1)	-----	-----	MDD	D	Q	F	C	L	R	W	N	N	H	Q	S	T	L	S	V	F	D	T	L	L	E	N	E	T	L	V	D	C	T	L	A	A	E	G	K	F	L	K	A	H	K	V	V	L	S	A	C	S	P	Y	F	A	T	L	L	Q			
Ttk 1-131 aa	(1)	-----	-----	MK	M	A	S	Q	R	F	C	L	R	W	N	N	H	Q	S	N	L	S	V	F	D	Q	L	L	H	A	E	T	F	T	D	V	T	L	A	V	E	G	Q	H	L	K	A	H	K	M	V	L	S	A	C	S	P	Y	F	N	T	L	F	V

		82	90	100	110	120	130	140	158	Section 2																																																																		
Ab PB 53-197 aa	(82)	ANPC	-EHP	IVIL	RDV	RCD	DVEN	LLS	FMY	N	GEV	N	SHE	-	QLP	D	F	L	K	T	A	H	L	L	Q	I	R	G	L	A	D	V	N	G	G	P	Y	S	K	-----																																				
CG41099 PB 33-164 aa	(60)	SN	IQ	--	QLD	-WS	DL	N	E	D	V	V	L	S	L	R	W	I	Y	T	D	L	I	D	L	Q	N	D	G	L	A	D	L	L	K	A	A	H	R	F	G	L	P	S	L	L	G	I	C	E	R	A	L	V	T	S	V	G	V	R	S	C	I	R	F	Y	C									
GAF PC 1-131 aa	(65)	NT	PC	-K	HP	V	V	M	L	A	G	V	N	A	N	D	L	E	A	L	L	E	F	V	Y	R	G	E	V	S	D	H	A	-	Q	L	P	S	L	L	Q	A	A	Q	C	L	N	I	Q	G	L	A	P	Q	T	V	T	K	D	D	Y	T	H	S	-----											
Lolal 1-127 aa	(64)	EN	PS	-K	HP	I	I	L	K	D	V	S	Y	I	H	L	Q	A	I	L	E	F	M	Y	A	G	E	V	N	S	Q	E	-	Q	L	P	A	F	L	K	T	A	D	R	L	K	V	K	G	L	A	E	T	P	S	S	I	K	R	E	G	-----														
Bab2 PA 194-313 aa	(61)	DN	PC	-Q	HP	I	I	M	R	D	V	S	W	S	D	L	K	A	L	V	E	F	M	Y	K	G	E	I	N	V	C	Q	D	-	Q	I	N	P	L	L	K	V	A	E	T	L	K	I	R	G	L	A	E	V	S	A	G	R	-----																	
Psq/BTB V 1-141 aa	(66)	EN	PC	K	H	P	T	I	I	L	P	A	D	I	I	F	T	D	L	K	T	I	I	D	F	V	Y	R	G	E	I	D	V	T	E	S	-	E	L	Q	G	L	L	R	T	A	E	Q	L	K	I	K	G	L	C	E	T	A	E	N	A	D	D	L	N	D	A	A	T	A	T	I	T	V	S	E
Mod(mdg4) 1-131 aa	(63)	Q	M	P	S	N	T	H	A	I	V	F	L	N	N	V	S	H	S	A	L	K	D	L	I	Q	F	M	Y	C	G	E	V	N	K	Q	D	-	A	L	P	A	F	I	S	T	A	E	S	L	Q	I	K	G	L	T	D	N	D	P	A	P	Q	P	P	Q	E	S	S	P	-----					
BtbVII PA 1-119 aa	(62)	T	N	P	C	-Q	HP	I	V	I	L	K	D	V	Q	Y	D	D	L	K	T	M	V	D	F	M	Y	Y	G	E	V	N	S	Q	E	-	Q	L	P	H	I	L	K	T	A	E	M	L	K	I	K	G	L	A	E	M	P	T	-----																	
Lola PA 1-120 aa	(63)	E	Q	Y	D	-K	HP	I	F	I	L	K	D	V	K	Y	Q	E	L	R	A	M	M	D	Y	M	Y	R	G	E	V	N	I	S	Q	D	-	Q	L	A	A	L	L	K	A	A	E	S	L	Q	I	K	G	L	S	D	N	R	T	-----																
Ttk 1-131 aa	(64)	S	H	P	E	-K	HP	I	V	I	L	K	D	V	P	Y	S	D	M	K	S	L	L	D	F	M	Y	R	G	E	V	S	V	D	Q	E	-	R	L	T	A	F	L	R	V	A	E	S	L	R	I	K	G	L	T	E	V	N	D	D	K	P	S	P	A	A	A	A	A	A	A	-----				

CG41099 BTB alignment with BTB domains of Ttk-group members

