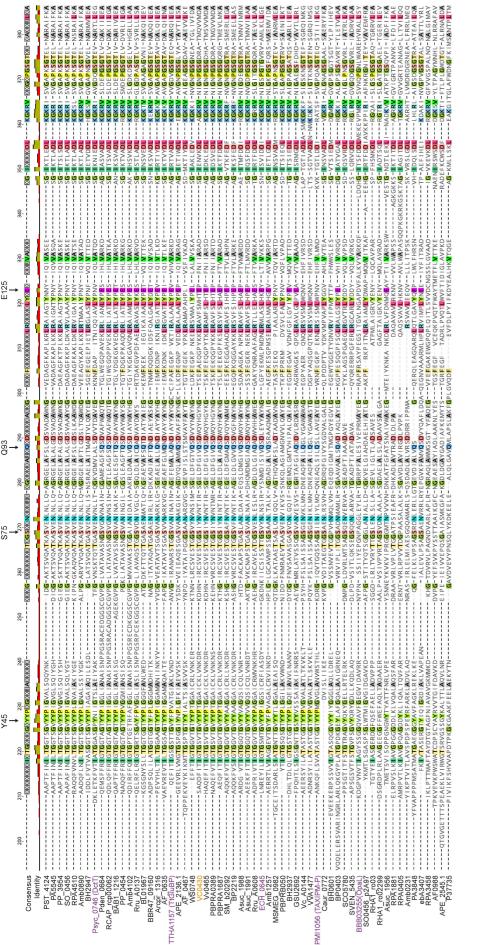
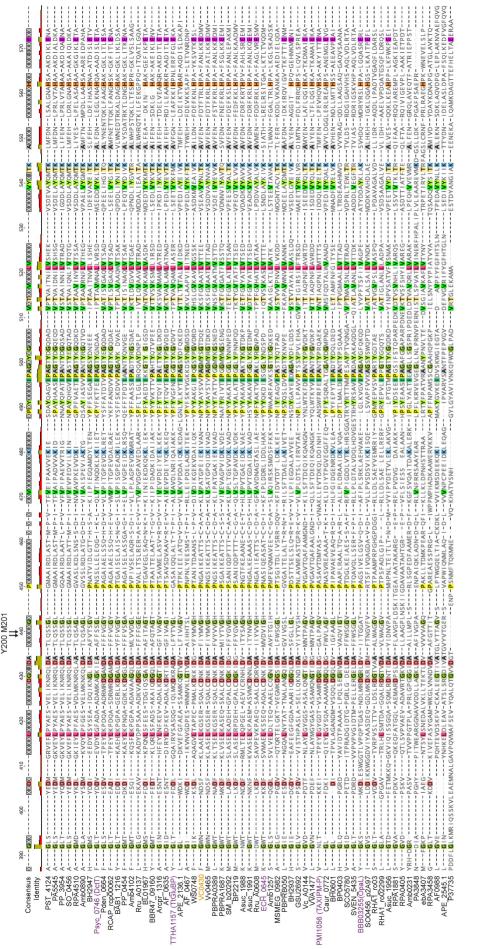
**Data S1. Multiple sequence alignment of 59 TAXI SBPs.** Sequence alignment to accompany the cladogram in Figure 1. Protein names are colour coded to match the tree in Figure 1 and the binding site residues mutated to alanine are indicated with an arrow.



TKNL P   PLINPGAERFWK -AKNL P   PLINPGAERFWK -AKNL P   PLINPGAERFWK -AKNL P   PLINPGAERFWK -AKNL P   PLINPGAERFWK -AKS - P   PLINPGAERFWK -VS - P   PLINPGAERFW -CGGA   P FINGAERFW -CGGA   P FINGAERFWK -VGGA   P		
	ν	- <b>E</b> AGVLK
	ΔΚ	
		- Eknl L P
- AKS - P PLHPGAEKY - EVGM-PVP HPGAERY - GOGM-VVP HPGAERY - TEGA-G P FHPGAERF - TEGA-G P FHPGAERF - TSSL-G P FHPGAERF - VKGA-G P FHPGAERF	INI - PADELHARKIKIK AAAS - PADELHARKIKKIK	
EVGM-PVPFHPGAERW QQGM-VAPIHPGAKKW QQGA-GIPFHPGAERFI TGGA-GIPFHPGAERFI TSSL-GIPFHPGAERFI VKGA-GIPFHAGAEKFI VKGA-GIPFHAGAEKW		
	L	
		-EQAAK
TSSL-GIPLHPGAERF		
VKGA-GIPFHAGAEKY	T SSI- G PLUP GALERY W.	
	VKGA-GIBFHAGAEK <mark>YY</mark> K	
LDKL-GIQLHGGASAY		
VQGI-AVPLHPGAMRY		KEGIIDRPGPMQP
LEGLGDIDI <mark>HPGAAKYFK</mark>		
KNGV-SIPVHPGACKY		
MAGI-SIPIHPGAYKY		
LEGL-SAPLHPAAEAY		KVGLLK
TAGN-SIPLHPGAVKY	TAGN-S   <b>PLHPG</b> AVK <mark>Y</mark> K	
SAGI-SI <mark>PLHPGA</mark> VK <mark>Y</mark>	SdGI-SI <mark>PLHPGA</mark> XXXX	EVGLLK
KNGL-SIPLHPGAIRY	KNGL-SIPLHPGAIRYYK	-EAGLLTK
KDGL-TAPLHDGAKKY	KDGL-TAPLHDGAKKWY	
KUGL-SAPLHPGAEKY	KUGL VAR HPROKENYK V DIA PROKENYK	
PAOS-TVPVHPGALRY		
AKSS-ITPMHDGAERY	AKSS-ITPMHDGAERYYK	-EIGAIK
SDGI-PIRLHEGAEAA	- SDGI - PIRLHEGAEAAAV-	
RETS-PVPLHPGAKA	RETS-PV <b>PLHPGA</b> AKALD	-ELGAAN
GQLK-GIPLHPGAQKY	60LK-61 <b>PLH6GA</b> QK <b>X</b> LN	- EQTQ
	TOUAL PURDENT RADOVCY	
AGI -PI PI HPGAARY		
LKGV-SVPLHLGAYRY		
ITGI-ANKLHPGAVKF	- ITGI-ANK <b>LHPGA</b> VKFWT	X
LRNE-VVPLHVGAIRY	LRNE-VVPLHVGAIRYYY	PESV
GRGL-SIPLHDGAVEA	GRGLSIPLHDGAVEAFE	-KL <b>G</b> APPLPEGR
IYTD-PLELHEGARRY		-SVKP
FUVG-ULKLHPGAAF		
IVTA-GVPIHPGAAAVBR		
AKNPNLFELHPGAAKYER		
EKDA-ALPAHRGAAF	DRTEMERNSDY I WGLVLLLSGLGS-AGAWERSYLTRDEREAGAKMRDRALAMVAKARKAETLEALDALOHE I DK I LRDTL	YDDGGAIEDLEPFSLVLE0FHHAVMDRBAALSASGPGLIPVDPA <b>T</b> LPA <b>A</b> HA
DKDA-VIPVQPGAAY	DKDa-VIPPGEAAATOBEEKSFLDRYSDLIWFSLMGLSLMGS-AGAWFASFLRKDERTSTASQRERLLDMLATARRCSSAEDLDTMQTEADAILRDTLTAYBCCAIDSAALTEKSFLDRYSDLIWFSLMGLSLMGS-AGAWFASFLRKDERTSTASQRERLLDMLATARRCSSAEDLDTMQTEADAILRDTLTAYBCCAIDSAALTEKSFLDRYSDLIWFSLMGLSLMGS-AGAWFASFLRKDERTSTASQRERLLDMLATARRCSSAEDLDTMQTEADAILRDTLTAYBCCAIDSAALTEKSFLDRYSDLIWFSLMGLSLMGS-AGAWFASFLRKDERTSTASQRERLLDMLATARRCSSAEDLDTMQTEADAILRDTLTAYBCCAIDSAALTEKSFLDRYSDLIWFSLMGLSLMGS-AGAWFASFLRKDERTSTASQRERLLDMLATARRCSSAEDLDTMQTEADAILRDTLTAYBCCAIDSAALTEKSFLDRYSDLIWFSLMGLSAALTEKSFLDRYSDLIWFSLMGLSAALTAYBCCAIDSAALTAYBCCAIDSAALTAYBCCAIDSAA	SAALT
EKAA-LIAI <mark>HPGA</mark> QQ <mark>Y</mark>	EKAA-LIAIHPEAGQQYVSGEIKTLFDRYADVVFIGLYAAGILGSGAVALYGMVFRRAPVHAGSRAHT-LAALRERARAARDGQELDAVEMEIEAVLDGVLSGLADGAISPKAELEGFRLAYDAARDA	ł
TLRLHEDAERY	XKSGLPLLQRYLPFRIASLADRYIILLIPFIAILIPLMKSIGPLYRWRIRARIYRWYRYIRDIDRKLDSGTDAEQLRSEIERLEKLES-ELNTVEVPLSYYHE-LYELHLLNFVIKRLHG	
ALGK-GWSYFPPMEQH	dlgk.vep.Wep.Wep.Hrac	
CIKEADDE-VADIHDGAVKALK		GL I KRQEV LAAAWKQYAAAAP SGDQEFRD – – G
AITESLAULVPVHPGLARFLKTTT		



	Market in the second se	Consensus Identity PST 4124 PA5545 PP_3954 SO_0456 SO_0456	AVAVAVAVA VAVA		-	-	20	99	e.	09 	100		130	140	<u>P</u> -	160	170	180	190
MILE	Michaeline (Michaeline (Michae	PST 4124 PA5545 PP 3954 SO <sup>0</sup> 456							3		VVVVV	~~~~~						VVV	
MI FVV	MI FUV	PA5545 PP 3954 SO 0456					NB I		·		kBIGII	AAAAFTAST	AAV						
MIT Control of the co	MI F FVV	PP 3954 SO 0456					NSL-				RRFGLF	TLAATVTEST							
MIK I	MI FVV	SO_0456					- UNP-				LRLAL -	-ASTLFAVSA	AAQ						
MICHART CONTRACT CONT	MICHARDON CONTRACT NOT CONTRACT						- I XIX		N		KRFIAV	SAALTLSLSA	ATMA						
MIRKS MIF	MI FVV	RPA4510					MKA-				EGV	AAAAVIVLAA	vPqA						
MI FW	MI FUV	Amb0890							X		RVVFGA	VLATILAVPA							
MFKYF	MI FVV	BH294/					I XXV		KFY			A SAMAL VACE							
MI FVV	MI FVV	Pden 0664									TI FAAF	A L AA S F GOAA	AA						
MI F FVV	MI F W	RCAP rcn00062					MKF-				VSFKSL	AGAALAVGLN.	140GV						
MI FLV	M F F V	BAB1 1216					MKF-				SKIRRL.	AVAAVAGAIA	LGAS			FA			
MIFKVF	MIFKVF	PP_0454					MSM-		X		SWI KTL	<b>TLALAVAGAA</b>	VTSAAST/						
MFKYF	MFKYF	Amb4102	MIFW				YPLPVMRR-		AVPAR		MPIRSI	VIAALLLLL	TGLG						
MEKYF	MEKYF	Rru_A0137					MTR-		RGL		FALVPQ	VLGMAVGMAC	MVAPAVV					RPSKA-	
MFKYF	MFKYF	BL0196/																	
MEKYF	искурство с с с с с с с с с с с с с с с с с с с	DBR4/_U9160													DEV	DSET			
MEKYF	MICK						MKK -					I FI AAI I GC	A00P		35	FKTT		TTPATT	TT
WEKVF	MFKYF	TTHA1157 (TtGluBP)					MRK-					- I LAALTLAG							
MFKYF	MEKYF	APE 2136.1					- ONMAMNQ-		R		ADAIMIAGA	AVVIVILLIA	T1A5					-907	
MKF	MKF	AF_0467	MFKYFC				- FQQQ I MKK -		ARLW		KVLALL	FLAISIAFSC	СТОТЕКР					TETAAT	TPT
MKR	MCR MCR MCR MCR MCR MCR MCR MCR MCR MCR	WS0748										GL SAL LVTSS							
MCR	WICH	1/1/1450										I KVGA I AAAV	WGAGAVNGADAN						
MICH	MICH	PRPRA0389									MAFKKL	LOMSALAGVV	MTAGMA						
MGK	MGK	PBPRA1687					MKR-				V222151	LVGFISLVVS	LTAH						
MGYH	MGYH	SM b20292					MKH-				RITLRG	AQ I AAL SAAL	FFSG					GAA	
MICK	MGYH	BP2219					MGK -		SVKHT		GHRKAFSLA	AACAAVALAW	AAPT						
MGYH MEF	MGVH	Asuc 1988					MSK-				IAKF	I LWAGL SLTA	VL SAQ						
MGYH MKK	MGYH MEK	Asuc_1991					- XXK				LFKL	<b>SLVAGIALAS</b>	LNAH						
6гүн Мг	MGYH MICK	Rru_A0608					MRF -				FAVLFA	LTVAAMPAGF						ALA	
06YH MYG	06YH 0ETVQHRK I I T	ECH_0645					MKK				Λλη JV	FISVLFNN	1 ASS						
MTM THE TRANSFER AND TH	MTK	Amb1257					MKR-					LIPALMAGLA	VLAQT					- AGA	
ВЕТV9HRK I I T	METV9HRK I I T	MSMEG 0982					- GKAAAIKK-					VI TI AVELELI							
METVOHRK I I T	METVGHRK I I T	09091494					N Y C					AL ILAVSLPF	AAEN						
METVGHRK I I T	METVGHRK I I T	Delloco														DPPA-D1GEEQ			
MTMF I RWL I L SACLLLAACSRAPDTE I L QRDVGQTLAATYGPDL FD I VM AT	MTMF1RWL1LSACLLLAACSRAPDTE1LQRDVGqTLAATYGPDLFD1WK1	2002032	WETVOUDK     T									AAITSEGI IG							
MTMF I RWL I LSACLL LAACSRAPDTE I LQRDVGQTLAATYGPDL FD I VALTRET	MTMF I RWL I LSACLLLAACSRAPDTE I LQRDVGqTLAATYGPDLFD LWARR MKR	VU AU 1477					- XXK -		N		LLMKSL	AVANVCFSAS	NVAAANV						
WITHFIRWLILSACSRAPDTEILQRDVGQTLAATYGPDLFDIVWLR	WTMFI RWL ILSACSRAPDTE ILQRDVGQTLAATYGPDLFD I VALTR	MI1056 (TAXIPM-P)					MR I -		RKT		LAIGIVAV	I AVVS LAMI G	3KK EN						
MTMFI RWL IL SACLLLAACSRAPDTE IL QRDVGQTLAATYGPDLFD1VALRR	MTMFIRWLILSACLLLAACSRAPDTEILQRDVGqTLAATYGPDLFDIVALRK	Caur_0772					-AYA-												
MINI-IKWL ILSACLLLAACSKAPDIEILQRUVGQILLAATIYGFDLFUJVARK	MINH IKWL ILSACLLLAACSKAPDI E ILQKUVGQI LAATYGPDLPU VARK	BH0601					MKK-	S			SLLSA	VGVSLLVTAA	CGGGSD			STGAD		EAG	
ALL REVALUE CONTINUE DE LE CONTRACTION DE LE CONTRACTIÓN DE LE CON	Mail	BP0403	MTMF I RWL I L SACLL	LAACSRAPDTL	EILQRDVGQT	LAATYGPDL	FDIVALRR-	5W	TAPPGQTRRV	/YYDVVLGLKKDLTLGAN	VDQPGAAAL VSL	LGAGPRS1SC	VKSSGNAAGDQIVAH.	ASAI YQRDAEQ0.	WHVAPASETAT	EAPSLDTGAPPF	PVTRQLLQTLEQ	TRSVPYSASS	TAQHV
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MIS	MI S	SO0456 n2497					ML				RN	VCGLAIAFES	LGAALGAA-					AES	
MIT	WIT	RHAT ro03					MIS-		RR		QF 1 GGV	AVAVAL SGCA	RAQP						
MXF	MXF	RHA1 ro02299					MIT-		RR		ALLRGV	VAAGATAATG	SVLASVLA-					ACS	
MASP ==DIGSDTMEANLPSTRSP ==	MARP == D= D= D5525E == 05 SFTR == D= N=NULT    L1/TT.5    G1/AS == 0.000000000000000000000000000000000	Asuc 1956					- YAK-		ł.		КНОТСК	I A I AAL CFSN	IMAQA						
MASTORL FRLADG5DTMEAULOPSTRSP	MSTORL RILADGSDTMEANLOPSIRSP	RPA1881					MASP	DGSGSE-	SFRTR		1	ALAAVLTFIL	VAVG					VLALVF	λ
MIX MIX MIX MIX MIX MIX MIX MIX MIX MIX	MR MR MR MR MR MR MR MR MR MR	RPA0405						0	AMLQPSLKSP		5 5	ILAIILSLIC	1 ASA						
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ur van Leider Verwarken en de lander ve	00 88 MRR	PA3848											× * * * * * * * * * * * * * * * * * * *						
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MLE	MAE						MKR-					I VIGVELAG	CAAFFK					PEGAT	
WIT	35	APE 2545 1					MAE -		NRNL		- AVGAVVVL I	I L VAGYML L G	GGEEOAGGEEOA					P-AATP	TET
		D37735					- L IM				RIIGAL	VGATAL SLAL	SVPA						