

Supplementary information S2 | **JmjC domain multiple sequence alignment using proteins that contain only a JmjC domain.** Multiple sequence alignment of the JmjC (Jumonji C) domain of proteins found within the JmjC-domain-only group. Fe(II)-binding (red), α KG-binding (blue), and conserved residues (black and grey) are shaded in each orthologue to show similarities and differences between related proteins within each group.

sp	SPAC25H1:	-----LYAKDMHLFRHLDPAFPYSTPDI FADDWLNAYVIDCESDDFR--	FAYLGS	SHLTTGL	HHTD	VYASHS	FVSNLC	GVK	WLFID--	PKDLQT
ce	1E200 :	-----HNMCSVQLVNPQTYYDRWYLCEVIQEQFGCFVGANTY----	LTPAG	SSGF	FPHW	DEID--	AFLLQ	VEGR	KYWR	WNA----
dm	CG2982 :	-----NPSYILRLRQVCTVLQEFHCKVGANLY----	LTPPN	SQGF	FAPH	YDIE--	AFVIQ	VEGR	KRWL	LYE----
hs	NO66 :	-----FSTTVWQFLAVLQEQFGSMAGSNVY----	LTPPN	SQGF	FAPH	YDIE--	AFVLQ	LEGR	KRLW	RVYR----
mm	NO66 :	-----FSPTVWQFLAVLQEQFGSMAGSNVY----	LTPPD	SQGF	FAPH	YDIE--	AFVLQ	LEGR	KRLW	RVYR----
hs	MINA53 :	-----FDQKRATIQFHQPQRKDELWRIQEKLECYFGSLVGSNVY----	ITPAG	SQGL	PPHY	DDVE--	VFILQ	LEGE	CKHW	RLYH----
mm	Mina53 :	-----DFDQKRATIQFHQPQRKDELWRIQEKLECYFGSLVGSNVY----	ITPAG	SQGL	PPHY	DDVE--	VFILQ	LEGE	CKHW	RLYH----
ce	5L609 :	-----LYLAQHRLFDQVPHLKRVDVII PDVCFGESSN--	PENVD	MM	WIGP	QDTS	PLHD	PR--	KMFM	VQVHGKPLFRMVA--
dm	CG13902 :	-----EYLAQHELFAQI PALKEDISIPDYCTISNEDT--	PGAVD	IK--	AWL	PAGT	VS	PMHY	DPK--	HNL
hs	JMJD5 :	-----GYLAQHQLFDQI PELKQDISIPDYCSLDGGE--	EEBIT	IN--	AWF	GQGT	IS	PLHD	DPQ--	QNF
mm	Jmj5 :	-----GYLAQHQLFDQI PELKRDISIPDYCCLNGE--	EEBIT	IN--	AWF	GQGT	IS	PLHD	DPQ--	QNF
dm	CG10133 :	-----IQKQNSLNSVDLPELAADLRVSDLDFAQQSFN--	KPPDA	VN--	FWL	GDER	AVT	SMKH	DPY--	ENV
hs	PLA2G4B :	-----VQKQCSNLPSELPLQLPDL--ESHVPWASEALG--	KMPDA	VN--	FWL	GAAA	AVT	SLHK	DHY--	ENL
mm	Pla2g4b :	-----VQKQCSNLPTELPLQLLSDI--ESHVPWASESLG--	KMPDA	VN--	FWL	GDA	AVT	SLHK	DHY--	ENL
hs	FIH :	-----LYLQQTLNLDTVGRKIVMDPLGFNWNWINKQ	GKRG	WQLT	SNLL	LIG	MEGN	VT	PAHY	DEQ--
mm	Fih :	-----LYLQQTLNLDTVGRKIVMDPLGFNWNWINKQ	GKRG	WQLT	SNLL	LIG	MEGN	VT	PAHY	DEQ--
dm	CG12879 :	KRTKSSQLLNMQQFLRKYGVLDGSDTHWAAQYKKA	DEV	PLS	CRS	SGI	GF	SS	FGFP--	DIGN
hs	HSPBAP1 :	-----Y----ADYKYFVSLFEDKTDLF----	QDV	KWS	D	FG	P	GR	NQ	EST--
mm	Hspbap1 :	-----Y----ADYKYFVTLFEDKTDVF----	QEV	VSD	D	FG	P	GR	NQ	EST--
ce	3g50 :	-----GTGVPPFFHFGPG--FAEVIHGSKRWFLYP--	YEQ	RPN						
hs	LOC339123 :	-----PTSLGNDTLVFFGDNNFTEWASLFRHYS	PP	PP	GL	T	P	A	P	A
mm	2610003J06Rik :	-----LYFFGDNNFTEWASLFRHYSPPFRLLGTT	P	P	A	P	A	P	A	P
dm	CG5383 :	-----HRRRKLDDYVVPKYFRDDL--QYCGENRR	P	P	P	P	P	P	P	P
ce	4F419 :	-----RKTKKLSEDSVVPKFEDDLF--HYADDKR	P	P	P	P	P	P	P	P
hs	PTDSR :	-----PKRRKLLLEDYKVPKFFTDLF--QYAGE	K	R	P	P	P	P	P	P
mm	Ptdsr :	-----PKRRKLLLEDYKVPKFFTDLF--QYAGE	K	R	P	P	P	P	P	P
dm	CG7200 :	-----LYLKDWHLAAQMP--GYNFYKVPKYFASD	W	L	N	E	Q	I	Q	G
hs	JMJD4 :	-----LYLKDWHLCRDFP--VEDVFTLVPYFSSD	W	L	N	E	W	D	L	D
mm	Jmj4 :	-----SLVNDL--EDIFTLPVYFSSDWLNEF	W	D	L	N	V	D	D	Y