

Figure 3 - Figure Supplement 1

a

Ub-binding

		.1.....10.....20.....30.....40.....50.....	
Sc	Swd1	-MNILLQDPFAVLKEHPEKLTHTIENPLRTECLQFSPCGDYALGCANGALVIYDMDTFR	59
Sp	Swd1	-MNLELLDPFSI-PDYPEALTTTLKHGH-ATSIRFSTNGYHLASGLVNGSVVIWDLSTFS	57
Kl	Swd1	MANLLLQDPFGVLKEYPEKLTHTLEVPAAVCVKFSRPGDYLA VGCSNGAIIYDMDSLK	60
Dm	RBBP5	-MNLELLESFG-QNYPEEFDGSLDCISLAVTCAFNKYGTLLAVGCNDGRIVIWDFLTRG	57
Xt	RBBP5	-MNLELLESFG-QNYPEEADGTLD CISMALTCTFNRWGTLLAVGCNDGRIVIWDFLTRG	57
Mm	RBBP5	-MNLELLESFG-QNYPEEADGTLD CISMALTCTFNRWGTLLAVGCNDGRIVIWDFLTRG	57
Hs	RBBP5	-MNLELLESFG-QNYPEEADGTLD CISMALTCTFNRWGTLLAVGCNDGRIVIWDFLTRG	57
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Loop1

Loop2

	250.....260.....270.....280.....290.....300	
Sc	Swd1	N-----SAVELTLEHKYQDVINKLQWNCILFSNNTAEYLVASTHGS	SAHELYIWETTSG 302
Sp	Swd1	-----NPEVEHKFQDVVNRLQWNSCGFSQT-GEFVFA-TTYQ	MAHAIYVWERGMG 288
Kl	Swd1	ESEGGSSHSVSIIELEHKYQDIINRLQWNTIFFSNHSGEYLVASAHGS	SAHDLYLWETSSG 310
Dm	RBBP5	LG-----KDGEPEPIQKLQDLVNKTTWKKCCFSGD-GEYICAGS--	ARQHAILYWEKSIG 283
Xt	RBBP5	CG-----RDGEPEPMQKLQDLVNRTPWKKCCFSGD-GEYIVAGS--	ARQHAILYWEKSIG 284
Mm	RBBP5	CG-----RDGEPEPMQKLQDLVNRTPWKKCCFSGD-GEYIVAGS--	ARQHAILYWEKSIG 284
Hs	RBBP5	CG-----RDGEPEPMQKLQDLVNRTPWKKCCFSGD-GEYIVAGS--	ARQHAILYWEKSIG 284
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Ub-binding

	390.....400.....410.....420...426	
Sc	Swd1	LEQEEIIAIDLRTREQYDVRGN-----NLLVERFTIPTDYTRIIMQSS-----	426
Sp	Swd1	----EEYFTSVVKILP---HD-----SSAEQPFVMPPTLSSS-----	398
Kl	Swd1	MTEAEIIAIDLCTPEKYDVRGN-----DISMPSFVIPIDYEGVIIQQHWAHQEQ----	439
Dm	RBBP5	AQQDEEIEVDVQKVEPVAAFCSSDEEGEDENALQFLMAPEVED--PEDGWTGQDGLEPS	422
Xt	RBBP5	GDAAEDEEVDVTSVDPIAAFCSSDEDLEDTKALLYLPIAPEVED--PEENPYGPP--PD	421
Mm	RBBP5	ADAAEDEEVDVTSVDPIAAFCSSDEELEDKALLYLPIAPEVED--PEENPYGPP--PD	421
Hs	RBBP5	ADAAEDEEVDVTSVDPIAAFCSSDEELEDKALLYLPIAPEVED--PEENPYGPP--PD	421
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b

RxR motif

	890.....900.....910.....920.....930.....	
Sc	Set1	REESSNKEPSDSVPQEVSRRDNRASNRRFQQDIEAQKAAIGTESELLSLNQLNK-RKKP	939
Kl	Set1	GTESTNQEADLEQDNHNASSRLNRVFRRFQQDIEAQRAAIGFESDLLSLNQGTK-RKKP	859
Sp	Set1	-----ISHSTRITSRMNRVNRRRLAAGVE--KSQLPAEADLLRNFNALKA-RKKQ	782
Mm	Set1A	-----GDTQGTRNV-LSERRSEQRRLLSAIG---TSAIMSDLLKLNLKF-RKKK	1578
Hs	Set1A	-----VDTGTRNV-LSERRSEQRRLLSAIG---TSAIMSDLLKLNLKF-RKKK	1569
Hs	Set1B	-----SIPAPHASTRA-GSERRSEQRRLSSFT----GSCDSLLKFNQLKF-RKKK	1828
Hs	MLL1	-----EVQLKSARRA-----TSMD----L---PMPMRFRHLKKTKEA	3830
Hs	MLL2	-----EVQLRSTRRA-----TSLE----L---PMAMRFRHLKKTKEA	2576
Hs	MLL3	-----STSTSKSFQSTVTGELNAPYSKQFVHSKSSQYRKMKTEWKSNN	4772
Hs	MLL4	-----STSMSKAYQSTFTGETNTPYSKQFVHSKSSQYRRLRTEWKNN	5398
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C

Ub-binding loop

		..130.....140.....150.....160.....170.....180.....	
Sc	Bre2	IKEGPTYWEVEVIRGGNKKFADGVNNKENADDSVDEVQSGIYEKMHKQVNDTPHLRFGVC	187
Sp	Bre2	MTSGEWYFEIKIEKGGG-----DDGAHVRIGVS	412
Kl	Bre2	MKEGKIYWEVEVK-----NVSDTSHIRCGIS	139
Dm	Ash2	VNRGCWYFEVTIE-----EMPDGAATRLGWG	369
Xt	Ash2L	VRKGAWYFEIFVD-----EMPPDTAARLGS	396
Mm	Ash2L	VRKGAWYFEITVD-----EMPPDTAARLGS	436
Hs	Ash2L	VRKGAWYFEITVD-----EMPPDTAARLGS	441
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