

Smed-mbd2/3	171	QIFWHKRLADNYAFNPNTNEKVRSEVLPKEFQNAAGPGIDNNLQFSIVSCIYNSTKNNIPVLGQSNHKASEIKNPCLLIITANQGVKQVITDDIIN	268
Sman-mbd2/3	187	QLFWEKRLADNYAFDPDTEGSEFKPISLPGKIGASVGVQPAQLVSHLIHALSSSSKSIPTIGEEQQPASEIKNPVCVINHLPQMTITFVITDDIR	284
Dmel-mbd2/3	228	QLFWEKRLRLRACHDSSQ-EEELDDITPQITRTIVQ-INVNEQTVQVSATLALHM---NAGHVGQSTKADLTKNAMAFNPQELMHAIITSEDDR	320
Ppec-mbd2/3	138	QLFWEKRLQGMHCDIEE-ETLQSMELPPEGLFAVG-PDMSSEGLVQSTASSLHLS---TQPMIGTQSGHQIEKNPQGVINTPEQPMCKPLVTEADIK	230
Bf1o-mbd2/3	177	QLFWEKRLQGNHACDIAE-EVINKMELPKSLEGL-PDWNEDTLQSIASSLHLS---NNPITGTQTPASTVEKNPAVNLNTDQPLMKVSVSDIEB	269
Drer-mbd2	136	QLFWEKRLKGLRSWDVSE-EVLTMDLPTGLQSIG-PDSSDETLLSATASALHMS---SAPITGTQSS-AAEKNPSIWINTQPLCKAFSVTDEHIR	226
Xlae-mbd2	136	QLFWEKRLQGLSASDVE-QVLRFMELPKGLQGVG-PNNDETLALAAISALHTS---SAPITGQLSA-TVEKNPSVWLNTQPLCKAFVITDDIR	226
Hsap-mbd2	280	QLFWEKRLQGLSASDVTE-QIITKMLPKGLQGVG-PGSDNETLLSASVASALHTS---SAPITGVQSA-AVEKNPAVNLNTSQPLCKAFVITDDIR	370
Ggal-mbd2	137	QLFWEKRLQGLSASDVG-ETLRKMLPRGLQALG-FVPDDVTLLSASVASALHYG---SVPVTGQLSS-AAEKNPAVWLNSSQPLCKAFVITDDIR	227
Hsap-mbd3	136	QLFWEKRLSGLNADFAIE-ELVKTMDLPKGLQGVG-PGSDNETLLSASVASALHTS---TMPITGQLSA-AVEKNPQVWLNTSQPLCKAFVITDDIR	226
Ggal-mbd3	80	QLFWEKRLSGLNADFAIE-ELVKTMDLPKGLQGVG-PGCTDETLLSASIASALHTS---TMPITGQLSA-AVEKNPQVWLNTSQPLCKAFVITDDIR	170
Xlae-mbd3	156	QLFWEKRLSGLNADFAIE-ELVKTMDLPKGLQGVG-PGCTDETLLSASIASALHTS---TMPITGQLSA-AVEKNPQVWLNTSQPLCKAFVITDDIR	246
Drer-mbd3	135	QLFWEKRLSGLNADFAIE-ELVKTMDLPKGLQGVG-PGSDTKLLSASIASALHTS---SAPITGQLSA-AVEKNPQVWLNTSQPLCKAFVITDDIR	225

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Sequence logo and alignment of MBD domain proteins. The sequence logo at the top shows conservation across 10 positions: β_1 , β_2 , β_3 , β_4 , α helix, and hairpin. Below is a multiple sequence alignment of 18 proteins. Conserved residues are highlighted in red.

Protein	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50															
Smed-MBD2/3	H	Q	T	S	L	P	P	G	W	K	R	E	E	L	I	K	P	T	G	L	Y	A	G	K	T	D	I	V	Y	--	T	S	P	T	G	Q	K	I	R	S	K	A	E	M	Q	K	I	L	G	G	----	S	Y	D	V	S	N	F	D	W	H	S	G	K	F
Hsap_MBD1	L	D	C	P	A	L	G	P	G	W	K	R	E	V	F	F	K	S	G	A	T	C	G	R	S	D	T	Y	----	Q	S	P	T	G	D	R	I	R	S	K	V	E	L	T	R	Y	L	G	P	----	A	C	D	L	T	L	F	D	F	K	Q	G	I		
Mmus_MBD1	Q	D	C	P	A	L	G	P	G	W	K	R	E	S	F	F	K	S	G	A	S	F	G	S	D	T	Y	----	Q	S	P	T	G	E	K	I	R	S	K	V	E	L	T	R	Y	L	G	P	----	A	C	D	L	T	L	F	D	F	K	Q	G	I			
Xlae_MBD1	E	D	W	P	L	L	G	P	G	W	K	R	N	V	V	R	K	S	G	A	T	C	G	H	S	D	T	Y	----	R	S	P	A	G	K	I	R	S	K	V	E	L	A	K	Y	L	G	S	----	A	V	D	L	S	F	F	D	F	R	----					
Hsap_MBD2	M	D	C	P	A	L	G	P	G	W	K	E	V	I	F	F	K	S	G	L	S	A	G	K	S	D	V	Y	----	F	S	P	S	G	K	K	F	R	S	K	P	Q	L	A	R	Y	L	G	N	----	T	V	D	L	S	S	F	D	F	T	G	K	M		
Mmus_MBD2	M	D	C	P	A	L	G	P	G	W	K	E	V	I	F	F	K	S	G	L	S	A	G	K	S	D	V	Y	----	F	S	P	S	G	K	K	F	R	S	K	P	Q	L	A	R	Y	L	G	N	----	A	V	D	L	S	S	F	D	F	T	G	K	M		
Xlae_MBD2	--	E	C	P	A	L	G	P	A	G	W	K	E	V	I	F	F	K	S	G	L	S	A	G	K	S	D	V	Y	----	Y	S	P	G	K	K	F	R	S	K	P	Q	L	A	R	Y	L	G	N	----	S	V	D	L	S	S	F	D	F	T	G	K	M		
Hsap_MBD3	W	E	C	P	A	L	P	Q	G	W	E	R	E	V	P	P	R	S	G	L	S	A	G	H	R	D	V	F	Y	----	Y	S	P	S	G	K	K	F	R	S	K	P	Q	L	A	R	Y	L	G	G	----	S	M	D	L	S	T	F	D	F	T	G	K	M	
Mmus_MBD3	W	E	C	P	A	L	P	Q	G	W	E	R	E	V	P	P	R	S	G	L	S	A	G	H	R	D	V	F	Y	----	Y	S	P	S	G	K	K	F	R	S	K	P	Q	L	A	R	Y	L	G	G	----	S	M	D	L	S	T	F	D	F	T	G	K	M	
Xlae_MBD3	W	E	C	S	A	L	P	Q	G	W	K	E	V	T	P	R	S	G	L	S	A	G	K	S	D	V	Y	----	Y	S	P	S	G	K	K	F	R	S	K	P	Q	L	A	R	Y	L	G	N	----	S	M	D	L	S	T	F	D	F	T	G	K	M			
Athali_MBD1	P	G	L	P	R	T	P	R	G	F	K	R	S	L	I	L	R	K	D	Y	S	K	----	M	D	A	Y	----	I	T	P	T	G	K	K	L	R	S	R	N	E	I																							