Table S1 : Prey Interaction Domains.

Bait	Prey	Prey size (aa)	Start of ID[a]	End of ID[b]	ID[c]
Med5	Med1	566	137	566	137-566
Med5	Med16	974	-20	510	1-510
Med7	Med10	157	2	157	101-157
			33	157	
			73	157	
			98	157	
			101	157	
Med7	Med4	284	-3	284	76-260
			20	284	
			71	284	
			76	260	
Med7	Med21	140	-6	140	58-140
			8	140	
			43	140	
			44	140	
			58	140	
Med10	Med7	222	45	222	111-203
			63	222	
			79	212	
			89	222	
			92	222	
			101	222	
			110	222	
			111	203	
Med10	Med14	1082	4	287	4-287
Med10	Med31	127	9	127	9-127
Med11	Med22	121	1	121	58-121
			58	121	
Med17	Med6	295	28	221	28-221
Med17	Med8	223	71	218	71-218
Med17	Med13	1420	790	905	790-905
Med17	Med21	140	-4	140	1-140
Med18	Med8	223	38	223	190-223
			52	223	
			75	223	
			86	223	
			98	223	
			120	223	
			132	223	
			157	223	
			163	223	
			182	223	
			190	223	

Med21	Med3	431	59	268	59-268
Med21	Med4	284	71	235	71-235
Med21	Med7	222	29	146	131-146
			43	222	
			55	222	
			63	222	
			79	213	
			95	222	
			105	222	
			106	222	
			110	222	
			111	208	
			115	222	
			131	222	
Med21	Med10	157	36	157	74-157
			41	157	
			73	157	
			74	157	
Med21	Med31	127	1	127	1-127

[a] The position of the N-terminus of the Mediator subunit fragment is indicated for each selected clone.

[b] The position of the C-terminus of the Mediator subunit fragment is indicated for each selected clone.

[c] For a given prey selected by one particular Mediator subunit, the ID is defined by the clone which encodes the fragment beginning closest to the C-terminus of the protein and the clone whose encoded fragment finishes closest to the N-terminus.

Figure S1 legend : Med8 C-terminal conserved motif

Alignments compare Med8 C-terminus from *S. cerevisiae* (Sc, upper line) and human (Hs, lowerline) with that from *S. pombe* (Sp), *A. fumigata* (Af) , *D. discoideum* (Dd), *A. thaliana* (At), *C. elegans* (Ce), and *D. melanogaster* (Dm). Flanking numbers indicate start positions in the complete peptide sequences. Solid and shaded backgrounds indicate identical or similar amino acids (aa), respectively, in at least two aligned sequences. Amino acids considered similar were R/K/H, A/S/T, I/L/V/M/C/F/Y/W, G/P, and E/D/Q/N. Positions are indicated with an asterisk if they harbor identical or similar aa in all eight sequences, or with a plus sign for three out of eight sequences. Predicted helical (H) secondary conformations are indicated above the alignment.

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