

Table S1 Mediator subunits are conserved within the crop plants.

Module	Subunit	<i>A. thaliana</i>	L (aa)	Mw	pI	Domains	<i>G. max</i> (Identity %)	<i>Z. mays</i> (Identity %)	<i>O. sativa</i> (Identity %)
Head	MED6	AT3G21350	298	33411	4.7	PF04916; PT1811104; PF030223809; G2DR.A.1.10.450.580	Glyma08g21290 (80.7)	GRMZM2G017537 (66.7)	Os06g11370 (43.4)
	MED8	AT2G03070	524	58157	9.97	PT1813552	Glyma13g45020 (80.5)	GRMZM2G168913 (49.7)	Os03g31010 (35.7)
	MED11	AT3G01435	115	13322	4.78	PF10200; PT18122890	Glyma03g32550 (66.1)	GRMZM2G071626 (51.8)	Os02g09600 (67.9)
							Glyma19g35290 (66.7)	GRMZM2G145996 (61.2)	Os02g49640 (52.7)
	MED17	AT5G20170	653	73404	6.32	PF10156; PT1813114	Glyma05g08320 (42.4)	GRMZM2G129806 (34.4)	Os12g44140 (41.0)
							Glyma14g01070 (54.1)		
							Glyma17g12660 (42.4)		
	MED18	AT2G22370	219	23365	6.5	PT1813221	Glyma09g06000 (79.8)	GRMZM2G090480 (48.1)	Os02g10050 (54.0)
							Glyma15g17250 (64.7)		
							Glyma18g18520 (63.3)		
	MED19	AT5G12230	221	25697	9.96	PT1812356	Glyma04g00310 (61.0)	GRMZM2G063688 (58.0)	Os03g44010 (59.8)
							AT5G19480	207	23824
		Glyma07g06450 (69.8)	GRMZM2G327174 (60.0)						
		Glyma16g03060 (69.8)							
	MED20	AT2G28230	219	25127	8.38	PF08612; PT1812465	Glyma13g16910 (76.7)	AC203031.3_FGP002 (44.2)	Os09g27140 (43.1)
							AT4G09070	219	25123
		AT2G28020	70	7870	6.52	PT1812465			
	MED22	AT1G07950	154	16563	4.97	PT1812454; PF06176; G2DR.A.1.20.58.1600	Glyma08g17030 (78.6)	GRMZM2G153766 (66.7)	Os01g04110 (60.5)
							Glyma15g33520 (74.0)		Os08g37480 (61.8)
		AT1G16430	150	16179	5.22	PT1812454; PF06176; G2DR.A.1.20.58.1600			
MED28	AT3G52860	156	17961	6.04	PT1813017	Glyma05g31930 (43.1)	GRMZM2G130010 (66.7)	Os05g06290 (74.4)	
						Glyma08g15230 (63.4)			
MED30	AT5G63480	189	19814	4.34	PT1813486	Glyma04g37350 (47.3)	GRMZM2G143242 (41.4)	Os04g31910 (74.3)	
						Glyma06g17740 (48.2)	GRMZM2G175188 (40.9)		
Middle	MED1	AT2G15890	203	23154	5.65	PT1813645	Glyma07g20870 (54.6)	GRMZM2G009958 (36.8)	Os03g55670 (35.2)
	MED4	AT5G02850	426	46155	4.64	PF10018; PT1813208	Glyma06g20060 (62.6)	GRMZM2G331754 (52.5)	Os09g36890 (54.3)
							Glyma08g39660 (64.5)	GRMZM2G452067 (52.1)	Os11g05150 (64.0)
						Glyma13g04800 (62.9)			
	MED7	AT5G03220	168	19425	6.36	PF05960; PT1812142N; SDP140718	Glyma07g03300 (54.8)	GRMZM2G061672 (58.2)	Os04g56640 (75.8)
							Glyma08g22810 (72.7)	GRMZM2G066981 (79.3)	
	MED9	AT1G55080	244	28586	5.95	PT1813108	Glyma07g01150 (62.1)	GRMZM2G160527 (68.2)	Os01g31629 (63)
							Glyma08g20540 (58.6)		
	MED10	AT1G26665	189	20912	5.06	PT1813345; PF09748	Glyma08g40780 (80.6)	GRMZM2G110500 (50.5)	Os09g35920 (52.5)
							AT5G41910	186	20726
	MED14	AT3G04740	1703	185507	7.43	PT1812809; PF08638	Glyma03g40750 (69.4)		
							Glyma19g43440 (70.6)		Os09g10960 (55.2)
	MED21	AT4G04780	139	15041	4.14	PT1813381; PT11221; 140718; G2DR.A.1.20.58.476; SDP140718	Glyma10g41060 (60.5)	GRMZM2G074280 (60.5)	Os08g04150 (73.7)
	MED26	AT3G10820	580	65817	6.95	SDS0505; PT1815141; G2DR.A.1.21.40.240; PF08711	Glyma04g39470 (32.1)	AC194104.3_FGP007 (51.0)	Os10g10270 (33.3)
							Glyma06g15430 (32.1)	GRMZM2G153409 (45.8)	Os03g24950 (50.0)

						PS11319; SGP47676; C280163;	Glyma19g127800 (59.7)	GRMZM2G180033 (47.9)	Os05g34210 (46.7)
						G12DA.1.26.930.10	Glyma03g124700 (60.6)	GRMZM2G702950 (44.9)	
	ATSG05140	436	49135	7.07	SM00506; PT0811541;		Glyma02g157800 (67.2)	AC218932.3_FGP009 (37.5)	
						G12DA.1.25.40.200; PF08711;			
						PS11319; SGP47676; C280163;			
						G12DA.1.26.930.10			
	ATSG09850	353	40058	4.93	SM00506; PT0811541;				
						G12DA.1.25.40.200; PF08711;			
						PS11319; SGP47676; C280163;			
						G12DA.1.26.930.10			
	MED31	ATSG19910	226	26604	9.45		Glyma10g38750 (100)	GRMZM2G139683 (93.8)	Os07g07020 (93.8)
							Glyma20g28990 (100)		Os10g41450 (57.7)
Tail	MED2/29/32	AT1G11760	151	16013	4.45	PT0821528; PT0833989	Glyma04g14710 (65.8)	GRMZM2G441565 (58.4)	Os10g40070 (47.3)
							Glyma09g34810 (65.8)		
	MED3/27	AT3G09180	402	44510	8.15	PF11571; PT0813110	Glyma03g36030 (51.6)	GRMZM2G071319 (50.0)	Os01g15850 (45.2)
							Glyma19g03150 (69.9)		
	MED5/24/33	AT2G48110	1275	139562	6.48	PT0833739	Glyma03g30760 (51.4)	GRMZM2G106790 (56.7)	Os05g24684 (33.8)
		AT3G23590	1309	143093	7.11	PT0833739	Glyma05g09220 (59.7)	GRMZM2G150754 (40.9)	Os07g11000 (55.2)
							Glyma13g28070 (67.2)	GRMZM2G151983 (34.2)	Os07g48350 (37.2)
							Glyma15g10970 (66.4)	GRMZM2G358491 (40.0)	
							Glyma18g45100 (38.5)		
							Glyma19g00780 (58.5)		
	MED15	AT1G15770	293	32657	9.3	PT0833137	Glyma08g22950 (66.1)	GRMZM2G020920 (64.7)	Os04g03860 (26.9)
		AT1G15780	1335	146345	9.72	PT0833137; G12DA.1.10.246.20; PF16087	Glyma13g44470 (70.4)	GRMZM2G164878 (70.6)	Os08g45080 (65.4)
							Glyma15g00790 (67.8)		
		AT2G10440	935	105506	8.99	PT0833137; PF16087			
	MED16	AT4G04920	1278	138185	6.13	PT0833130	Glyma13g24970 (73.4)	GRMZM2G119657 (65.6)	Os10g35560 (61.9)
							Glyma13g31480 (72.2)		
							Glyma15g07830 (68.6)		
	MED23	AT1G23230	1615	180094	7.36	PT0812091; PF11537	Glyma09g22260 (71.4)	GRMZM2G089684 (59.9)	Os02g49992 (50.0)
	MED25	AT1G25540	836	89566	8.34	PT0810270; SM00327VWVF_A3; PF11260; PT0812143	Glyma02g10880 (54.5)	GRMZM2G138178 (36.8)	Os09g13610 (82.8)
Kinase	MED12	AT4G00450	2235	247224	8.93		Glyma03g01150 (59.3)	GRMZM2G114459 (43.2)	Os07g45400 (46.1)
							Glyma07g07710 (50.6)	GRMZM5G828278 (43.4)	Os10g40260 (37.9)
							Glyma09g39550 (59.6)		
							Glyma18g46700 (58.3)		
	MED13	AT1G55325	2001	217267	6.19		Glyma18g00280 (63.7)	GRMZM2G153792 (52.2)	Os05g37500 (51.8)
							Glyma11g256800 (64.0)		
	CDK8	ATSG63610	470	52797	9.62	SM00226; PS00011; PS00100; PF00009; SGP56112; PS00107; G12DA.1.10.510.10; PT0824056-SPQ; PT0811205-SP13; PT0811205; S6112; PT0824056;	Glyma04g38510 (40.4)	GRMZM2G166771 (32.0)	Os10g42950 (48.1)
							Glyma08g00510 (80.0)		
							Glyma08g10810 (40.7)		

CYCC1	AT5G48630	256	30214	6.91	PERF025750; PF00134; S0F47954; S0B0385; PT0B10B26-SF7; 47954; C200043	Glyma08g46170 (50.8)	GRMZM2G408242 (70.7)	Os09g32680 (77.5)	
	AT5G48640	253	29914	6.43	S0B0385; G2D5A.1.10.472.10; PERF025750; PF00134; 47954; PT0B10B26; PT0B10B26-SF7; C200043	Glyma18g33140 (52.4)			
Unknown	MED34	AT1G31360	705	79368	7.49	PF00271; TK3B00044; S0B0400; PF00270; S0B0407; PF00570; PT0B13710; P530067; P551192; PF00382; G2D5A.3.40.30.300; S0F72540; P551194; PT0B13710-SF12; PT0B13710-SF72; C200046; C200079; G2D5A.1.10.10.10; G2D5A.1.10.100.00; PF16124; S0F47919; S0B00956	Glyma09g34860 (62.5)	GRMZM2G451856 (43.1)	Os04g35420 (40.7) Os11g48090 (78.9)
MED35	AT1G44910	958	109381	6.43	PF00397; P530020; S0B0406; S0B0441; PF01040; S0F31045; PT0B11064; S0F31099; G2D5A.1.10.10.440; G2D5A.2.20.70.10; PT0B11064-SF21; C200201; P531676	Glyma10g255700 (42.2)		Os01g34780 (64.3)	
					GlymaU0290000 (68.3)				
					Glyma17g35120 (73.2)				
					Glyma20g27240 (59.4)				
	AT3G19670	992	113568	6.91	PF00397; P530020; S0B0406; S0B0441; PF01040; S0F31045; PT0B11064; S0F31099; G2D5A.1.10.10.440; G2D5A.2.20.70.10; PT0B11064-SF21; C200201; P531676				
	AT3G19840	835	92806	8.68	S0B0441; S0F31099; PF00397; P501109; P530020; S0F31045; S0B0406; PF01040; PT0B13777; G2D5A.2.20.70.10; G2D5A.1.10.10.440				
MED36	AT4G25630	320	33653	10.69	PF01200; PR00052; PT0B10315; PERF000540; S0F33335 G2D5A.3.40.30.150; S0B01206; G2D5A.3.30.200.20; MF_00011	Glyma04g37770 (84.7)	GRMZM2G150648 (94.9)	Os02g57590 (96.6)	
					Glyma11g237200 (77.2)	GRMZM2G105480 (51.5)	Os05g08360 (64.3)		
					Glyma06g17310 (85.5)				
					Glyma18g02340 (67.3)				
	AT5G52470	308	32829	10.8	PF01200; PR00052; PT0B10315; PERF000540; S0F33335 G2D5A.3.40.30.150;				

					100026	PT10810175-0F1171	
					CD10241: G12DA.3.20.1276.10		
AT5G42020	668	73561	4.84	P001036	P000301	P000271	
				PF000112	P000126	PT10810175	
				P011207	PT10810175-0F1171		
				S0F10067	G12DA.3.50.648.10		
				S0F100620	S0F100614		
				G12DA.2.60.14.10			
				G12DA.3.30.428.40			
				100004	PT10810175-0F1171		
				CD10241: G12DA.3.20.1276.10			

The numbers within the brackets indicate sequence identities (%) between Arabidopsis Mediator subunits and their orthologues in other species. The source databases of *A. thaliana*, *G. max*, *Z. mays* and *O. sativa* are from *Arabidopsis thaliana TAIR10* (<https://www.arabidopsis.org>), *Glycine max Wm82.a2.v1* (<https://phytozome.jgi.doe.gov>), *Oryza sativa V7 JGI* (<https://phytozome.jgi.doe.gov>) and *Zea mays Ensembl 18* (<https://phytozome.jgi.doe.gov>), respectively. The Arabidopsis Mediator sequences were downloaded from TAIR10 (<https://www.arabidopsis.org>) by name search; and their homologs were identified by BLAST in this database. For identifying Mediator homologs in *G. max*, *Z. mays* and *O. sativa*, BLAST searches were performed based on the seed sequences from *Arabidopsis* using the BLOSUM 62 substitution matrix and an iteration threshold of 0.1. The proteins with the presence of common MED domains were selected. All the data are from websites, <https://www.arabidopsis.org> and <https://phytozome.jgi.doe.gov>.

L, protein length; Mw, Molecular weight; pI, Isoelectric points.

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