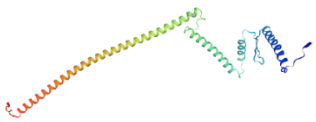
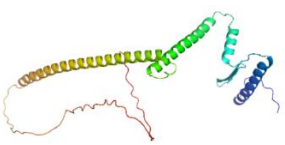
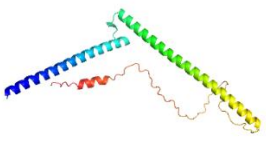
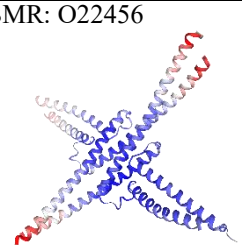
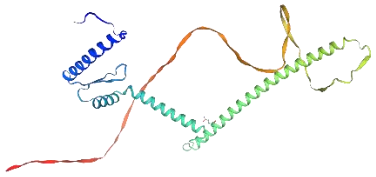
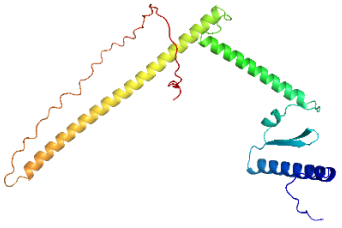
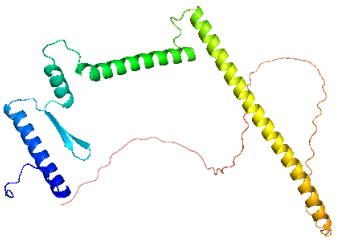
Selected results of a BLASTx search on NCBI against the transcripts of *Actinidia arguta*

Transcript ID	Scientific Name	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
64734(Sl_AGL9)	*Actinidia chinensis*	SEP3	147	306	30%	4,00E-40	89.19%	245	ADU15477.1
	Actinidia rufa	AGAMOUS-like 6	60.8	89.3	16%	4,00E-11	49.25%	183	GFY92414.1
	Arabidopsis thaliana	SEP3	95.9	198	29%	5e-25	76.92%	251	NP_564214.2
15357(At_AGL15)	*Actinidia chinensis*	SEP1	134	240	35%	2,00E-34	37.66%	238	ADU15478.1
	Actinidia rufa	AGAMOUS-like 15	450	450	23%	2,00E-151	93.25%	248	GFZ02645.1
29968(At_AGL61)	*Actinidia rufa*	AGAMOUS-like 62	150	150	11%	2,00E-40	43.16%	218	GFY89491.1
	Actinidia rufa	AGAMOUS-like 61	135	135	10%	2,00E-35	43.45%	193	GFY90130.1
1393(At_AGL61)	*Actinidia rufa*	AGAMOUS-like 62	103	103	75%	3,00E-28	58.44%	218	GFY89491.1
	Actinidia rufa	AGAMOUS-like 61	100	100	75%	9,00E-26	58.44%	471	GFZ16939.1
46683(At_AGL61)	*Actinidia rufa*	AGAMOUS-like 62	96.7	156	29%	5,00E-22	39.47%	218	GFY89491.1
	Actinidia rufa	AGAMOUS-like 61	64.3	112	27%	4,00E-11	33.88%	193	GFY90130.1
10198(At_AGL61)	*Actinidia rufa*	AGAMOUS-like 61	79.0	79.0	24%	1,00E-14	37.41%	471	GFZ16939.1
	Actinidia rufa	AGAMOUS-like 62	71.2	71.2	24%	3,00E-13	34.01%	218	GFY89491.1
7944(Arufa_AGL62)	*Actinidia rufa*	AGAMOUS-like 62	429	429	51%	1,00E-151	96.76%	219	GFY88618.1
	Actinidia rufa	AGAMOUS-like 62	134	134	50%	2,00E-36	36.32%	218	GFY89491.1
104080(At_AGL62)	*Actinidia rufa*	AGAMOUS-like 62	122	122	25%	3,00E-31	38.89%	218	GFY89491.1
	Actinidia rufa	AGAMOUS-like 61	117	117	25%	1,00E-29	42.86%	193	GFY90130.1
68068(At_AGL62)	*Actinidia rufa*	AGAMOUS-like 62	133	133	54%	5,00E-37	46.78%	218	GFY89491.1
	Actinidia rufa	AGAMOUS-like 61	139	139	53%	3,00E-37	52.73%	471	GFZ16939.1
17213(At_AGL80)	*Actinidia rufa*	AGAMOUS-like 80	334	334	48%	2,00E-114	93.07%	202	GFZ02879.1
	Actinidia rufa	AGAMOUS-like 80	166	166	41%	3,00E-48	58.43%	242	GFY89127.1
32624(At_AGL80)	*Actinidia rufa*	AGAMOUS-like 80	72.4	72.4	5%	8,00E-13	41.46%	242	GFY89127.1
	Actinidia rufa	AGAMOUS-like 80	71.6	71.6	5%	2,00E-12	40.65%	240	GFY94340.1

	64734(Sl_AGL9)			
	***Solanum lycopersicum* AGL9**	***Actinidia chinensis* SEP3**	***Actinidia rufa* AGAMOUS-like 6**	***Arabidopsis thaliana* SEP3**
UniProtKB	Q42464 (AGL9_SOLLC)	F4ZKM5 (F4ZKM5_ACTCH)	A0A7J0F155 (A0A7J0F155_9ERIC)	O22456 (SEP3_ARATH)
Protein name	Agamous-like MADS-box protein AGL9 homolog Alternative name(s): TM5	Agamous-like MADS-box protein AGL9 homolog	AGAMOUS-like 6	Developmental protein SEPALLATA 3 Alternative name: Agamous-like MADS-box protein AGL9
Sequence length (aa) Mass (kDa)	224 25,999	245 28,031	183 21,068	251 29,066
Function	Probable transcription factor active in inflorescence development and floral organogenesis.	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity; RNA polymerase II transcription regulatory region sequence-specific DNA binding	**GO - Molecular Function:** DNA-binding transcription factor activity	Probable transcription factor active in inflorescence development and floral organogenesis. Functions with SEPALLATA1/AGL2 and SEPALLATA2/AGL4 to ensure proper development of petals, stamens and carpels and to prevent the indeterminate growth of the flower meristem. Interacts with APETALA1, AGAMOUS or APETALA3/PISTILLATA to form complexes, that could be involved in genes regulation during floral meristem development. Binds specifically to the CArG box DNA sequence 5'-CC (A/T)6 GG-3'.
Subcellular location	Nucleus	Nucleus	Nucleus	Nucleus
Chain	PRO_0000199468 (1-224 aa) Agamous-like MADS-box protein AGL9 homolog	AF-F4ZKM5-F1 (1-245 aa)	AF-A0A7J0F155-F1 (1-183 aa)	PRO_0000199485 (1-251aa) Developmental protein SEPALLATA 3
Expression	Tissue specificity: Flower specific.	-	-	Developmental stage: Expressed early during flower development within petals, stamens, and carpels.
Protein-protein interaction databases	STRING: 4081.Q42464	-	-	STRING: 3702.O22456
3D structure databases	SMR: Q42464 	AlphaFoldDB: F4ZKM5 	AlphaFoldDB: A0A7J0F155 	SMR: O22456 

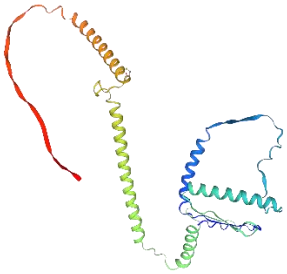
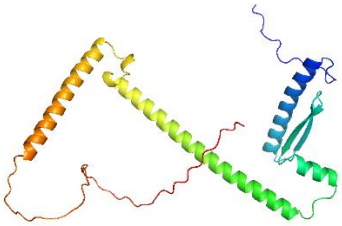
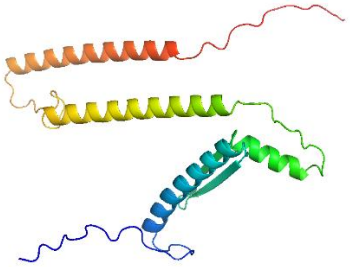
Family & Domains	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR050142 MADS-box/MEF2_TF (3-170 aa) IPR033896 MEF2-like_N (2-76 aa) IPR002487 TF_Kbox (PROSITE: 89-179 aa: Pfam: 91-173 aa) IPR002100 TF_MADSbox (SMART: 1-60 aa; PROSITE: 1-61 aa; PROSITE: 3-57 aa; PRINTS: 3-23, 23-38, 38-59 aa) IPR036879 TF_MADSbox_sf (14-111 aa) **Pfam**: PF01486 K-box 1 hit (91-173 aa) PF00319 SRF-TF 1 hit (10-57 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS51297 K_BOX 1 hit (89-179 aa) PS00350 MADS_BOX_1 1 hit (3-57 aa) PS50066 MADS_BOX_2 1 hit (1-61 aa) **Supfam:** SSF55455 SRF-like 1 hit	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR050142 MADS-box/MEF2_TF (3-187 aa) IPR033896 MEF2-like_N (2-76 aa) IPR002487 TF_Kbox (PROSITE: 89-185 aa; Pfam: 91-173 aa) IPR002100 TF_MADSbox (SMART: 1-60 aa; PROSITE: 1-61 aa; PROSITE: 3-57 aa; PRINTS: 3-23, 23-38, 38-59 aa) IPR036879 TF_MADSbox_sf (2 -75 aa) **Pfam**: PF01486 K-box 1 hit (91-173 aa) PF00319 SRF-TF 1 hit (10-57 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS51297 K_BOX 1 hit PS00350 MADS_BOX_1 1 hit PS50066 MADS_BOX_2 1 hit **Supfam:** SSF55455 SRF-like 1 hit	**InterPro**: IPR050142 MADS-box/MEF2_TF (4-121 aa) IPR002487 TF_Kbox (PROSITE: 24-114 aa; Pfam: 20-108 aa) **Pfam**: PF01486 K-box 1 hit (20-108 aa) **Prosite:** PS51297 K_BOX 1 hit (24-114 aa)	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR050142 MADS-box/MEF2_TF (3-198 aa) IPR033896 MEF2-like_N (2-76 aa) IPR002487 TF_Kbox (PROSITE: 91-181 aa: Pfam: 93-175 aa) IPR002100 TF_MADSbox (SMART: 1-60 aa; PROSITE: 1-61 aa; PROSITE: 3-57 aa; PRINTS: 3-23, 23-38, 38-59 aa) IPR036879 TF_MADSbox_sf (2-76 aa) **Pfam**: PF01486 K-box 1 hit (93-175 aa) PF00319 SRF-TF 1 hit (10-57 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS51297 K_BOX 1 hit (91-181 aa) PS00350 MADS_BOX_1 1 hit (3-57 aa) PS50066 MADS_BOX_2 1 hit (1-61 aa) **Supfam:** SSF55455 SRF-like 1 hit

	15357(At_AGL15)		
	***Arabidopsis thaliana* AGL15**	***Actinidia chinensis* SEP1**	***Actinidia rufa* AGAMOUS-like 15**
UniProtKB	Q38847 (AGL15_ARATH)	F4ZKM6 (F4ZKM6_ACTCH)	A0A7J0FVE2 (A0A7J0FVE2_9ERIC)
Protein name	Agamous-like MADS-box protein AGL15	SEP 1	AGAMOUS-like 15
Sequence length (aa) Mass (kDa)	268 30,329	238 28,031	248 28,010
Function	Transcription factor involved in the negative regulation of flowering, probably through the photoperiodic pathway. Acts both as an activator and as a repressor of transcription. Binds DNA in a sequence-specific manner in large CArG motif 5'-CC (A/T)8 GG-3'. Participates probably in the regulation of programs active during the early stages of embryo development. Prevents premature perianth senescence and abscission, fruits development and seed desiccation.	Probable transcription factor.	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: cis-regulatory region sequence-specific DNA binding; DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity

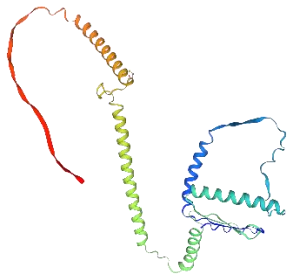
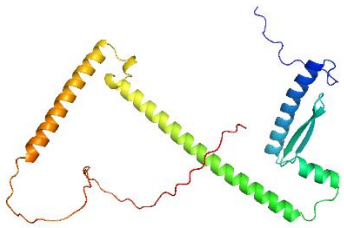
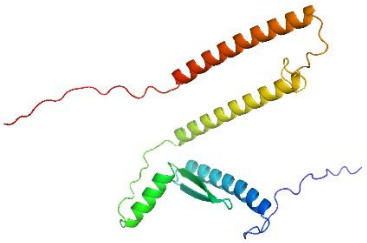
	Stimulates the expression of at least DTA4, LEC2, FUS3, ABI3, AT4G38680/CSP2 and GRP2B/CSP4. Can enhance somatic embryo development in vitro.		
Subcellular location	Cytoplasm Nucleus Note: Associated with the chromosomes during mitosis. Accumulates in the egg cytoplasm before fertilization but moves into the nucleus of the fertilized egg.	Nucleus	Nucleus
Chain	PRO_0000199474 (1-268 aa) Agamous-like MADS-box protein AGL15	AF-F4ZKM6-F1 (1-238 aa)	AF-A0A7J0FVE2-F1 (1-248 aa)
Expression	**Tissue specificity:** Expressed at low levels in flowers and siliques. Also present in seedlings. Detected during embryogenesis and accumulates during early seed development (at protein level). Expressed in shoot apices and the base of leaf petioles. **Induction:** By auxin (2,4-D). Feedback loop leading to direct down-regulation by itself. **Developmental stage:** During the reproductive phase, accumulates in immature buds and at the base of the floral organs, and in the receptacle, ovules, anther filaments, and stigma and style of open flowers. Accumulates before fertilization in the cytoplasm in the cells of the egg apparatus and moves into the nucleus during early stages of development following fertilization in the suspensor, embryo, and endosperm, mainly double fertilization derived tissues (at protein level). Highly expressed in developing embryos. In young seedlings, present in the shoot and root apices, lateral root primordia and throughout the vascular system.	-	-
Protein-protein interaction databases	STRING: 3702.Q38847	-	-
3D structure databases	SMR: Q38847 	AlphaFoldDB: F4ZKM6 	AlphaFoldDB: A0A7J0FVE2 
Family & Domains	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR050142 MADS-box/MEF2_TF (3-220 aa, 3-242 aa)	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR050142 MADS-box/MEF2_TF (3-183 aa)	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR050142 MADS-box/MEF2_TF (3-166 aa, 3-179 aa)

	IPR033896 MEF2-like_N (2-78 aa) IPR002487 TF_Kbox (80-170 aa) IPR002100 TF_MADSbox (SMART: 1-60 aa; PROSITE: 1-61 aa; PROSITE: 3-57 aa; PRINTS: 3-23, 23-38, 38-59 aa) IPR036879 TF_MADSbox_sf (2-81 aa) **Pfam**: PF01486 K-box 1 hit (75-165 aa) PF00319 SRF-TF 1 hit (10-57 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS51297 K_BOX 1 hit (80-170 aa) PS00350 MADS_BOX_1 1 hit (3-57 aa) PS50066 MADS_BOX_2 1 hit (1-61 aa) **Supfam:** SSF55455 SRF-like 1 hit	IPR033896 MEF2-like_N (2-71 aa) IPR002487 TF_Kbox (81-171 aa) IPR002100 TF_MADSbox (SMART: 1-60 aa; PROSITE: 1-61 aa; PROSITE: 3-57 aa; PRINTS: 3-23, 23-38, 38-59 aa) IPR036879 TF_MADSbox_sf (2 - 79 aa) **Pfam**: PF01486 K-box 1 hit (80-165 aa) PF00319 SRF-TF 1 hit (10-57 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS51297 K_BOX 1 hit PS00350 MADS_BOX_1 1 hit PS50066 MADS_BOX_2 1 hit **Supfam:** SSF55455 SRF-like 1 hit	IPR033896 MEF2-like_N (2-77 aa) IPR002487 TF_Kbox (86-176 aa) IPR002100 TF_MADSbox (SMART: 1-60 aa; PROSITE: 1-61 aa; PROSITE: 3-57 aa; PRINTS: 3-23, 23-38, 38-59 aa) IPR036879 TF_MADSbox_sf (2 - 77 aa) **Pfam**: PF01486 K-box 1 hit (83-170 aa) PF00319 SRF-TF 1 hit (10-57 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS51297 K_BOX 1 hit PS00350 MADS_BOX_1 1 hit PS50066 MADS_BOX_2 1 hit **Supfam:** SSF55455 SRF-like 1 hit

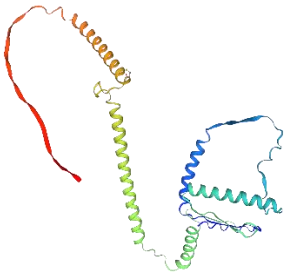
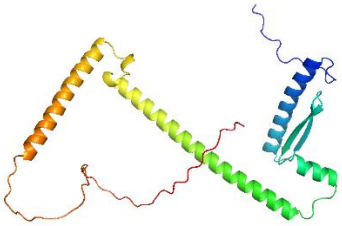
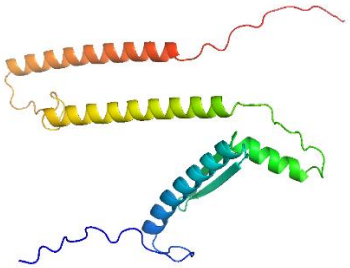
	29968(At_AGL61)		
	***Arabidopsis thaliana* AGL61**	***Actinidia rufa* AGAMOUS-like 62**	***Actinidia rufa* AGAMOUS-like 61**
UniProtKB	Q4PSU4 (AGL61_ARATH)	A0A7J0ESN3 (A0A7J0ESN3_9ERIC)	A0A7J0EUU1 (A0A7J0EUU1_9ERIC)
Protein name	Agamous-like MADS-box protein AGL61 Alternative name: Protein DIANA	AGAMOUS-like 62	AGAMOUS-like 61
Sequence length (aa) Mass (kDa)	264 30,264	218 24,695	193 21,195
Function	Probable transcription factor. Controls central cell differentiation during female gametophyte development. **Miscellaneous** Plants lacking AGL61 show a reduced size of the central cell and a reduced or absent central cell vacuole. When fertilized, the central cell fails to give rise to endosperm and the embryo sac degenerates. However, mutated female gametophytesol are not defective in pollen tube guidance and the synergid function is not impaired.	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity; RNA polymerase II cis-regulatory region sequence-specific DNA binding	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity; RNA polymerase II cis-regulatory region sequence-specific DNA binding
Subcellular location	Nucleus Note: The transport to the nucleus is dependent on dimerization with AGL80.	Nucleus	Nucleus
Chain	PRO_0000363649 (1-264 aa) Agamous-like MADS-box protein AGL61	AF-A0A7J0ESN3-F1 (1-218 aa)	AF-A0A7J0EUU1-F1 (1-193 aa)
Expression	**Tissue specificity** Expressed exclusively in the central cell of the female gametophyte and in early endosperm. **Developmental stage** Expressed in the final stages of embryo sac development.	-	-

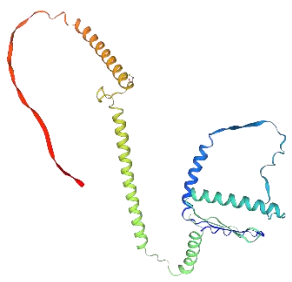
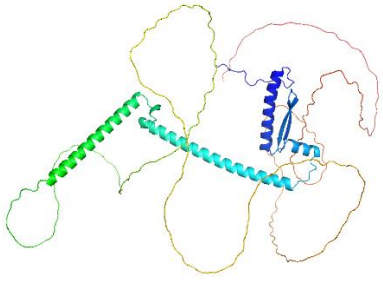
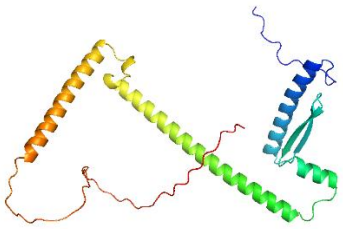
Protein-protein interaction databases	STRING: 3702.Q4PSU4	-	-
3D structure databases	SMR: Q4PSU4 	AlphaFoldDB: A0A7J0ESN3 	AlphaFoldDB: A0A7J0EUU1 
Family & Domains	**CDD:** cd00265MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (63-135 aa) IPR002100 TF_MADSbox (SMART: 62-121 aa; PROSITE: 62-122 aa; PRINTS: 64-84aa, 84-99aa, 99-120 aa) IPR036879 TF_MADSbox_sf (63-140 aa) **Pfam**: PF00319 SRF-TF 1 hit (71-118 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (62-122 aa) **Supfam:** SSF55455 SRF-like 1 hit	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (8-78 aa) IPR002100 TF_MADSbox (SMART: 7-66 aa; PROSITE: 7-67 aa; PRINTS: 9-29, 29-44, 44-65 aa) IPR036879 TF_MADSbox_sf (7-83 aa) **Pfam**: PF00319 SRF-TF 1 hit (16-63 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (7-67 aa) **Supfam:** SSF55455 SRF-like 1 hit	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (11-86 aa) IPR002100 TF_MADSbox (SMART: 10-69 aa; PROSITE: 10-70 aa; PRINTS: 12-32, 32-47, 47-68 aa) IPR036879 TF_MADSbox_sf (10-84 aa) **Pfam**: PF00319 SRF-TF 1 hit (19-66 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (10-70 aa) **Supfam:** SSF55455 SRF-like 1 hit

	1393(At_AGL61)		
	***Arabidopsis thaliana* AGL61**	***Actinidia rufa* AGAMOUS-like 62**	***Actinidia rufa* AGAMOUS-like 61**
UniProtKB	Q4PSU4 (AGL61_ARATH)	A0A7J0ESN3 (A0A7J0ESN3_9ERIC)	A0A7J0EUU1 (A0A7J0EUU1_9ERIC)
Protein name	Agamous-like MADS-box protein AGL61 Alternative name: Protein DIANA	AGAMOUS-like 62	AGAMOUS-like 61
Sequence length (aa) Mass (kDa)	264 30,264	218 24,695	193 21,195
Function	Probable transcription factor. Controls central cell differentiation during female gametophyte development. **Miscellaneous** Plants lacking AGL61 show a reduced size of the central cell and a reduced or absent central cell vacuole. When fertilized, the central cell fails to give rise to endosperm and the embryo sac degenerates. However, mutated female gametophytesol are not defective in pollen tube guidance and the synergid function is not impaired.	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity; RNA polymerase II cis-regulatory region sequence-specific DNA binding	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity; RNA polymerase II cis-regulatory region sequence-specific DNA binding

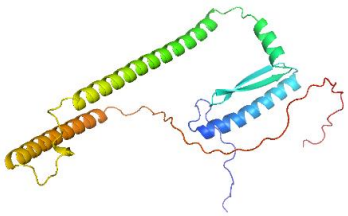
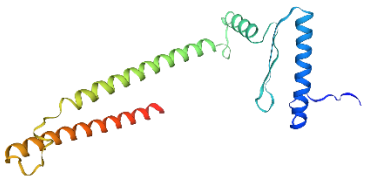
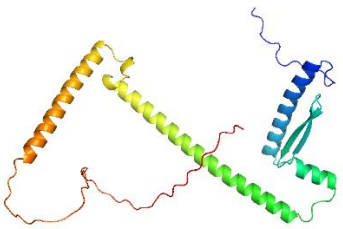
Subcellular location	Nucleus Note: The transport to the nucleus is dependent on dimerization with AGL80.	Nucleus	Nucleus
Chain	PRO_0000363649 (1-264 aa) Agamous-like MADS-box protein AGL61	AF-A0A7J0ESN3-F1 (1-218 aa)	AF-A0A7J0EUU1-F1 (1-193 aa)
Expression	**Tissue specificity** Expressed exclusively in the central cell of the female gametophyte and in early endosperm. **Developmental stage** Expressed in the final stages of embryo sac development.	-	-
Protein-protein interaction databases	STRING: 3702.Q4PSU4	-	-
3D structure databases	SMR: Q4PSU4 	AlphaFoldDB: A0A7J0ESN3 	AlphaFoldDB: A0A7J0EUU1 
Family & Domains	**CDD:** cd00265MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (63-135 aa) IPR002100 TF_MADSbox (SMART: 62-121 aa; PROSITE: 62-122 aa; PRINTS: 64-84aa, 84-99aa, 99-120 aa) IPR036879 TF_MADSbox_sf (63-140 aa) **Pfam**: PF00319 SRF-TF 1 hit (71-118 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (62-122 aa) **Supfam:** SSF55455 SRF-like 1 hit	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (8-78 aa) IPR002100 TF_MADSbox (SMART: 7-66 aa; PROSITE: 7-67 aa; PRINTS: 9-29, 29-44, 44-65 aa) IPR036879 TF_MADSbox_sf (7-83 aa) **Pfam**: PF00319 SRF-TF 1 hit (16-63 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (7-67 aa) **Supfam:** SSF55455 SRF-like 1 hit	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (11-86 aa) IPR002100 TF_MADSbox (SMART: 10-69 aa; PROSITE: 10-70 aa; PRINTS: 12-32, 32-47, 47-68 aa) IPR036879 TF_MADSbox_sf (10-84 aa) **Pfam**: PF00319 SRF-TF 1 hit (19-66 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (10-70 aa) **Supfam:** SSF55455 SRF-like 1 hit

	46683(At_AGL61)		
	***Arabidopsis thaliana* AGL61**	***Actinidia rufa* AGAMOUS-like 62**	***Actinidia rufa* AGAMOUS-like 61**
UniProtKB	Q4PSU4 (AGL61_ARATH)	A0A7J0ESN3 (A0A7J0ESN3_9ERIC)	A0A7J0EUU1 (A0A7J0EUU1_9ERIC)
Protein name	Agamous-like MADS-box protein AGL61 Alternative name: Protein DIANA	AGAMOUS-like 62	AGAMOUS-like 61
Sequence length (aa) Mass (kDa)	264 30,264	218 24,695	193 21,195

Function	Probable transcription factor. Controls central cell differentiation during female gametophyte development. **Miscellaneous** Plants lacking AGL61 show a reduced size of the central cell and a reduced or absent central cell vacuole. When fertilized, the central cell fails to give rise to endosperm and the embryo sac degenerates. However, mutated female gametophytesol are not defective in pollen tube guidance and the synergid function is not impaired.	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity; RNA polymerase II cis-regulatory region sequence-specific DNA binding	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity; RNA polymerase II cis-regulatory region sequence-specific DNA binding
Subcellular location	Nucleus Note: The transport to the nucleus is dependent on dimerization with AGL80.	Nucleus	Nucleus
Chain	PRO_0000363649 (1-264 aa) Agamous-like MADS-box protein AGL61	AF-A0A7J0ESN3-F1 (1-218 aa)	AF-A0A7J0EUU1-F1 (1-193 aa)
Expression	**Tissue specificity** Expressed exclusively in the central cell of the female gametophyte and in early endosperm. **Developmental stage** Expressed in the final stages of embryo sac development.	-	-
Protein-protein interaction databases	STRING: 3702.Q4PSU4	-	-
3D structure databases	SMR: Q4PSU4 	AlphaFoldDB: A0A7J0ESN3 	AlphaFoldDB: A0A7J0EUU1 
Family & Domains	**CDD:** cd00265MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (63-135 aa) IPR002100 TF_MADSbox (SMART: 62-121 aa; PROSITE: 62-122 aa; PRINTS: 64-84aa, 84-99aa, 99-120 aa) IPR036879 TF_MADSbox_sf (63-140 aa) **Pfam**: PF00319 SRF-TF 1 hit (71-118 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (62-122 aa) **Supfam:** SSF55455 SRF-like 1 hit	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (8-78 aa) IPR002100 TF_MADSbox (SMART: 7-66 aa; PROSITE: 7-67 aa; PRINTS: 9-29, 29-44, 44-65 aa) IPR036879 TF_MADSbox_sf (7-83 aa) **Pfam**: PF00319 SRF-TF 1 hit (16-63 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (7-67 aa) **Supfam:** SSF55455 SRF-like 1 hit	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (11-86 aa) IPR002100 TF_MADSbox (SMART: 10-69 aa; PROSITE: 10-70 aa; PRINTS: 12-32, 32-47, 47-68 aa) IPR036879 TF_MADSbox_sf (10-84 aa) **Pfam**: PF00319 SRF-TF 1 hit (19-66 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (10-70 aa) **Supfam:** SSF55455 SRF-like 1 hit

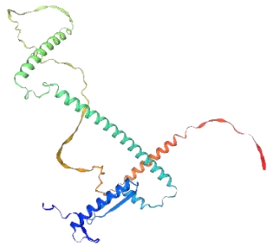
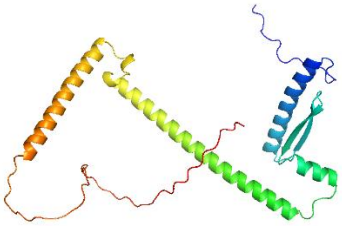
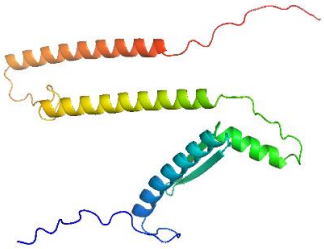
	10198(At_AGL61)		
	***Arabidopsis thaliana* AGL61**	***Actinidia rufa* AGAMOUS-like 61**	***Actinidia rufa* AGAMOUS-like 62**
UniProtKB	Q4PSU4 (AGL61_ARATH)	A0A7J0H1G5 (A0A7J0H1G5_9ERIC)	A0A7J0ESN3 (A0A7J0ESN3_9ERIC)
Protein name	Agamous-like MADS-box protein AGL61 Alternative name: Protein DIANA	AGAMOUS-like 61	AGAMOUS-like 62
Sequence length (aa) Mass (kDa)	264 30,264	471 48,501	218 24,695
Function	Probable transcription factor. Controls central cell differentiation during female gametophyte development. **Miscellaneous** Plants lacking AGL61 show a reduced size of the central cell and a reduced or absent central cell vacuole. When fertilized, the central cell fails to give rise to endosperm and the embryo sac degenerates. However, mutated female gametophytesol are not defective in pollen tube guidance and the synergid function is not impaired.	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity; RNA polymerase II cis-regulatory region sequence-specific DNA binding	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity; RNA polymerase II cis-regulatory region sequence-specific DNA binding
Subcellular location	Nucleus Note: The transport to the nucleus is dependent on dimerization with AGL80.	Nucleus	Nucleus
Chain	PRO_0000363649 (1-264 aa) Agamous-like MADS-box protein AGL61	AF-A0A7J0H1G5-F1 (1-471 aa)	AF-A0A7J0ESN3-F1 (1-218 aa)
Expression	**Tissue specificity** Expressed exclusively in the central cell of the female gametophyte and in early endosperm. **Developmental stage** Expressed in the final stages of embryo sac development.	-	-
Protein-protein interaction databases	STRING: 3702.Q4PSU4	-	-
3D structure databases	SMR: Q4PSU4 	AlphaFoldDB: A0A7J0H1G5 	AlphaFoldDB: A0A7J0ESN3 
Family & Domains	**CDD:** cd00265MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (63-135 aa) IPR002100 TF_MADSbox (SMART: 62-121 aa; PROSITE: 62-122 aa; PRINTS: 64-84, 84-99, 99-120 aa)	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (8-79 aa) IPR002100 TF_MADSbox (SMART: 7-66 aa; PROSITE: 7-67 aa; PRINTS: 9-29, 29-44, 44-65 aa) IPR036879 TF_MADSbox_sf (8-78 aa)	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (8-78 aa) IPR002100 TF_MADSbox (SMART: 7-66 aa; PROSITE: 7-67 aa; PRINTS: 9-29, 29-44, 44-65 aa)

	IPR036879 TF_MADSbox_sf (63-140 aa) **Pfam**: PF00319 SRF-TF 1 hit (71-118 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (62-122 aa) **Supfam:** SSF55455 SRF-like 1 hit	**Pfam**: PF00319 SRF-TF 1 hit (16-63 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (7-67 aa) **Supfam:** SSF55455 SRF-like 1 hit	IPR036879 TF_MADSbox_sf (7-83 aa) **Pfam**: PF00319 SRF-TF 1 hit (16-63 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (7-67 aa) **Supfam:** SSF55455 SRF-like 1 hit

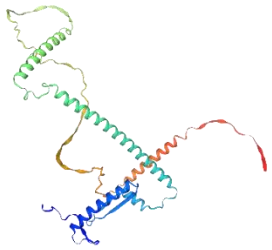
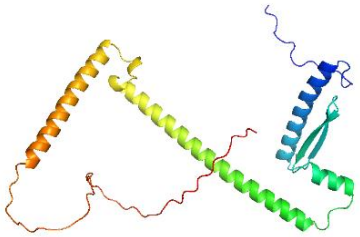
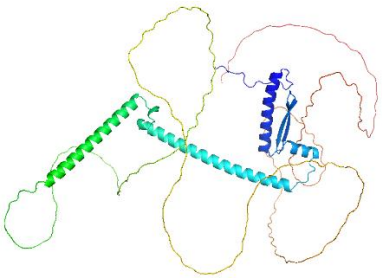
	7944(Arufa_AGL62)		
	***Actinidia rufa* AGAMOUS-like 62**	***Arabidopsis thaliana* AGL29**	***Actinidia rufa* AGAMOUS-like 62**
UniProtKB	A0A7J0EQ66 (A0A7J0EQ66_9ERIC)	O64703 (AGL29_ARATH)	A0A7J0ESN3 (A0A7J0ESN3_9ERIC)
Protein name	AGAMOUS-like 62	Agamous-like MADS-box protein AGL29	AGAMOUS-like 62
Sequence length (aa)	219	172	218
Mass (kDa)	25,170	19,753	24,695
Function	**GO - Molecular Function**: cis-regulatory region sequence-specific DNA binding; DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity	Probable transcription factor.	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity; RNA polymerase II cis-regulatory region sequence-specific DNA binding
Subcellular location	Nucleus	Nucleus	Nucleus
Chain	AF-A0A7J0EQ66-F1 (1-219 aa)	PRO_0000433965 (1-172 aa) Agamous-like MADS-box protein AGL29	AF-A0A7J0ESN3-F1 (1-218 aa)
Expression	-	**Tissue specificity** Expressed in pollen. **Developmental stage** During embryogenesis, expressed in the chalazal endosperm.	-
Protein-protein interaction databases	-	STRING: 3702.O64703	-
3D structure databases	AlphaFoldDB: A0A7J0EQ66 	SMR: O64703 	AlphaFoldDB: A0A7J0ESN3 
Family & Domains	**InterPro**: IPR002100 TF_MADSbox (SMART: 6-68 aa; PROSITE: 10-69 aa; PRINTS: 11-31 aa, 31-46 aa, 46-67 aa)	**InterPro**: IPR002100TF_MADSbox (SMART: 1-60 aa; PROSITE: 1-61 aa; PRINTS: 3-23 aa, 23-38 aa, 38-59 aa) IPR036879TF_MADSbox_sf (2-76 aa)	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (8-78 aa)

	IPR036879 TF_MADSbox_sf (12-88 aa) **Pfam**: PF00319 SRF-TF 1 hit (19-65 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (17-69 aa) **Supfam:** SSF55455SRF-like 1 hit	**Pfam**: PF00319 SRF-TF 1 hit (12-57 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (1-61 aa) **Supfam:** SSF55455 SRF-like 1 hit	IPR002100 TF_MADSbox (SMART: 7-66 aa; PROSITE: 7-67 aa; PRINTS: 9-29, 29-44, 44-65 aa) IPR036879 TF_MADSbox_sf (7-83 aa) **Pfam**: PF00319 SRF-TF 1 hit (16-63 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (7-67 aa) **Supfam:** SSF55455 SRF-like 1 hit

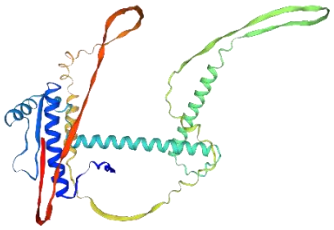
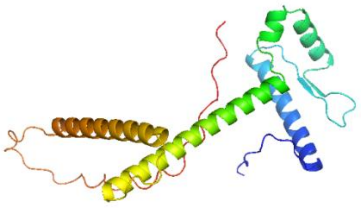
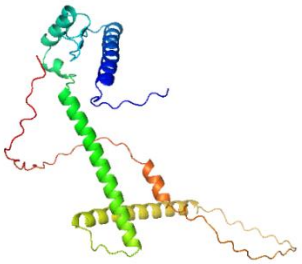
	104080(At_AGL62)		
	***Arabidopsis thaliana* AGL62**	***Actinidia rufa* AGAMOUS-like 62**	***Actinidia rufa* AGAMOUS-like 61**
UniProtKB	Q9FKK2 (AGL62_ARATH)	A0A7J0ESN3 (A0A7J0ESN3_9ERIC)	A0A7J0EUU1 (A0A7J0EUU1_9ERIC)
Protein name	Agamous-like MADS-box protein AGL62	AGAMOUS-like 62	AGAMOUS-like 61
Sequence length (aa) Mass (kDa)	299 34,588	218 24,695	193 21,195
Catalytic activity	-	-	-
Function	Probable transcription factor. Required for suppression of cellularization and promotion of nuclear proliferation during early endosperm development. The FERTILIZATION-INDEPENDENT SEED (FIS) polycomb complex is required for suppression of ALG62 expression at the end of the syncytial phase of endosperm development. **Miscellaneous** Plants lacking AGL62 show a premature endosperm cellularization and a seed-lethal phenotype.	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity; RNA polymerase II cis-regulatory region sequence-specific DNA binding	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity; RNA polymerase II cis-regulatory region sequence-specific DNA binding
Subcellular location	Nucleus	Nucleus	Nucleus
Chain	PRO_0000363650 (1-299 aa) Agamous-like MADS-box protein AGL62	AF-A0A7J0ESN3-F1 (1-218 aa)	AF-A0A7J0EUU1-F1 (1-193 aa)
Expression	**Tissue specificity** Expressed in the endosperm but not in the embryo. Detected in young siliques, roots, leaves, stems, young flowers and anthers. **Developmental stage** Expressed during the syncytial endosperm development.	-	-
Protein-protein interaction databases	STRING: 3702.Q9FKK2	-	-

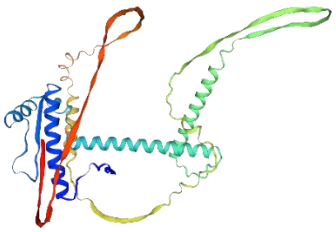
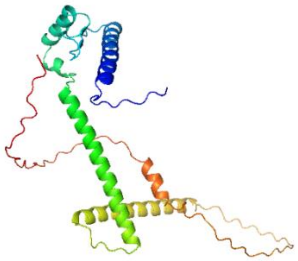
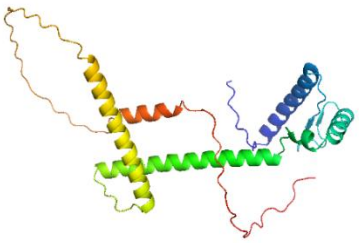
3D structure databases	SMR: Q9FKK2 	AlphaFoldDB: A0A7J0ESN3 	AlphaFoldDB: A0A7J0EUU1 
Family & Domains	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (7-78 aa) IPR002100 TF_MADSbox (SMART: 6-65 aa; PROSITE: 6-66 aa; PRINTS: 8-28 aa, 28-43 aa, 43-64 aa) IPR036879 TF_MADSbox_sf (7-86 aa) **Pfam**: PF00319 SRF-TF 1 hit (15-62 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (6-66 aa) **Supfam:** SSF55455 SRF-like 1 hit	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (8-78 aa) IPR002100 TF_MADSbox (SMART: 7-66 aa; PROSITE: 7-67 aa; PRINTS: 9-29, 29-44, 44-65 aa) IPR036879 TF_MADSbox_sf (7-83 aa) **Pfam**: PF00319 SRF-TF 1 hit (16-63 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (7-67 aa) **Supfam:** SSF55455 SRF-like 1 hit	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (11-86 aa) IPR002100 TF_MADSbox (SMART: 10-69 aa; PROSITE: 10-70 aa; PRINTS: 12-32, 32-47, 47-68 aa) IPR036879 TF_MADSbox_sf (10-84 aa) **Pfam**: PF00319 SRF-TF 1 hit (19-66 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (10-70 aa) **Supfam:** SSF55455 SRF-like 1 hit

	68068(At_AGL62)		
	***Arabidopsis thaliana* AGL62**	***Actinidia rufa* AGAMOUS-like 62**	***Actinidia rufa* AGAMOUS-like 61**
UniProtKB	Q9FKK2 (AGL62_ARATH)	A0A7J0ESN3 (A0A7J0ESN3_9ERIC)	A0A7J0H1G5 (A0A7J0H1G5_9ERIC)
Protein name	Agamous-like MADS-box protein AGL62	AGAMOUS-like 62	AGAMOUS-like 61
Sequence length (aa) Mass (kDa)	299 34,588	218 24,695	471 48,501
Function	Probable transcription factor. Required for suppression of cellularization and promotion of nuclear proliferation during early endosperm development. The FERTILIZATION-INDEPENDENT SEED (FIS) polycomb complex is required for suppression of ALG62 expression at the end of the syncytial phase of endosperm development. **Miscellaneous** Plants lacking AGL62 show a premature endosperm cellularization and a seed-lethal phenotype.	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity; RNA polymerase II cis-regulatory region sequence-specific DNA binding	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity; RNA polymerase II cis-regulatory region sequence-specific DNA binding
Subcellular location	Nucleus	Nucleus	Nucleus
Chain	PRO_0000363650 (1-299 aa) Agamous-like MADS-box protein AGL62	AF-A0A7J0ESN3-F1 (1-218 aa)	AF-A0A7J0H1G5-F1 (1-471)

Expression	**Tissue specificity** Expressed in the endosperm but not in the embryo. Detected in young siliques, roots, leaves, stems, young flowers and anthers. **Developmental stage** Expressed during the syncytial endosperm development.	-	-
Protein-protein interaction databases	STRING: 3702.Q9FKK2	-	-
3D structure databases	SMR: Q9FKK2 	AlphaFoldDB: A0A7J0ESN3 	AlphaFoldDB: A0A7J0H1G5 
Family & Domains	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (7-78 aa) IPR002100 TF_MADSbox (SMART: 6-65 aa; PROSITE: 6-66 aa; PRINTS: 8-28 aa, 28-43 aa, 43-64 aa) IPR036879 TF_MADSbox_sf (7-86 aa) **Pfam**: PF00319 SRF-TF 1 hit (15-62 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (6-66 aa) **Supfam:** SSF55455 SRF-like 1 hit	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (8-78 aa) IPR002100 TF_MADSbox (SMART: 7-66 aa; PROSITE: 7-67 aa; PRINTS: 9-29, 29-44, 44-65 aa) IPR036879 TF_MADSbox_sf (7-83 aa) **Pfam**: PF00319 SRF-TF 1 hit (16-63 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (7-67 aa) **Supfam:** SSF55455 SRF-like 1 hit	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR033896 MEF2-like_N (8-79 aa) IPR002100 TF_MADSbox (SMART: 7-66 aa; PROSITE: 7-67 aa; PRINTS: 9-29, 29-44, 44-65 aa) IPR036879 TF_MADSbox_sf (8-78 aa) **Pfam**: PF00319 SRF-TF 1 hit (16-63 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (7-67 aa) **Supfam:** SSF55455 SRF-like 1 hit

	17213(At_AGL80)		
	***Arabidopsis thaliana* AGL80**	***Actinidia rufa* AGAMOUS-like 80**	***Actinidia rufa* AGAMOUS-like 80**
UniProtKB	Q9FJK3 (AGL80_ARATH)	A0A7J0FW04 (A0A7J0FW04_9ERIC)	A0A7J0EU74 (A0A7J0EU74_9ERIC)
Protein name	Agamous-like MADS-box protein AGL80	AGAMOUS-like 80	AGAMOUS-like 80
Sequence length (aa) Mass (kDa)	321 36,825	202 23,426	242 28,010
Function	Probable transcription factor. Controls central cell differentiation during female gametophyte development. Required for the expression of DEMETER and DD46, but not for the expression of FIS2. Probable transcription factor that may function in the maintenance of the proper function of the central cell in pollen tube attraction.	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: cis-regulatory region sequence-specific DNA binding; DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: cis-regulatory region sequence-specific DNA binding; DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity

	Miscellaneous Plants lacking AGL80 (mutant fem111) have defects in central cell and endosperm development.		
Subcellular location	Nucleus	Nucleus	Nucleus
Chain	PRO_0000363651 (1-321 aa) Agamous-like MADS-box protein AGL80	AF-A0A7J0FW04-F1 (1-202 aa)	AF-A0A7J0F6N5-F1 (1-240 aa)
Expression	**Tissue specificity** Expressed in the central cell of the female gametophyte and in early endosperm. Also detected in ovaries, young siliques, roots, leaves, stems, young flowers and anthers.	-	-
Protein-protein interaction databases	STRING: 3702.Q9FJK3	-	-
3D structure databases	SMR: Q9FJK3 	AlphaFoldDB: A0A7J0FW04 	AlphaFoldDB: AF-A0A7J0EU74-F1 
Family & Domains	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR050142 MADS-box/MEF2_TF (3-272 aa) IPR033897 MEF2-like_N (2-85 aa) IPR002100 TF_MADSbox (SMART: 1-60 aa; PROSITE: 1-49 aa; PRINTS: 3-23 aa, 23-38 aa) IPR036879 TF_MADSbox_sf (7-86 aa) **Pfam**: PF00319 SRF-TF 1 hit (10-51 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (1-49 aa) **Supfam:** SSF55455 SRF-like 1 hit	**CDD:** cd00266MADS_SRF_like 1 hit **InterPro**: IPR033897 SRF-like_MADS-box (2-85 aa) IPR036879 TF_MADSbox_sf (14-119 aa) IPR002100 TF_MADSbox (SMART: 1-60 aa; PROSITE: 1-49 aa; PRINTS: 3-23, 23-38, 38-59 aa) **Pfam**: PF00319 SRF-TF 1 hit (10-51 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit **Supfam:** SSF55455 SRF-like 1 hit	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR050142 MADS-box/MEF2_TF (3-160 aa) IPR033897 MEF2-like_N (2-85 aa) IPR002100 TF_MADSbox (SMART: 1-60 aa; PROSITE: 1-49 aa; PROSITE: 3-57 aa; PRINTS: 3-23, 23-38 aa) IPR036879 TF_MADSbox_sf (13-97 aa) **Pfam**: PF00319 SRF-TF 1 hit (10-51 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit **Supfam:** SSF55455 SRF-like 1 hit

	32624(At_AGL80)		
	***Arabidopsis thaliana* AGL80**	***Actinidia rufa* AGAMOUS-like 80**	***Actinidia rufa* AGAMOUS-like 80**
UniProtKB	Q9FJK3 (AGL80_ARATH)	A0A7J0EU74 (A0A7J0EU74_9ERIC)	A0A7J0F6N5 (A0A7J0F6N5_9ERIC)
Protein name	Agamous-like MADS-box protein AGL80	AGAMOUS-like 80	AGAMOUS-like 80
Sequence length (aa) Mass (kDa)	321 36,825	242 28,010	240 27,367
Function	Probable transcription factor. Controls central cell differentiation during female gametophyte development. Required for the expression of DEMETER and DD46, but not for the expression of FIS2. Probable transcription factor that may function in the maintenance of the proper function of the central cell in pollen tube attraction. **Miscellaneous** Plants lacking AGL80 (mutant fem111) have defects in central cell and endosperm development.	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: cis-regulatory region sequence-specific DNA binding; DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity	**GO - Biological Process**: positive regulation of transcription by RNA polymerase II **GO - Molecular Function**: cis-regulatory region sequence-specific DNA binding; DNA-binding transcription factor activity, RNA polymerase II-specific; protein dimerization activity
Subcellular location	Nucleus	Nucleus	Nucleus
Chain	PRO_0000363651 (1-321 aa) Agamous-like MADS-box protein AGL80	AF-A0A7J0FVE2-F1 (1-242 aa)	AF-A0A7J0FVE2-F1 (1-248 aa)
Expression	**Tissue specificity** Expressed in the central cell of the female gametophyte and in early endosperm. Also detected in ovaries, young siliques, roots, leaves, stems, young flowers and anthers.	-	-
Protein-protein interaction databases	STRING: 3702.Q9FJK3	-	-
3D structure databases	SMR: Q9FJK3 	AlphaFoldDB: AF-A0A7J0EU74-F1 	AlphaFoldDB: A0A7J0F6N5 
Family & Domains	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR050142 MADS-box/MEF2_TF (3-272 aa) IPR033897 MEF2-like_N (2-85 aa) IPR002100 TF_MADSbox (SMART: 1-60 aa; PROSITE: 1-49 aa; PRINTS: 3-23 aa, 23-38 aa) IPR036879 TF_MADSbox_sf (7-86 aa)	**CDD:** cd00265 MADS_MEF2_like 1 hit **InterPro**: IPR050142 MADS-box/MEF2_TF (3-160 aa) IPR033897 MEF2-like_N (2-85 aa) IPR002100 TF_MADSbox (SMART: 1-60 aa; PROSITE: 1-49 aa; PROSITE: 3-57 aa; PRINTS: 3-23, 23-38 aa) IPR036879 TF_MADSbox_sf (13-97 aa) **Pfam**: PF00319 SRF-TF 1 hit (10-51 aa) **Prints:**	**CDD:** cd00266MADS_SRF_like 1 hit **InterPro**: IPR050142 MADS-box/MEF2_TF (3-169 aa) IPR033897 SRF-like_MADS-box (2-85 aa) IPR002100 TF_MADSbox (SMART: 1-60 aa; PROSITE: 1-49 aa; PROSITE: 3-57 aa; PRINTS: 3-23, 23-38 aa) IPR036879 TF_MADSbox_sf (13-97 aa) **Pfam**: PF00319 SRF-TF 1 hit (10-51 aa)

	Pfam: PF00319 SRF-TF 1 hit (10-51 aa) **Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit (1-49 aa) **Supfam:** SSF55455 SRF-like 1 hit	PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit **Supfam:** SSF55455 SRF-like 1 hit	**Prints:** PR00404 MADSDOMAIN **Prosite:** PS50066 MADS_BOX_2 1 hit **Supfam:** SSF55455 SRF-like 1 hit