

Table S5. List of proteins identified in the **gel slice e** (55-40 kDa) for each extraction procedures. Statistical parameters, number of unique peptides found for each protein, total spectra number assigned to each protein, protein molecular weight and Citrus Genome Database sequence or Uniprot ID are reported. NCBI description and accession ID obtained through BLAST search (blastp) of the recognized clementine proteins are also shown. The gray lanes specify the putative allergen identified.

procedure	rank	log(e)	log(l)	% measured	% corrected	unique peptides	spectra n°	MW	Citrus Genome/Uniprot Database ID	NCBI description and accession
1	1	-157	5,57	37	49	17	51	59,8	clementine0.9_006425m	ATP synthase beta subunit 1 [Gossypium hirsutum] ACS83602.1
	1	-114	5,36	42	59	13	51	36	clementine0.9_015142m	glyceraldehyde-3-phosphate dehydrogenase [Nicotiana tabacum] CAB39974.1
	2	-156	5,48	52	57	17	51	47,8	tr D7NHW9 D7NHW9_PONTR	Enolase; EC 4.2.1.11;
	2	-80	5,05	39	44	11	29	38,6	clementine0.9_014051m	fructose-bisphosphate aldolase- like [Solanum tuberosum] ABB29926.1
	3	-66	5,32	25	35	9	20	53,1	clementine0.9_008773m	adenosylhomocysteinase-like [Glycine max] XP_003531217.1
	3	-66,5	4	29	46	9	20	44,1	clementine0.9_011921m	predicted protein [Populus trichocarpa] >gb EEF06342.1 XP_002322215.1
	4	-65	5	25	38	8	22	54,9	clementine0.9_007969m	ATPase subunit 1 [Citrullus lanatus] >gb ACV96623.1 YP_003587244.1
	4	-48,4	5,09	4	5	2	2	0	clementine0.9_010848m	glyceraldehyde 3-phosphate dehydrogenase [Nicotiana langsdorffii x Nicotiana sanderiae] ABV02033.1

5	-52,3	4	21	26	7	14	51,5	clementine0.9_009373m	UDP-glucose pyrophosphorylase [Populus deltoides] AEF13021.1
5	-40	4,72	29	39	6	11	32,4	clementine0.9_017250m	PAE [Litchi chinensis] ACF05806.1
6	-51	4,82	26	30	8	12	53,8	clementine0.9_007973m	dihydrolipoamide dehydrogenase, putative [Ricinus communis] >gb EEF43150.1 XP_002519286.1
6	-33,5	4	30	46	6	10	39	clementine0.9_014139m	Glutamine synthetase nodule isozyme; Sgb AAA34239.1 P32289.1
7	-39	4,7	14	34	6	11	48,8	tr D5MR69 D5MR69_9ROSI Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit.	
7	-30,9	4,66	28	31	5	10	41,4	clementine0.9_013604m	UDP-arabinopyranose mutase 1 [Vitis vinifera] XP_002263490.1
8	-37	4	2,5	3	1	1	0	sp Q09MH0 RBL_CITSI Ribulose bisphosphate carboxylase large chain; RuBisCO large subunit.	
8	-30,3	4,17	8,4	14	3	7	39	clementine0.9_014130m	glutamine synthetase [Hevea brasiliensis] AAB61597.1
9	-35,1	4,95	19	26	6	10	49,3	clementine0.9_010162m	translation elongation factor 1A-2 [Gossypium hirsutum] ABA12218.1
9	-20,9	4,53	13	19	3	8	42,1	clementine0.9_035266m	probable fructose-bisphosphate aldolase 3, chloroplastic [Vitis vinifera] XP_002282753.1
10	-32	4	17	27	5	11	55,3	clementine0.9_007821m	mitochondrial-processing peptidase subunit alpha-like isoform 1 [Glycine max]

										XP_003525296.1
10	-19,7	4,57	14	21	3	6	37	clementine0.9_014847m	predicted protein [Populus trichocarpa] >gb EEE81435.1	XP_002302162.1
11	-28,7	4,72	13	19	4	7	56,2	clementine0.9_008261m	predicted protein [Populus trichocarpa] >gb EEE96547.1	XP_002318327.1
11	-19	4,38	9,5	12	4	8	59,8	clementine0.9_006425m	ATP synthase beta subunit 1 [Gossypium hirsutum]	ACS83602.1
12	-28,1	4,55	10	15	5	7	54,3	clementine0.9_008666m	vacuolar H ⁺ -ATPase B subunit [Citrus unshiu]	BAA75517.1
12	-18	4,28	12	17	3	8	42,7	clementine0.9_012612m	isocitrate dehydrogenase, putative [Ricinus communis] >gb EEF42934.1	XP_002519520.1
13	-25,9	4,49	10	13	4	7	53,7	clementine0.9_008700m	6-phosphogluconate dehydrogenase, decarboxylating-like isoform 2 [Vitis vinifera]	XP_002271021.1
13	-16	4,21	12	16	3	5	43,2	clementine0.9_012420m	glycolate oxidase [Gossypium hirsutum]	AEX09184.1
14	-20,7	4	22	37	4	6	36	clementine0.9_015530m	polygalacturonase-inhibitor protein [Citrus sp. cv. Sainumphung]	BAB82980.1
14	-15,2	4,32	3	3	1	1	0	clementine0.9_012004m	pectate lyase [Salix gilgiana]	BAB59066.1
15	-19	4,37	9,6	12	3	3	53,8	clementine0.9_008243m	glutathione reductase, cytosolic [Vitis vinifera] >emb CBI33364.3	XP_002285672.1

	15	-13,1	4,2	11	16	3	5	35,5	clementine0.9_015365m	malate dehydrogenase [Gossypium hirsutum] ACJ11738.1
	16	-14,9	4	7,7	15	3	7	55	clementine0.9_008512m	UDP-glucosyltransferase family 1 protein [Citrus sinensis] ACS87991.1
	16	-11,2	4	8	9	2	5	38,1	clementine0.9_014739m	predicted protein [Populus trichocarpa] >gb EEE82533.1 XP_002297728.1
	17	-12,5	4,01	7	11	3	4	49,8	clementine0.9_010297m	predicted protein [Populus trichocarpa] >gb ABK93982.1 XP_002331641.1
	17	-10,3	4,3	8	15	2	3	36	clementine0.9_015530m	polygalacturonase-inhibitor protein [Citrus sp. cv. Sainumphung] BAB82980.1
	18	-12,4	4,28	7,5	10	3	5	54,9	clementine0.9_007926m	predicted protein [Populus trichocarpa] >gb EEF10430.1 XP_002331178.1
2	1	-167	5,39	43	57	19	48	59,8	clementine0.9_006425m	ATP synthase beta subunit 1 [Gossypium hirsutum] ACS83602.1
	1	-116	5,56	36	52	13	56	36	clementine0.9_015142m	glyceraldehyde-3-phosphate dehydrogenase [Nicotiana tabacum] CAB39974.1
	2	-114	5,19	45	50	13	27	47,8	tr D7NHW9 D7NHW9_PONTR Enolase; EC 4.2.1.11	
	2	-95,7	5,48	18	27	5	10	47,1	clementine0.9_010848m	glyceraldehyde 3-phosphate dehydrogenase [Nicotiana langsdorffii x Nicotiana sanderiae] ABV02033.1

3	-51	4	16	23	7	15	49,3	clementine0.9_010162m	translation elongation factor 1A-2 [Gossypium hirsutum] ABA12218.1
3	-74	4	46	52	11	17	38,6	clementine0.9_014051m	fructose-bisphosphate aldolase-like [Solanum tuberosum] ABB29926.1
4	-45,8	4,67	15	36	7	14	48,8	tr D5MR69 D5MR69_9ROSI Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit; Flags: Fragment	
4	-39	4	14	18	6	10	59,8	clementine0.9_006425m	ATP synthase beta subunit 1 [Gossypium hirsutum] ACS83602.1
5	-27,1	4	14	28	5	6	55	clementine0.9_008512m	UDP-glucosyltransferase family 1 protein [Citrus sinensis] ACS87991.1
5	-38	4,76	14	22	5	15	44,1	clementine0.9_011921m	predicted protein [Populus trichocarpa] >gb EEF06342.1 XP_002322215.1
6	-23,6	4,43	11	18	4	7	55,3	clementine0.9_007821m	mitochondrial-processing peptidase subunit alpha-like isoform 1 [Glycine max] XP_003525296.1
6	-31,9	4,87	26	31	5	11	35,5	clementine0.9_014978m	malate dehydrogenase, putative [Ricinus communis] >gb EEF38101.1 XP_002524262.1
7	-20,5	4	12	17	4	6	56,2	clementine0.9_008261m	predicted protein [Populus trichocarpa] >gb EEE96547.1 XP_002318327.1
7	-31,3	4,79	26	35	5	8	32,4	clementine0.9_017250m	PAE [Litchi chinensis] ACF05806.1
8	-19,3	4,47	19	32	4	6	36	clementine0.9_015530m	polygalacturonase-inhibitor protein [Citrus sp. cv. Sainumphung]

8	-30,5	4,71	16	22	5	9	35,5	clementine0.9_015365m	BAB82980.1 malate dehydrogenase [Gossypium hirsutum]
9	-19	4,24	8,4	10	3	6	53,8	clementine0.9_008243m	ACJ11738.1 glutathione reductase, cytosolic [Vitis vinifera] >emb CBI33364.3 XP_002285672.1
9	-28,3	4	21	36	5	9	39	clementine0.9_014130m	AAB61597.1 glutamine synthetase [Hevea brasiliensis]
10	-17,2	4,3	8,5	16	3	4	51,8	clementine0.9_009303m	ACJ11726.1 serine hydroxymethyltransferase [Gossypium hirsutum]
10	-25,2	4	12	19	3	7	39	clementine0.9_014139m	P32289.1 Glutamine synthetase nodule isozyme; >gb AAA34239.1
11	-16,2	4,32	10	16	3	6	54,9	clementine0.9_007969m	YP_003587244.1 ATPase subunit 1 [Citrullus lanatus] >gb ACV96623.1
11	-21,4	4,58	13	33	4	6	46,3	clementine0.9_010705m	XP_002513044.1 Aspartic proteinase nepenthesin- 1 precursor, putative [Ricinus communis] >gb EEF49547.1
12	-15,3	4,54	34	78	3	6	24,2	clementine0.9_021092m	AFN02126.1 germin-like protein [Citrus limon]
12	-17	4,57	20	22	4	7	41,4	clementine0.9_013604m	XP_002263490.1 UDP-arabinopyranose mutase 1 [Vitis vinifera]
13	-15,5	4,43	13	23	3	3	36	clementine0.9_015530m	BAB82980.1 polygalacturonase-inhibitor protein [Citrus sp. cv. Sainumphung]

	14	-14,2	4,07	15	20	3	3	42	clementine0.9_013166m	actin 1 [Populus trichocarpa] >ref XP_002522194.1 P_002298710.1
	15	-11,8	4,32	13	30	2	3	22,8	clementine0.9_022028m	uncharacterized protein LOC100499779 precursor [Glycine max] >gb ACU13579.1 NP_001235916.1
	16	-10,6	4	11	33	2	6	29,6	clementine0.9_018182m	uncharacterized protein LOC100817630 [Glycine max] XP_003533986.1
3	1	-129	5,03	44	48	16	28	47,8	tr D7NHW9 D7NHW9_PONTR Enolase; EC 4.2.1.11	
	1	-127	5,62	36	50	16	71	36	clementine0.9_015142m	glyceraldehyde-3-phosphate dehydrogenase [Nicotiana tabacum] CAB39974.1
	2	-104	4,93	28	37	13	26	59,8	clementine0.9_006425m	ATP synthase beta subunit 1 [Gossypium hirsutum] ACS83602.1
	2	-106	5,54	15	15	5	11	0	clementine0.9_010848m	glyceraldehyde 3-phosphate dehydrogenase [Nicotiana langsdorffii x Nicotiana sanderiae] ABV02033.1
	3	-33	4,34	14	17	5	9	51,5	clementine0.9_009373m	UDP-glucose pyrophosphorylase [Populus deltoides] AEF13021.1
	3	-72	5,25	44	62	10	23	35,5	clementine0.9_015365m	malate dehydrogenase [Gossypium hirsutum] ACJ11738.1
	4	-29	4,5	19	27	5	8	53,1	clementine0.9_008773m	adenosylhomocysteinase-like [Glycine max] XP_003531217.1

4	-69	5,25	45	55	10	18	35,5	clementine0.9_014978m	malate dehydrogenase, putative [Ricinus communis] >gb EEF38101.1 XP_002524262.1
5	-24,3	4	17	40	4	7	48,8	tr D5MR69 D5MR69_9ROSI Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit; Flags: Fragment.	
5	-65	5,09	37	42	9	20	38,6	clementine0.9_014051m	fructose-bisphosphate aldolase-like [Solanum tuberosum] ABB29926.1
6	-18,7	3,98	7,6	11	3	5	49,3	clementine0.9_010162m	translation elongation factor 1A-2 [Gossypium hirsutum] ABA12218.1
6	-60,5	5,08	23	37	8	22	44,1	clementine0.9_011921m	predicted protein [Populus trichocarpa] >gb EEF06342.1 XP_002322215.1
7	-18,2	4,22	12	19	3	7	54,9	clementine0.9_007969m	ATPase subunit 1 [Citrullus lanatus] >gb ACV96623.1 YP_003587244.1
7	-55,3	4,82	18	23	8	14	59,8	clementine0.9_006425m	ATP synthase beta subunit 1 [Gossypium hirsutum] ACS83602.1
8	-16,7	4,38	27	61	3	6	24,2	clementine0.9_021092m	germin-like protein [Citrus limon] AFN02126.1
8	-44,5	4,97	24	32	6	11	32,4	clementine0.9_017250m	PAE [Litchi chinensis] ACF05806.1
9	-14,1	4,34	8,4	15	3	5	49,7	clementine0.9_010064m	tubulin alpha-1 chain [Vitis vinifera] XP_002285721.1
9	-37,1	4	28	34	6	10	42,6	clementine0.9_012687m	protein disulfide isomerase, putative [Ricinus communis] >gb EEF47293.1 XP_002515309.1

10	-14	4	9,4	15	3	4	55,3	clementine0.9_007821m	mitochondrial-processing peptidase subunit alpha-like isoform 1 [Glycine max] XP_003525296.1	
10	-35,5	4,84	26	33	5	12	43,2	clementine0.9_012420m	glycolate oxidase [Gossypium hirsutum] AEX09184.1	
11	-28,2	4,76	28	31	5	8	41,4	clementine0.9_013604m	UDP-arabinopyranose mutase 1 [Vitis vinifera] XP_002263490.1	
12	-26,3	4	15	22	4	8	42,7	clementine0.9_012612m	isocitrate dehydrogenase, putative [Ricinus communis] >gb EEF42934.1 XP_002519520.1	
13	-24,9	4,72	17	23	4	8	42,1	clementine0.9_035266m	PREDICTED: probable fructose- biphosphate aldolase 3, chloroplastic [Vitis vinifera] XP_002282753.1	
14	-20	4,66	12	19	3	9	39	clementine0.9_014139m	Glutamine synthetase nodule isozyme; >gb AAA34239.1 P32289.1	
15	-15,5	4	34	78	3	5	24,2	clementine0.9_021092m	germin like protein [Citrus limon] AFN02126.1	
16	-14,4	4,54	10	16	3	6	39	clementine0.9_013981m	isocitrate dehydrogenase, putative [Ricinus communis] >gb EEF33583.1 XP_002528761.1	
17	-12,3	4,38	11	33	2	4	29,6	clementine0.9_018182m	uncharacterized protein LOC100817630 [Glycine max] XP_003533986.1	
4	1	-129	5,3	38	50	16	36	59,8	clementine0.9_006425m	ATP synthase beta subunit 1 [Gossypium hirsutum] ACS83602.1

1	-114	5,36	42	59	13	51	36	clementine0.9_015142m	glyceraldehyde-3-phosphate dehydrogenase [Nicotiana tabacum] CAB39974.1
1	-138	5,49	44	63	16	55	36	clementine0.9_015142m	glyceraldehyde-3-phosphate dehydrogenase [Nicotiana tabacum] CAB39974.1
2	-99,9	5,3	42	46	12	33	47,8	tr D7NHW9 D7NHW9_PONTR	Enolase; EC 4.2.1.11;
2	-80	5,05	39	44	11	29	38,6	clementine0.9_014051m	fructose-bisphosphate aldolase-like [Solanum tuberosum] ABB29926.1
2	-81	5,3	8,1	8	3	6	0	clementine0.9_010848m	glyceraldehyde 3-phosphate dehydrogenase [Nicotiana langsdorffii x Nicotiana sanderae] ABV02033.1
3	-36	4	41	93	6	10	24,2	clementine0.9_021092m	germin-like protein [Citrus limon] AFN02126.1
3	-66,5	4	29	46	9	20	44,1	clementine0.9_011921m	predicted protein [Populus trichocarpa] >gb EEF06342.1 XP_002322215.1
3	-80	4	45	51	12	21	38,6	clementine0.9_014051m	fructose-bisphosphate aldolase-like [Solanum tuberosum] ABB29926.1
4	-28	4	15	18	5	5	51,5	clementine0.9_009373m	UDP-glucose pyrophosphorylase [Populus deltoides] AEF13021.1
4	-48,4	5,09	4	5	2	2	0	clementine0.9_010848m	glyceraldehyde 3-phosphate dehydrogenase [Nicotiana langsdorffii x Nicotiana sanderae] ABV02033.1

4	-60,9	4,8	21	34	8	19	44,1	clementine0.9_011921m	predicted protein [Populus trichocarpa] >gb EEF06342.1 XP_002322215.1
5	-28	4,45	12	29	5	9	48,8	tr D5MR69 D5MR69_9ROSI Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit; Flags: Fragment	
5	-40	4,72	29	39	6	11	32,4	clementine0.9_017250m	PAE [Litchi chinensis] ACF05806.1
5	-35,1	4,38	14	18	6	8	59,8	clementine0.9_006425m	ATP synthase beta subunit 1 [Gossypium hirsutum] ACS83602.1
6	-25,8	4,47	18	30	4	7	55,3	clementine0.9_007821m	mitochondrial-processing peptidase subunit alpha-like isoform 1 [Glycine max] XP_003525296.1
6	-33,5	4	30	46	6	10	39	clementine0.9_014139m	Glutamine synthetase nodule isozyme; gb AAA34239.1 P32289.1
6	-31,7	4,76	26	33	5	11	43,2	clementine0.9_012420m	glycolate oxidase [Gossypium hirsutum] AEX09184.1
7	-22,6	4	12	17	4	8	49,3	clementine0.9_010162m	translation elongation factor 1A-2 [Gossypium hirsutum] ABA12218.1
7	-30,9	4,66	28	31	5	10	41,4	clementine0.9_013604m	UDP-arabinopyranose mutase 1 [Vitis vinifera] XP_002263490.1
7	-25,7	4	16	23	5	10	35,5	clementine0.9_015365m	malate dehydrogenase [Gossypium hirsutum] ACJ11738.1
8	-21,4	4,53	14	16	4	7	46,9	clementine0.9_011556m	dead box ATP-dependent RNA helicase, putative [Ricinus communis] >gb EEF41044.1 XP_002521376.1
8	-30,3	4,17	8,4	14	3	7	39	clementine0.9_014130m	glutamine synthetase [Hevea

8	-24,2	4,2	17	28	5	10	39	clementine0.9_014130m	brasiliensis] AAB61597.1 glutamine synthetase [Hevea brasiliensis] AAB61597.1
9	-20,3	4	15	21	4	7	53,1	clementine0.9_008773m	adenosylhomocysteinase-like [Glycine max] XP_003531217.1
9	-20,9	4,53	13	19	3	8	42,1	clementine0.9_035266m	probable fructose-bisphosphate aldolase 3, chloroplastic [Vitis vinifera] XP_002282753.1
9	-18	4,49	15	18	4	6	42,6	clementine0.9_012687m	protein disulfide isomerase, putative [Ricinus communis] >gb EEF47293.1 XP_002515309.1
10	-17,2	4,32	11	15	3	7	46,5	tr Q9SW73 Q9SW73_CITLI NADP-isocitrate dehydrogenase	
10	-19,7	4,57	14	21	3	6	37	clementine0.9_014847m	predicted protein [Populus trichocarpa] >gb EEE81435.1 XP_002302162.1
10	-17	4,32	13	15	3	5	41,4	clementine0.9_013604m	UDP-arabinopyranose mutase 1 [Vitis vinifera] XP_002263490.1
11	-16,5	4,42	8,1	12	3	5	54,9	clementine0.9_007969m	ATPase subunit 1 [Citrus lanatus] >gb ACV96623.1 YP_003587244.1
11	-19	4,38	9,5	12	4	8	59,8	clementine0.9_006425m	ATP synthase beta subunit 1 [Gossypium hirsutum] ACS83602.1
11	-16,5	4,76	21	26	3	9	35,5	clementine0.9_014978m	malate dehydrogenase, putative [Ricinus communis] >gb EEF38101.1 XP_002524262.1

12	-16	4,62	12	21	3	6	36	clementine0.9_015530m	polygalacturonase-inhibitor protein [Citrus sp. cv. Sainumphung] BAB82980.1
12	-18	4,28	12	17	3	8	42,7	clementine0.9_012612m	isocitrate dehydrogenase, putative [Ricinus communis] >gb EEF42934.1 XP_002519520.1
12	-15,8	4,46	11	15	3	6	32,4	clementine0.9_017250m	PAE [Litchi chinensis] ACF05806.1
13	-15,4	4,55	8,4	15	3	6	49,7	clementine0.9_010064m	tubulin alpha-1 chain [Vitis vinifera] XP_002285721.1
13	-16	4,21	12	16	3	5	43,2	clementine0.9_012420m	glycolate oxidase [Gossypium hirsutum] AEX09184.1
13	-15,3	4,42	12	19	3	7	39	clementine0.9_014139m	Glutamine synthetase nodule isozyme; gb AAA34239.1 P32289.1
14	-15,4	4,42	9,6	15	3	6	44,6	clementine0.9_011862m	60S ribosomal protein L4 [Vitis vinifera] XP_002274975.1
14	-15,2	4,32	3	3	1	1	0	clementine0.9_012004m	pectate lyase [Salix gilgiana] BAB59066.1
15	-14,2	4,28	11	15	3	4	47,7	clementine0.9_011353m	translation elongation factor [Citrus maxima] ACP43319.1
15	-13,1	4,2	11	16	3	5	35,5	clementine0.9_015365m	malate dehydrogenase [Gossypium hirsutum] ACJ11738.1
16	-11,2	4	8	9	2	5	38,1	clementine0.9_014739m	predicted protein [Populus trichocarpa] >gb EEE82533.1 XP_002297728.1
17	-10,3	4,3	8	15	2	3	36	clementine0.9_015530m	polygalacturonase-inhibitor protein [Citrus sp. cv.

Sainumphung]

[BAB82980.1](#)
