Physiological and proteomic approaches to address the active role of ozone in kiwifruit postharvest ripening

Ioannis S. Minas, Georgia Tanou, Maya Belghazi, Dominique Job, Georgios Manganaris, Athanassios Molassiotis and Miltiadis Vasilakakis

Supplementary Material

(Supplementary Table S1 and Table S2 and Supplementary Figures S1, S2 and S3)

Table S1

Quantification of protein zones from 1D-gels of kiwifruit proteins

Protein zones relative quantities from 1DE-gels of kiwifruit proteins

Protein extracts have been analyzed by one-dimensional electrophoresis and 1D-gels were submitted to image analysis as described in Experimental procedures,

Legend:

Zone *N°*, protein zone label on the reference 1-DE gel presented in Figure 6;

C1 (Mean), average of zone relative quantities of Control kiwifruits samples exposed to 1 day self-life following 5 months cold storage as obtained from densitometric analysis of individual zones from proteins in 1DE-gels stained with coomassie blue from three different gels and independent extractions;

C6 (Mean), average of zone relative quantities of Control kiwifruits samples exposed to 6 days self-life following 5 months cold storage as obtained from densitometric analysis of individual zones from proteins in 1DE-gels stained with coomassie blue from three different gels and independent extractions;

Ration Mean C6/Mean C1, The C6 (Mean) zone relative quantity divided by the C1 (Mean) zone relative quantity;

p values C6/C1, p value between zone relative quantities of individual zones from three different gels and independent extractions of C1 samples and zone relative quantities of individual zones from three different gels and independent extractions of C6 samples;

C12 (Mean), average of zone relative quantities of Control kiwifruits samples exposed to 12 days self-life following 5 months cold storage as obtained from densitometric analysis of individual zones from proteins in 1DE-gels stained with coomassie blue from three different gels and independent extractions;

Ration Mean C12/Mean C1, The C12 (Mean) zone relative quantity divided by the C1 (Mean) zone relative quantity;

p values C12/C1, p value between zone relative quantities of individual zones from three different gels and independent extractions of C1 samples and zone relative quantities of individual zones from three different gels and independent extractions of C12 samples;

O1 (Mean), average of zone relative quantities of Ozone-treated kiwifruit samples that exposed to 1 day self-life following 5 months cold storage as obtained from densitometric analysis of individual zones from proteins in 1DE-gels stained with coomassie blue from three different gels and independent extractions;

Ration Mean O1/Mean C1, The O1 (Mean) zone relative quantity divided by the C1 (Mean) zone relative quantity;

p values O1/C1, p value between zone relative quantities of individual zones from three different gels and independent extractions of C1 samples and zone relative quantities of individual zones from three different gels and independent extractions of O1 sampes;

O6 (Mean), average of zone relative quantities of Ozone-treated kiwifruit samples that exposed to 6 days self-life following 5 months cold storage as obtained from densitometric analysis of individual zones from proteins in 1DE-gels stained with coomassie blue from three different gels and independent extractions;

Ration Mean O6/Mean O1, The O6 (Mean) zone relative quantity divided by the O1 (Mean) zone relative quantity;

p values O6/O1, p value between zone relative quantities of individual zones from three different gels and independent extractions of O1 samples and zone relative quantities of individual zones from three different gels and independent extractions of O6 samples;

Ration Mean O6/Mean C6, The O6 (Mean) zone relative quantity divided by the C6 (Mean) zone relative quantity;

p values O6/C6, p value between zone relative quantities of individual zones from three different gels and independent extractions of C6 plants and zone relative quantities of individual zones from three different gels and independent extractions of O6 plants;

O12 (Mean), average of zone relative quantities of Ozone-treated kiwifruit samples that exposed to 12 days self-life following 5 months cold storage as obtained from densitometric analysis of individual zones from proteins in 1DE-gels stained with coomassie blue from three different gels and independent extractions;

Ration Mean O12/Mean O1, The O12 (Mean) zone relative quantity divided by the O1 (Mean) zone relative quantity;

p values O12/O1, p value between zone relative quantities of individual zones from three different gels and independent extractions of O1 samples and zone relative quantities of individual zones from three different gels and independent extractions of O12 samples;

Ration Mean O12/Mean C12, The O12 (Mean) zone relative quantity divided by the C12 (Mean) zone relative quantity;

p values O12/C12, p value between zone relative quantities of individual zones from three different gels and independent extractions of C12 samples and zone relative quantities of individual zones from three different gels and independent extractions of O12 samples.

Zone N°	C1 (Mean)	C6 (Mean)	Ratio Mean C6/Mean C1	p values C6/C1	C12 (Mean)	Ratio Mean C12/Mean C1	p values C12/C1	O1 (Mean)	Ratio Mean O1/Mean C1	p values O1/C1	O6 (Mean)	Ratio Mean O6/Mean O1	p values O6/O1	Ratio Mean O6/Mean C6	p values O6/C6	O12 (Mean)	Ratio Mean O12/Mean O1	p values O12/O1	Ratio Mean O12/Mean C12	p values O12/C12
1	29	21	0,72	0,52	22	0,76	0,53	38	1,31	0,58	26	0,68	0,47	1,24	0,68	28	0,74	0,46	1,27	0,40
2	29	21	0,72	0,24	22	0,76	0,49	32	1,10	0,79	26	0,81	0,58	1,24	0,27	23	0,72	0,39	1,05	0,97
3	49	33	0,67	0,30	42	0,86	0,71	54	1,10	0,77	39	0,72	0,50	1,18	0,75	41	0,76	0,45	0,98	0,94
4	50	153	3,06	0,00	269	5,38	0,00	50	1,00	0,98	67	1,34	0,32	0,44	0,01	146	2,92	0,01	0,54	0,00
5	94	121	1,29	0,65	114	1,21	0,64	112	1,19	0,69	115	1,03	0,94	0,95	0,91	118	1,05	0,88	1,04	0,90
6	119	123	1,03	0,88	105	0,88	0,46	120	1,01	0,97	109	0,91	0,74	0,89	0,68	115	0,96	0,87	1,10	0,62
7	70	61	0,87	0,44	49	0,70	0,32	62	0,89	0,79	51	0,82	0,68	0,84	0,26	47	0,76	0,63	0,96	0,94
8	65	60	0,91	0,82	84	1,29	0,40	96	1,48	0,18	71	0,74	0,23	1,18	0,64	73	0,76	0,21	0,87	0,54
9	877	881	1,00	0,97	989	1,13	0,31	1401	1,60	0,01	1327	0,95	0,57	1,51	0,02	1211	0,86	0,24	1,22	0,16
10	36	27	0,75	0,12	28	0,78	0,11	42	1,17	0,53	29	0,69	0,30	1,07	0,89	33	0,79	0,61	1,18	0,70
11	48	33	0,69	0,43	42	0,88	0,75	54	1,13	0,82	43	0,80	0,71	1,30	0,60	42	0,78	0,64	1,00	1,00
12	38	37	0,97	0,93	56	1,47	0,44	54	1,42	0,19	42	8,00	0,68	1,14	0,86	53	0,98	0,88	0,95	0,89
13	144	100	0,69	0,13	143	0,99	0,98	100	0,69	0,15	119	1,19	0,62	1,19	0,60	129	1,29	0,57	0,90	0,80
14	145	427	2,94	0,00	378	2,61	0,00	161	1,11	0,57	256	1,59	0,03	0,60	0,00	192	1,19	0,23	0,51	0,00
15	283	520	1,84	0,00	542	1,92	0,00	272	0,96	0,69	401	1,47	0,01	0,77	0,02	485	1,78	0,01	0,89	0,09
16	48	33	0,69	0,34	35	0,73	0,50	45	0,94	0,91	46	1,02	0,99	1,39	0,62	40	0,89	0,79	1,14	0,76
17	23	20	0,87	0,45	27	1,17	0,82	31	1,35	0,39	25	0,81	0,58	1,25	0,62	23	0,74	0,34	0,85	0,77
18	51	76	1,49	0,07	144	2,82	0,00	64	1,25	0,36	75	1,17	0,46	0,99	0,95	137	2,14	0,01	0,95	0,65
19	48	47	0,98	0,87	36	0,75	0,11	44	0,92	0,79	34	0,77	0,61	0,72	0,44	38	0,86	0,74	1,06	0,84
20	57	57	1,00	1,00	50	0,88	0,72	57	1,00	0,98	40	0,70	0,21	0,70	0,42	55	0,96	0,92	1,10	0,81
21	13106	11715	0,89	0,29	10231	0,78	0,06	12607	0,96	0,59	11239	0,89	0,35	0,96	0,77	11706	0,93	0,32	1,14	0,50
22	2392	2016	0,84	0,39	1744	0,73	0,31	2463	1,03	0,89	2809	1,14	0,57	1,39	0,18	2570	1,04	0,68	1,47	0,13
23	2348	2418	1,03	0,70	2425	1,03	0,60	2134	0,91	0,18	2526	1,18	0,19	1,04	0,71	2145	1,01	0,95	0,88	0,20
24	3950	4356	1,10	0,12	4030	1,02	0,77	3987	1,01	0,86	4163	1,04	0,64	0,96	0,61	3891	0,98	0,89	0,97	0,84
25	1984	2000	1,01	0,98	2372	1,20	0,37	1765	0,89	0,80	2285	1,29	0,52	1,14	0,69	1533	0,87	0,76	0,65	0,12
26	2346	2456	1,05	0,82	3662	1,56	0,01	2155	0,92	0,63	2096	0,97	0,88	0,85	0,69	3234	1,50	0,02	0,88	0,08
27	61	62	1,02	0,95	53	0,87	0,41	77	1,26	0,55	66	0,86	0,77	1,06	0,92	53	0,69	0,39	1,00	0,97
28	1173	1743	1,49	0,15	1610	1,37	0,23	1339	1,14	0,72	1558	1,16	0,56	0,89	0,39	1194	0,89	0,73	0,74	0,18
29	1932	2113	1,09	0,30	2172	1,12	0,34	2098	1,09	0,65	2324	1,11	0,63	1,10	0,55	2047	0,98	0,88	0,94	0,59
30	397	459	1,16	0,24	490	1,23	0,07	405	1,02	0,85	423	1,04	0,61	0,92	0,38	421	1,04	0,74	0,86	0,15
31	479	611	1,28	0,36	591	1,23	0,43	497	1,04	0,90	517	1,04	0,90	0,85	0,54	407	0,82	0,54	0,69	0,22

Table S2

The list and detailed information of the identified kiwifruit proteins

Zone No[a]	**Acces. Number[b]**	**Protein name[c]**	**Organism[d]**	**Subcellular localization[e]**	**Matching criteria[f]**	**Functional categories[g]**	**Carbonylation status[h]**	**Theor. pI/Mw[i]**	**% cov[j]**	**Score[k]**	**MW**	**emPAI[l]**	**Peptides**		
													m/z	**Mass (exp)**	**Sequences[m]**
1	gi|15293147	Zinc finger (Ran-binding) family protein	*Arabidopsis thaliana*	Chloroplast	100% to gi|18405190 *Arabidopsis thaliana*, E value: 0.0	04.05.01.04-Transcription/transcriptional control	N	6.72 / 94747	2	61	94747	NA	433.6970	865.3794	K.DTGVGDFR.N
													546.7087	1091.4028	R.GSNGSSANRSR.G
2	gi|414979	Ferredoxin-dependent glutamate synthase	*Spinacia oleracea*	Cytosol		01.01-Metabolism/Amino acid	N	5.82 / 161734	1	132	161734	0.05	567.2051	1132.3956	R.LCEAADEAVR.N + Carbamidomethyl (C)
													721.8458	1441.6770	K.LVAEAGIGTVASGVAK.G
3		Unidentified				30-Unknown	N								
4	gi|2267006	HSP 70	*Oryza sativa*	Endoplasmic reticulum		06.01-Protein destination and storage/Folding and stability	N	5.30 / 73495	11	378	73495	0.18	495.2370	988.4594	R.LSQEEIDR.M
													499.7431	997.4716	K.NQAAVNPER.T
													578.3146	1154.6146	K.DAGVIAGLNVAR.I
													754.8508	1507.6870	R.ITPSWVAFTDSER.L
													830.4340	1658.8534	R.IINEPTAAAIAYGLDK.K
													1027.9727	2053.9308	R.VEIESLFDGTDFSEPLTR.A
	gi|7939619	Beta-galactosidase	*Solanum lycopersicum*	Apoplast		01.05-Metabolism/Sugars and polysaccharides	N	8.54 / 92864	2	129	92864	0.08	641.2565	1280.4984	K.CLSNCGEASQR.W + 2 Carbamidomethyl (C)
													648.2650	1294.5154	K.KCLSNCGEASQR.W
													701.8378	1401.6610	R.STPEMWPGIIQK.A + Oxidation (M)
5	gi|6969976	HSP 70	*Malus x domestica*	Cytosol		06.01-Protein destination and storage/Folding and stability	N	5.17 / 71171	10	291	71171	0.29	640.8095	1279.6044	R.EIAEAYLGSSIK.N
													693.8479	1385.6812	K.ELESICNPIIAK.M + Carbamidomethyl (C)
													744.3309	1486.6472	R.TTPSYVAFTDTER.L
													830.4066	1658.7986	R.IINEPTAAAIAYGLDK.K
													840.8955	1679.7764	K.NAVVTVPAYFNDSQR.Q

	gi|123656	HSP 70	*Spinacia oleracea*	Chloroplast		06.01-Protein destination and storage/Folding and stability	N	5.34 / 71686	10	258	71686	0.22	640.8095	1279.6044	K.EIAEAYLGSTVK.N
													693.8479	1385.6812	K.ELESICNPIIAK.M + Carbamidomethyl (C)
													737.3080	1472.6014	R.TTPSYVAFTDSER.L
													830.4066	1658.7986	R.IINEPTAAAIAYGLDK.K
													840.8955	1679.7764	K.NAVVTVPAYFNDSQR.Q
	gi|225434994	HSP 70 ATP binding isoform	*Vitis vinifera*	Unclear		06.01-Protein destination and storage/Folding and stability	N	5.14 / 71297	8	251	71297	0.23	693.8479	1385.6812	K.ELESLCNPIIAK.M + Carbamidomethyl (C)
													744.3309	1486.6472	R.TTPSYVAFTDTER.L
													830.4066	1658.7986	R.IINEPTAAAIAYGLDK.K
													840.8955	1679.7764	K.NAVVTVPAYFNDSQR.Q
	gi|15223533	HSP 70 early responsive to	*Arabidopsis thaliana*	Cytosol		06.01-Protein destination and storage/Folding and stability	N	5.22 / 68314	9	197	68314	0.17	640.8095	1279.6044	R.EIAEAYLGSSIK.N
													737.3080	1472.6014	R.TTPSYVAFTDSER.L
													830.4066	1658.7986	R.IINEPTAAAIAYGLDK.K
													840.8955	1679.7764	K.NAVVTVPAYFNDSQR.Q
6	gi|224092266	Malate dehydrogenase	*Populus trichocarpa*	Cytosol	99% to gi|255550956 *Ricinus communis*, E value: 0.0	02.10-Energy/TCA pathway	N	6.63 / 63056	2	99	63056	0.06	408.2159	814.4172	K.APLEETR.K
													430.7483	859.4820	K.IWLVDSK.G
7	gi|27805582	Maturase	*Phoenix dactylifera*	Chloroplast		04.22-Transcription/mRNA processing	N	9.50 / 61445	1	54		NA	491.7240	981.4334	R.FSCAGTLAR.K + Carbamidomethyl (C)
													491.7254	981.4362	R.FSCANTLAR.K
8	gi|224136806	Enolase	*Populus trichocarpa*	Cytosol	100% to gi|255539693 *Ricinus communis*, E value: 0.0	02.01-Energy/Glycolysis	N	5.67 / 47897	12	253	47898	0.35	401.2318	800.4490	K.EGLELLK.T
													456.2119	910.4092	R.DGGSDYLGK.G
													459.7583	917.5020	K.SCNALLLK.V + Carbamidomethyl (C)
													754.3864	1506.7582	R.IEEELGSAAVYAGAK.F
													787.4296	1572.8446	K.VNQIGSVTESIEAVK.M
	gi|147838248	Agglutinin	*Vitis vinifera*	Cytosol	99% to gi|57233444 *Triticum aestivum*, E	03.26-Cell growth/division/Growth regulators	N	5.58 / 53256	3	92	53256	0 .07	507.2876	1012.5606	R.VDKNVVALR.N

					value: 2e-102										
													540.7498	1079.4850	R.NLGNNNFCK.R + Carbamidomethyl (C)
	gi|21487	Leucine aminopeptidase	*Solanum tuberosum*	Chloroplast		06.13-Protein destination and storage/Proteolysis	N	5.75 / 58144	4	85	58144	0.13	636.3203	1270.6260	K.GLTFDSGGYNLK.T
													659.8163	1317.6180	K.TIEVNNTDAEGR.L
	gi|1483563	Leucine aminopeptidase	*Petroselinum crispum*	Cytosol		06.13-Protein destination and storage/Proteolysis	N	5.33 / 30831	8	85	30831	0.13	636.3203	1270.6260	K.GLTFDSGGYNIK.T
													659.8163	1317.6180	K.TIEVNNTDAEGR.L
	gi|39818375	ATP synthase (F1) subunit beta	*Solanum tuberosum*	Mitochondria	94% to gi|114421 *Nicotiana plumbaginifolia.* E value: 7e-111	07.22-Transporters/Transport ATPases	N	9.14 / 34107	11	167	34107	0.37	587.3332	1172.6518	K.VVDLLAPYQR.G
													640.3279	1278.6412	K.ITDEFTGAGAIGK.V
													705.4077	1408.8008	R.VLNTGSPITVPVGR.S
9	gi|160419153	Pectinesterase	*Actinidia deliciosa*	Apoplast		09.01-Cell structure/Cell wall	N	6.67 / 35346	24	347	35346	0.66	635.2999	1268.5852	R.GISFENYAGPSK.H
													641.3004	1280.5862	K.TNLMFIGDGIGK.T + Oxidation (M)
													682.8447	1363.6748	R.SSTVAVVGTGFIAR.G
													717.7950	1433.5754	K.EGAYFEYVDVDK.K
													751.3982	1500.7818	K.VAAAADLIPVLSSFK.T
													844.8575	1687.7004	R.DDPNQNTGISILNCK.V + Carbamidomethyl (C)
	gi|119354	Enolase	*Solanum lycopersicum*	Cytosol		02.01-Energy/Glycolysis	N	5.68 / 47768	10	293	47768	0.25	401.2166	800.4186	K.EGLELLK.T
													456.1897	910.3648	R.DGGSDYLGK.G
													787.3738	1572.7330	K.VNQIGSVTESIEAVK.M
													914.3973	1826.7800	R.IEEELGSEAVYAGASFR.K
	gi|114421	ATP synthase (F1) subunit beta	*Nicotiana plumbaginifolia*	Mitochondria		07.22-Transporters/Transport ATPases	N	5.95 / 59819	8	142	59819	0.13	488.2625	974.5104	K.IGLFGGAGVGK.T
													587.3066	1172.5986	K.VVDLLAPYQR.G
													639.7943	1277.5740	R.TIAMDGTEGLVR.G + Oxidation (M)
													705.3753	1408.7360	R.VLNTGSPITVPVGR.A
	gi|15984	Actinidin	*Actinidia deliciosa*	Unclear	100% to gi|193806686 *Actinidia*	06.13-Protein destination and storage/Proteolysis	N	4.91 / 42131	7	135	42131	0.19	430.2292	858.4438	R.SAGAVVDIK.S

					deliciosa, E value: 0.0										
													948.4097	1894.8048	R.NVGGAGTCGIATMPSYPVK.Y + Carbamidomethyl (C); Oxidation (M)
	gi|225465417	Agglutinin	*Vitis vinifera*	Cytosol	99% to gi|57233444 *Triticum aestivum*, E value: 8e-107	03.26-Cell growth/division/Growth regulators	N	6.71 / 52943	5	104	52943	0.15	507.2548	1012.4950	R.VDKNVVALR.N
													520.2427	1038.4708	R.NIYNVNFR.L
													533.7222	1065.4298	K.GDNGNYLSAR.T
10	gi|160419153	Pectinesterase	*Actinidia deliciosa*	Apoplast		09.01-Cell structure/Cell wall	N	6.67 / 35346	24	596	35346	1.03	635.2853	1268.5560	R.GISFENYAGPSK.H
													641.2973	1280.5800	K.TNLMFIGDGIGK.T + Oxidation (M)
													682.8495	1363.6844	R.SSTVAVVGTGFIAR.G
													717.8038	1433.5930	K.EGAYFEYVDVDK.K
													751.3996	1500.7846	K.VAAAADLIPVLSSFK.T
													844.8546	1687.6946	R.DDPNQNTGISILNCK.V + Carbamidomethyl (C)
	gi|119354	Enolase	*Solanum lycopersicum*	Cytosol		02.01-Energy/Glycolysis	N	5.68 / 47768	18	418	47768	0.46	456.1935	910.3724	R.DGGSDYLGK.G
													787.3868	1572.7590	K.VNQIGSVTESIEAVK.M
													902.9301	1803.8456	R.AAVPSGASTGIYEALELR.D
													914.3930	1826.7714	R.IEEELGSEAVYAGASFR.K
													1162.4757	2322.9368	K.YGQDATNVGDEGGFAPNIQENK.E
	gi|6723469	Glutathione reductase	*Betula pendula*	Chloroplast		11.06-Disease/Defence/Detoxification	N	5.98 / 38913	7	108	38913	0.20	650.3249	1298.6352	R.LNLEAVGVELDK.T
													849.9080	1697.8014	K.IVGPNEVEVTQLDGTK.L
	gi|224074105	Alanine aminotransferase	*Populus trichocarpa*	Mitochondria	99% to gi|297839097 *Arabidopsis lyrata subsp. lyrata*, E value: 0.0	01.01-Metabolism/Amino acid	N	5.27 / 52650	3	78	52650	0.07	466.2394	930.4642	K.DGILSSLAR.R
													508.7481	1015.4816	R.DTIAAGIEAR.D

	gi|165960245	Endo-beta-1.4-glucanase	*Persea americana*	Apoplast	78% to gi|22208353 *Fragaria x ananassa*. E value: 2e-111	09.01-Cell structure/Cell wall	N	9.10 / 26600	8	120	26600	0.31	528.7289	1055.4432	K.VDSSFVSCR.G + Carbamidomethyl (C)
													688.8119	1375.6092	K.SQVDYILGDNPR.A
11	gi|15218869	Isocitrate dehydrogenase	*Arabidopsis thaliana*	Cytosol		02.10-Energy/TCA pathway	N	6.13 / 45717	5	89	45717	0.14	528.7632	1055.5118	R.ATDAVIKGPGK.L
													560.2580	1118.5014	K.CATITPDEGR.V + Carbamidomethyl (C)
	gi|22007862	Enolase	*Vitis vinifera*	Cytosol	86% to gi|225455555 *Vitis vinifera*. E value: 9e-80	02.01-Energy/Glycolysis	N	9.14 / 30878	16	254	30878	0.41	754.3586	1506.7026	R.IEEELGSAAVYAGAK.F
													755.8969	1509.7792	K.VQIVGDDLLVTNPK.R
													787.3854	1572.7562	K.VNQIGSVTESIEAVK.M
12	gi|22007862	Enolase	*Vitis vinifera*	Cytosol	86% to gi|225455555 *Vitis vinifera*. E value: 9e-80	02.01-Energy/Glycolysis	N	9.14 / 30878	16	176	30878	0.26	754.3529	1506.6912	R.IEEELGSAAVYAGAK.F
													755.8944	1509.7742	K.VQIVGDDLLVTNPK.R
													787.3898	1572.7650	K.VNQIGSVTESIEAVK.M
13	gi|225455555	Enolase	*Vitis vinifera*	Cytosol	100% to gi|255539693 *Ricinus communis*, E value: 0.0	02.01-Energy/Glycolysis	N	6.17 / 48080	16	336	48080	0.34	451.7304	901.4462	K.ACNALLLK.V + Carbamidomethyl (C)
													754.3381	1506.6616	R.IEEELGSAAVYAGAK.F
													755.8606	1509.7066	K.VQIVGDDLLVTNPK.R
													787.3634	1572.7122	K.VNQIGSVTESIEAVK.M
													1162.4537	2322.8928	K.YGQDATNVGDEGGFAPNIQENK.E
	gi|2078350	Transaldolase	*Solanum tuberosum*	Unclear		02.07-Energy/Pentose phosphate	N	5.79 / 47779	10	270	47779	0.35	542.7658	1083.5170	K.IGTPEALDLR.G
													600.2894	1198.5642	R.VTSVASFFVSR.V
													660.3091	1318.6036	R.LADDTEGTVEAAK.W
													691.3074	1380.6002	K.SFDSLLDSLQEK.A
	gi|1143381	Polygalacturonase inhibitor	*Actinidia deliciosa*	Apoplast		11.02-Disease/defense/Defense-related	N	8.72 / 36141	13	185	36141	0.35	442.6992	883.3838	K.FQFDLSK.V
													539.7690	1077.5234	K.TIQIVDFSR.N
													574.3029	1146.5912	K.IYGSLPVGLTK.L

													604.6218	1810.8436	K.VVFPQSLTSLDLNHNK.I
	gi|225430200	Hypothetical protein	*Vitis vinifera*	Unclear		30-Unknown	N	5.77 / 40308	9	133	40308	0.09	416.2051	830.3956	R.LGNEASIK.Q
													590.2793	1178.5440	R.DTIKVPYESK.G
													859.3913	1716.7680	K.QGDMLLVVPEGAFAVR.L + Oxidation (M)
	gi|149938958	Glutamate dehydrogenase	*Actinidia chinensis*	Mitochondria		01.01-Metabolism/Amino acid	N	6.28 / 44801	5	105	44801	0.17	579.7951	1157.5756	K.VVAVSDITGAVK.N
													581.7750	1161.5354	K.TAVADIPYGGAK.G
	gi|15239438	Hypothetical protein	*Arabidopsis thaliana*	Unclear		30-Unknown	N	6.92 / 39953	7	104	39953	NA	400.7224	799.4302	R.AIELVAGK.E
													416.2051	830.3956	R.LGNEASIK.Q
													590.2793	1178.5440	K.DTLKVPYESK.G
	gi|119023806	HSP 70 dnaK protein	*Selaginella lepidophylla*	Unclear	84% to gi|118366049 *Tetrahymena thermophila*. E value: 4e-97	06.01-Protein destination and storage/Folding and stability	N	8.84 / 24806	17	145		0.30	614.7817	1227.5488	R.VEIIANDQGNR.T
													737.3068	1472.5990	R.TTPSYVGFTESER.L
													841.3628	1680.7110	K.DAVVTVPAYFNDSQR.Q
14	gi|225430200	Hypothetical protein	*Vitis vinifera*	Unclear		30-Unknown	N	5.77 / 40308	9	163	40308	0.13	416.2136	830.4126	R.LGNEASIK.Q
													590.2910	1178.5674	R.DTIKVPYESK.G
													859.3954	1716.7762	K.QGDMLLVVPEGAFAVR.L + Oxidation (M)
	gi|2078350	Transaldolase	*Solanum tuberosum*	Unclear		02.07-Energy/Pentose phosphate	N	5.79 / 47779	4	105	47779	0.16	542.7762	1083.5378	K.IGTPEALDLR.G
													600.3019	1198.5892	R.VTSVASFFVSR.V
	gi|126896	Malate dehydrogenase	*Citrullus lanatus*	Mitochondria		02.10-Energy/TCA pathway	N	8.88 / 36178	6	95	36178	0.22	617.2701	1232.5256	R.TQDGGTEVVEAK.A
													659.8250	1317.6354	R.DDLFNINAGIVK.S
	gi|146216004	Cysteine protease	*Actinidia deliciosa*	Unclear		06.13-Protein destination and storage/Proteolysis	N	4.90 / 50759	6	81	50759	0.07	667.3204	1332.6262	K.CGIAVEPSYPIK.T + Carbamidomethyl (C)
													1145.0130	2288.0114	K.VVTIDDYEDVPVNNEQALC K.A
	gi|26563946	Alpha-galactosidase	*Mesembryanthemum crystallinum*	Apoplast	83% to gi|224113219 *Populus trichocarpa*. E value: 6e-119	01.05-Metabolism/Sugars and polysaccharides	N	4.96 / 26451	10	117	26451	0.14	557.2816	1112.5486	K.APLLIGCDVR.N + Carbamidomethyl (C)
													797.8928	1593.7710	K.EVIAVNQDPLGIQAK.K

	gi|117220428	Acyl-coenzyme A oxidase	*Oryza sativa Indica Group*	Peroxisome	98% to gi|115467984 *Oryza sativa Japonica Group.* E value: 7e-96	01.06-Metabolism/Lipid and sterol	N	10.27 / 42164	2	74	42164	NA	415.1843	414.1770	K.GGGPK.K
													421.7384	841.4622	-.VATVSIPR.T
	gi|57570980	Methylcrotonoyl-CoA carboxylase	*Citrus trifoliata*	Mitochondria	73% to gi|224103609 *Populus trichocarpa*. E value: 8e-26	01.01-Metabolism/Amino acid	N	10.06 / 30039	3	65		NA	428.7466	855.4786	R.LASLLSPR.M
													622.8170	1243.6194	R.LTISVIDSIKR.L
15	gi|7798706	Malate dehydrogenase	*Vitis vinifera*	Mitochondria		02.10-Energy/TCA pathway	N	8.79 / 36851	20	344	36851	0.63	610.2931	1218.5716	K.LFGVTTLDVVR.A
													617.2404	1232.4662	R.TQDGGTEVVEAK.A
													659.7871	1317.5596	R.DDLFNINAGIVK.S
													897.9518	1793.8890	K.VAVLGAAGGIGQPLALLMK.L + Oxidation (M)
													909.8804	1817.7462	K.NGVEEVLGLGPLSDYEK.Q
	gi|207667274	Malate dehydrogenase	*Brassica rapa subsp. Pekinensis*	Chloroplast		02.30-Energy/Photosynthesis	N	8.51 / 42292	9	201	42292	0.29	610.2931	1218.5716	K.LFGVTTLDVVR.A
													659.7871	1317.5596	R.DDLFNINAGIVK.T
													742.8005	1483.5864	K.AGAGSATLSMAYAAAR.F + Oxidation (M)
	gi|255553512	Hypothetical protein	*Ricinus communis*	Unclear		30-Unknown	N	8.88 / 39587	6	153	39587	0.20	500.7346	999.4546	R.ESAIAQILR.T
													895.8638	1789.7130	R.IDDFGSLCGPVLDQVR.V + Carbamidomethyl (C)
	gi|115469420	Glyceraldehyde-3-phosphate dehydrogenase	*Oryza sativa Japonica Group*	Chloroplast		02.30-Energy/Photosynthesis	N	8.78 / 43467	6	85		NA	406.1609	810.3072	K.LTGMAFR.V + Oxidation (M)
													1093.4230	2184.8314	K.GILGYTDEDVVSNDFIGDTR.S
													533.6902	1065.3658	K.GDNGNYLSAR.T
	gi|51112804	Fructose-bisphosphate aldolase	*Antirrhinum majus*	Cytosol	91% to gi|10800924 *Persea americana*. E value: 1e-131	02.01-Energy/Glycolysis	N	5.03 / 27405	9	152	27405	0.30	666.7944	1331.5742	K.VAPEVVAEYTVR.A
													730.8029	1459.5912	R.LSSINVENVESNR.R
	gi|5443161	Malate dehydrogenase	*Mesembryanthemum crystallinum*	Glyoxysomal	84% to gi|297739396 *Vitis vinifera*. E value: 6e-90	02.10-Energy/TCA pathway	N	9.35 / 35743	8	136	35743	0.21	659.7871	1317.5596	R.DDLFNINAGIVK.T
													742.8005	1483.5864	-.AGAGSATLSMAYAAVK.L + Oxidation (M)

	gi|124671212	Peroxidase	*Centaurea solstitialis*	Apoplast	80% to gi|225451467 *Vitis vinifera*. E value: 5e-100	11.06-Disease/Defence/Detoxification	N	5.15 / 28262	11	133	28262	0.29	741.8296	1481.6446	K.FSQTFTTIPATLR.L
													939.8761	1877.7376	K.DAQDNLSLAGDGFDTVIK.
	gi|143562221	Acyl-coenzyme A oxidase	*Triticum aestivum*	Peroxisome	92% to gi|125597167 *Oryza sativa Japonica Group*. E value: 8e-127	01.06-Metabolism/Lipid and sterol	N	11.20 / 24502	3	77	24502	NA	421.7087	841.4028	-.VATVSIPR.T
													689.2930	1376.5714	K.VLKCCYLIIPV.- + 2 Carbamidomethyl (C)
16	gi|7798706	Malate dehydrogenase	*Vitis vinifera*	Mitochondria		02.10-Energy/TCA pathway	N	8.79 / 36851	20	354	36851	0.63	610.2908	1218.5670	K.LFGVTTLDVVR.A
													617.2405	1232.4664	R.TQDGGTEVVEAK.A
													659.7856	1317.5566	R.DDLFNINAGIVK.S
													897.9502	1793.8858	K.VAVLGAAGGIGQPLALLMK.L + Oxidation (M)
													909.8799	1817.7452	K.NGVEEVLGLGPLSDYEK.Q
	gi|255575381	Fructose-bisphosphate aldolase	*Ricinus communis*	Cytosol		02.01-Energy/Glycolysis	N	6.57 / 38613	11	192	38613	0.20	416.1981	830.3816	R.ALQASTLK.A
													463.7140	925.4134	K.ENGVLPGIK.V
													577.7377	1153.4608	K.ANSEATLGTYK.G
													666.7935	1331.5724	K.VAPEVVAEYTVR.A
	gi|115473517	Malate dehydrogenase	*Oryza sativa (japonica cultivar-*	Glyoxysomal		02.10-Energy/TCA pathway	N	9.00 / 42195	10	167	42195	0.29	610.2908	1218.5670	K.LFGVTTLDVVR.A
													629.7750	1257.5354	R.IQNAGTEVVEAK.A
													888.9709	1775.9272	K.VAILGAAGGIGQPLSLLVK.M
													533.6907	1065.3668	K.GDNGNYLSAR.T
	gi|39791702	Hypothetical protein	*Solanum tuberosum*	Unclear	86% to gi|225450055 *Vitis vinifera*. E value: 2e-131	30-Unknown	N	8.34 / 35244	9	188	35244	0.22	500.7358	999.4570	R.ESALAQIIR.T
													553.2103	1104.4060	R.TCAQEEVLR.V + Carbamidomethyl (C)
													621.7668	1241.5190	K.GSLYALTFGASR.T
	gi|14493820	Malate dehydrogenase	*Beta vulgaris*	Chloroplast	90% to gi|225452831 *Vitis vinifera*. E value: 4e-108	02.30-Energy/Photosynthesis	N	6.14 / 23733	15	188	23733	0.56	610.2908	1218.5670	K.LFGVTTLDVVR.A
													629.7750	1257.5354	R.IQNAGTEVVEAK.A

													659.7856	1317.5566	R.DDLFNINAGIVK.T
	gi|8122436	Protein disufide isomerase	*Euphorbia esula*	Endoplasmic reticulum	85% to gi|224128376 *Populus trichocarpa*. E	06.01-Protein destination and storage/Folding and stability	N	4.79 / 20324	11	92	20324	NA	534.7303	1067.4460	K.YGVSGFPTLK.F
													728.2872	1454.5598	R.DLDDFVTFINEK.S
17	gi|115434198	fructose-bisphosphate aldolase	*Oryza sativa Japonica Group*	Chloroplast		02.30-Energy/Photosynthesis	N	8.81 / 41968	14	260	41968	0.41	436.7045	871.3944	R.ALQNSVLK.T
													465.2038	928.3930	K.ANSLAQLGR.Y
													593.1843	1184.3540	R.YTGEGESDEAK.K
													724.7763	1447.5380	R.GILAIDESNATCGK.R + Carbamidomethyl (C)
													749.8353	1497.6560	R.TVVSIPCGPSALAVK.E + Carbamidomethyl (C)
	gi|255575381	Fructose-bisphosphate aldolase	*Ricinus communis*	Cytosol		02.01-Energy/Glycolysis	N	6.57 / 38613	11	219	38613	0.20	416.1947	830.3748	R.ALQASTLK.A
													463.7041	925.3936	K.ENGVLPGIK.V
													577.7226	1153.4306	K.ANSEATLGTYK.G
													666.7870	1331.5594	K.VAPEVVAEYTVR.A
	gi|126896	Malate dehydrogenase	*Citrullus lanatus*	Mitochondria		02.10-Energy/TCA pathway	N	8.88 / 36178	11	188	36178	0.35	617.2349	1232.4552	R.TQDGGTEVVEAK.A
													659.7799	1317.5452	R.DDLFNINAGIVK.S
													897.9373	1793.8600	K.VAVLGAAGGIGQPLALLMK.L + Oxidation (M)
	gi|211906514	Lactoylglutathione lyase	*Gossypium hirsutum*	Chloroplast		11.06-Disease/Defence/Detoxification	N	5.69 / 32495	7	84	32495	0.25	639.7536	1277.4926	K.ITSFLDPDGWK.T
													646.7670	1291.5194	K.TVLVDNEDFLK.E
	gi|39791702	Hypothetical protein	*Solanum tuberosum*	Unclear	86% to gi|225450055 *Vitis vinifera*. E value: 2e-131	30-Unknown	N	8.34 / 35244	9	182	35244	0.36	500.7275	999.4404	R.ESALAQIIR.T
													553.2059	1104.3972	R.TCAQEEVLR.V + Carbamidomethyl (C)
													621.7590	1241.5034	K.GSLYALTFGASR.T
	gi|21093381	Glyceraldehyde-3-phosphate dehydrogenase	*Gossypium arboreum*	Cytosol	93% to gi|297738348 *Vitis vinifera*. E value: 2e-102	02.01-Energy/Glycolysis	N	8.82 / 24552	17	163	24566	0.33	400.6913	799.3680	K.VVISAPSK.D
													587.7751	1173.5356	K.AGIALNKNFVK.L

													717.7933	1433.5720	R.AASFNIIPSSTGAAK.A
													749.8376	1497.6606	R.VPTVDVSVVDLTVR.L
	gi|77498491	UDP-glucuronate decarboxylase	*Mimulus guttatus*	Chloroplast	89% to gi|224109544 *Populus trichocarpa*. E value: 2e-73	01.05-Metabolism/Sugars and polysaccharides	N	5.98 / 24658	17	145	24658	0.15	609.2802	1216.5458	R.VVSNFLAQAIR.D
													678.2720	1354.5294	K.IISVENTPDDPR.Q
													777.8266	1553.6386	R.DEPLTVQLPGTQTR.S
18	gi|255644696	Fructose-bisphosphate aldolase	*Glycine max*	Chloroplast	100% to gi|255570707 *Ricinus communis*, E value: 0.0	02.30-Energy/Photosynthesis	N	8.73 / 42518	11	191	42518	0.40	408.6692	815.3238	R.ASPETIAK.Y
													465.1975	928.3804	K.ANSLAQLGR.Y
													724.7711	1447.5276	R.GILAIDESNATCGK.R + Carbamidomethyl (C)
													749.8888	1497.7630	R.TVVSIPCGPSALAVK.E + Carbamidomethyl (C)
	gi|211906514	Lactoylglutathione lyase	*Gossypium hirsutum*	Chloroplast		11.06-Disease/Defence/Detoxification	N	5.69 / 32495	11	190	32495	0.39	561.2452	1120.4758	R.KPGPIPGINTK.I
													639.7951	1277.5756	K.ITSFLDPDGWK.T
													646.8068	1291.5990	K.TVLVDNEDFLK.E
	gi|4650842	Elongation factor	*Lithospermum erythrorhizon*	Cytosol		05.04-Protein synthesis/Translation factors	N	5.87 / 24836	14	123	24836	0.33	478.2025	954.3904	R.GGGQVIPTAR.R
													568.1896	1134.3646	K.EGALAEENMR.G + Oxidation (M)
													791.8389	1581.6632	K.EQMTPLSEFEDKL.- + Oxidation (M)
	gi|90318896	NADPH quinone oxidoreductase	*Taraxacum officinale*	Unclear	81% to gi|224078882 *Populus trichocarpa*. E value: 1e-110	02.20-Energy/Electron-transport	N	5.68 / 27692	17	118	27692	0.14	533.7004	1065.3862	K.VFVTAGSEEK.L
													866.4826	1730.9506	K.VAVPAGQVLPIPSGVSLK.D
													869.3909	1736.7672	K.IGDQVCALISGGGYAEK.V + Carbamidomethyl (C)
19	gi|950299	Xyloglucan endotransglycosylas	*Actinidia deliciosa*	Apoplast		09.01-Cell structure/Cell wall	N	8.49 / 34127	5	64	34127	0.11	862.4113	1722.8080	R.TGQPYILQTNVFTGGK.G
	gi|255575381	Fructose-bisphosphate aldolase	*Ricinus communis*	Cytosol		02.01-Energy/Glycolysis	N	6.57 / 38613	11	207	38613	0.20	416.2314	830.4482	R.ALQASTLK.A
													463.7449	925.4752	K.ENGVLPGIK.V
													577.7609	1153.5072	K.ANSEATLGTYK.G

													666.8210	1331.6274	K.VAPEVVAEYTVR.A
	gi|211906514	Lactoylglutathione lyase	*Gossypium hirsutum*	Chloroplast		11.06-Disease/Defence/Detoxification	N	5.69 / 32495	11	113	32495	0.16	639.7886	1277.5626	K.ITSFLDPDGWK.T
													646.8093	1291.6040	K.TVLVDNEDFLK.E
													733.3429	1464.6712	K.DPDGYIFELIQR.A
	gi|240255920	Beta-1.3-glucanase	*Arabidopsis thaliana*	Vacuole		03.26-Cell growth/division/Growth regulators	N	6.43 / 37688	6	75	37688	0.10	542.2597	1082.5048	K.NFGLFFPNK.Q
													729.8462	1457.6778	R.LYDPNQAALNALR.N
20	gi|255575381	Fructose-bisphosphate	*Ricinus communis*	Cytosol		02.01-Energy/Glycolysis	N	6.57 / 38613	8	115	38613	0.10	416.2275	830.4404	R.ALQASTLK.A
													463.7406	925.4666	K.ENGVLPGIK.V
													666.8163	1331.6180	K.VAPEVVAEYTVR.A
	gi|118488420	ATP synthase subunit E	*Populus trichocarpa*	Vacuole	99% to gi|255537687 *Ricinus communis*, E value: 2e-109	07.22-Transporters/Transport ATPases	N	7.79 / 26366	10	112	26366	0.31	582.2663	1162.5180	K.IVFENSLDAR.L
													731.8237	1461.6328	K.VLQAQDDVVNSMK.D + Oxidation (M)
21	gi|157829826	Actinidin chain A	*Actinidia deliciosa*	Unclear		06.13-Protein destination and storage/Proteolysis	N	4.23 /23543	41	4137	235463	3.49	430.2256	858.4366	R.SAGAVVDIK.S
													518.2269	1034.4392	-.LPSYVDWR.S
													866.3238	1730.6330	K.NSWDTTWGEEGYMR.I
													948.3859	1894.7572	R.NVGGAGTCGIATMPSYPVK
													1051.5106	2101.0066	K.IVTGVLISLSEQELIDCGR.T + Carbamidomethyl (C)
													1171.4719	2340.9292	K.SQGECGGCWAFSAIATVEG INK.I + 2 Carbamidomethyl (C)
	gi|157834287	Chymopapain	*Carica papaya*	Apoplast		06.13-Protein destination and storage/Proteolysis	N	9.37 / 23658	10	95	23658	0.82	1125.9779	2249.9412	K.NQGACGSPWAFSTIATVEG INK.I
													1171.4672	2340.9198	K.NQGACGSMWAFSTIATVE GINK.I + Carbamidomethyl (C)
													1174.4711	2346.9276	K.NQGACGSHWAFSTIATVEG INK.I + Carbamidomethyl (C)
22	gi|1170601	Fruit protein oxidoreductase	*Actinidia deliciosa*	Chloroplast		02.20-Energy/Electron-transport	N	7.88 / 35177	16	279	35177	0.50	573.3096	1144.6046	R.VLPAAAESLFK.V
													707.8539	1413.6932	K.EGDVVDLTQIIGR.G
													739.3560	1476.6974	R.SVPGTTSEVLCSLK.E + Carbamidomethyl (C)

													788.3823	1574.7500	R.QDTYIWTPVPISR.V
	gi|147784332	Triosephosphate isomerase	*Vitis vinifera*	Cytosol	99% to gi|211906460 *Gossypium hirsutum*, E value: 2e-127	02.01-Energy/Glycolysis	N	6.34 / 27181	15	265	27181	0.48	663.3062	1324.5978	R.IIYGGSVSGANCK.E + Carbamidomethyl (C)
													687.8286	1373.6426	K.VIACVGETLEQR.E + Carbamidomethyl (C)
													727.3199	1452.6252	R.ESGSTMEVVAAQTK.A + Oxidation (M)
	gi|117697496	Serine-rich protein	*Solanum lycopersicum*	Unclear	68% to gi|225430428 *Vitis vinifera*. E value: 3e-62	30-Unknown	N	5.53 / 25422	3	102	25422	0.15	413.7432	825.4718	K.ITNLLPR.K
													543.2819	1084.5492	-.MKITNLLPR.K
23	gi|1170601	Fruit protein oxidoreductase	*Actinidia deliciosa*	Chloroplast		02.20-Energy/Electron-transport	CC	7.88 / 35177	7	122	35177	0.23	573.3104	1144.6062	R.VLPAAAESLFK.V
													707.8557	1413.6968	K.EGDVVDLTQIIGR.G
	gi|92012845	Triosephosphate isomerase	*Nicotiana tabacum*	Cytosol	97% to gi|76573375 *Solanum tuberosum*. E value: 1e-69	02.01-Energy/Glycolysis	CC	8.96 / 32564	8	100	32564	0.12	687.8314	1373.6482	K.VIACVGETLEQR.E + Carbamidomethyl (C)
													732.3444	1462.6742	R.LLLNESNDFVGDK.V
24	gi|85701136	Kiwellin	*Actinidia deliciosa*	Apoplast		11.02-Disease/defense/Defense-related	CC	5.83 / 19955.09	60	1934	19955	5.93	490.1845	978.3544	K.VVDECDSR.H + Carbamidomethyl (C)
													525.6896	1049.3646	-.ISSCNGPCR.D + 2 Carbamidomethyl (C)
													526.1998	1050.3850	K.EHAGQPPCR.N + Carbamidomethyl (C)
													654.2804	1306.5462	K.NVGVVDITWSMA.- + Oxidation (M)
													740.7917	1479.5688	R.IVALSTGWYNGGSR.C
													782.3186	1562.6226	R.DLNDCDGQLICIK.G + 2 Carbamidomethyl (C)
													786.3009	1570.5872	K.CNDDPQVGTHICR.G + 2 Carbamidomethyl (C)
													936.9018	1871.7890	R.NNIVDGSNAVWSALGLDK.
													979.3901	1956.7656	K.SYPTYDCSPPVTSSTPAK.L + Carbamidomethyl (C)
													435.7298	869.4450	R.VVEALSPR.-
	gi|9456010	Alpha-expansin	*Solanum lycopersicum*	Apoplast	98% to gi|3747132 *Solanum lycopersicum*. E value: 4e-59	09.01-Cell structure/Cell wall	CC	8.12 / 17728	6	102	17728	0.22	473.2467	944.4788	K.AGIVPVSFR.K
													537.2581	1072.5016	K.AGIVPVSFRK.V

25	gi|190358875	Thaumatin	*Actinidia deliciosa*	Apoplast		11.02-Disease/defense/Defense-related	CC	8.29 / 24205	41	2190	24205	2.22	527.7004	1053.3862	R.TGCNFDGAGR.G + Carbamidomethyl (C)
													550.7059	1099.3972	R.CPDAYSYPK.D + Carbamidomethyl (C)
													678.3804	1354.7462	R.GQNWIINPGAGTK.G
													711.2686	1420.5226	R.APGGCNNPCTVFK.T + 2 Carbamidomethyl (C)
													824.3268	1646.6390	K.CTADINGQCPNELR.A + 2 Carbamidomethyl (C)
													903.2992	1804.5838	K.DDQTSTFTCPAGTNYK.V + Carbamidomethyl (C)
													1063.3784	2124.7422	K.TDQYCCNSGNCGLTNFSK.
	gi|112949627	Alpha-expansin	*Actinidia deliciosa*	Apoplast		09.01-Cell structure/Cell wall	CC	9.89 / 22989	4	227	22989	0.17	473.2577	944.5008	R.AGIVPVSFR.R
	gi|225444607	Phosphoinositide 5-phosphatase	*Vitis vinifera*	Unclear	98% to gi|255550313 *Ricinus communis*, E value: 0.0	12-Unclear classification	CC	6.28 / 95304	2	68		NA	518.2489	1034.4832	K.LLCMVDLTK.D
													637.2699	1272.5252	R.INEGNRSTGGLR.F
	gi|27248592	2-Cys peroxiredoxin	*Ipomoea nil*	Chloroplast	95% to gi|225440735 *Vitis vinifera*. E value: 2e-97	11.06-Disease/Defence/Detoxification	CC	5.88 / 29237	8	77	29237	NA	511.2606	1020.5066	K.YPLVSDVTK.S
													779.9015	1557.7884	K.SYNVLIPDQGIALR.G
26	gi|116791989	60S ribosomal protein	*Picea sitchensis*	Cytosol	99% to gi|40287508 *Capsicum annuum*, E value: 1e-81	05.01-Protein synthesis/Ribosomal proteins	CC	8.46 / 17788	13	82	17788	0.22	441.2190	880.4234	K.IGPLGLSPK.K
													619.3317	1236.6488	K.VAVVPSAAALVIK.A
	gi|51061329	Small GTP-binding protein	*Antirrhinum majus*	Chloroplast	93% to gi|255570175 *Ricinus communis*. E value: 4e-108	10.0410-Signal transduction/G proteins	CC	8.49 / 28765	10	133	28765	0.13	568.2561	1134.4976	K.YIIIGDTGVGK.S
													854.8400	1707.6654	K.IQEGVFDVSNESSGIK.V
27	gi|27544454	Pectinmethylesterase inhibitor	*Actinidia deliciosa*	Cytosol		09.01-Cell structure/Cell wall	N	4.97 / 19878	15	171	19878	0.42	686.3167	1370.6188	K.IIASLTNQATDPK.L
													753.3262	1504.6378	K.GLGQFSIDIAQASAK.Q
	gi|146737976	Thaumatin	*Actinidia deliciosa*	Apoplast		11.02-Disease/defense/Defense-related	N	7.92 / 21614	18	164	21614	0.63	527.6749	1053.3352	R.TGCNFDGAGR.G + Carbamidomethyl (C)
													711.2642	1420.5138	R.APGGCNNPCTVFK.T + 2 Carbamidomethyl (C)
													824.3041	1646.5936	K.CTADINGQCPNELR.A + 2 Carbamidomethyl (C)
	gi|255538956	Peptidyl-prolyl cis-trans isomerase	*Ricinus communis*	Cytosol		06.01-Protein destination and storage/Folding and stability	N	8.94 / 18142	15	89	18142	0.21	704.8013	1407.5880	R.IVMELFADTTPR.T + Oxidation (M)

													712.7964	1423.5782	K.VFFDMTVGGAPAGR.I
28	gi|281552896	Bet v 1 related allergen	*Actinidia chinensis*	Unclear		11.02-Disease/defense/Defense-related	CC	5.82 / 17479	42	582	17479	3.07	417.1697	832.3248	K.VSEEEIK.L
													617.2579	1232.5012	K.ILEGDGCAGTIK.E + Carbamidomethyl (C)
													638.7453	1275.4760	K.IVACPDGGSICK.N + 2 Carbamidomethyl (C)
													644.7900	1287.5654	K.AFILDGDTLVPK.V
													677.7414	1353.4682	M.GVVTYDMEIPSK.V + Oxidation (M)
													756.7594	1511.5042	K.ALEAYLLANPDYC.- + Carbamidomethyl (C)
	gi|62738429	Pectinmethylesterase inhibitor	*Actinidia chinensis*	Cytosol		09.01-Cell structure/Cell wall	CC	4.60 / 16414	30	338	16414	0.89	686.3095	1370.6044	K.IIASLTNQATDPK.L
													753.3401	1504.6656	K.GLGQFSIDIAQASAK.Q
													1067.8934	2133.7722	R.YETCSENYADAIDSLGQAK Q + Carbamidomethyl (C)
	gi|220682974	UDP-glucose-1-phosphate uridylyltransferase	*Saccharum officinarum*	Cytosol		01.05-Metabolism/Sugars and polysaccharides	CC	5.24 / 52260	5	126	52260	0.15	649.3019	1296.5892	K.LEIPDGAVLENK.D
													792.3529	1582.6912	R.ANPANPSIELGPEFK.K
	gi|8529430	Eukaryotic translation initiation factor 5A	*Medicago truncatula*	Unclear	96% to gi|217071678 *Medicago truncatula*. E value: 3e-83	05.04-Protein synthesis/Translation factors	CC	5.33 / 19955	16	153	19955	0.42	424.6937	847.3728	K.VVEVSTSK.T
													567.7457	1133.4768	K.TYPQQAGTIR.K
													685.8221	1369.6296	K.LPTDDNLLTQIK.E
29	gi|281552896	Bet v 1 related allergen	*Actinidia chinensis*	Unclear		11.02-Disease/defense/Defense-related	N	5.82 / 17479	27	159	17479	0.83	417.1681	832.3216	K.VSEEEIK.L
													617.2529	1232.4912	K.ILEGDGCAGTIK.E + Carbamidomethyl (C)
													638.7468	1275.4790	K.IVACPDGGSICK.N + 2 Carbamidomethyl (C)
													644.7963	1287.5780	K.AFILDGDTLVPK.V
	gi|48828052	Nucleoside diphosphate kinase	*Gossypium raimondii*	Cytosol	92% to gi|284433792 *Jatropha curcas*. E value: 4e-57	01.03-Metabolism/Nucleotides	N	6.20 / 15840	26	173	15840	0.25	482.1970	962.3794	R.GDFAIDIGR.N
													685.7789	1369.5432	R.NVIHGSDSVESAR.K
													784.3596	156..7046	K.IIGATNPAESAPGTIR.G
30		Unidentified				30-Unknown	N								
31	gi|75224035	Cystatin	*Actinidia deliciosa*	Apoplast		06.13-Protein destination and storage/Proteolysis	N	9.39/ /12748	21	307	12748	0.71	664.8123	1327.6100	R.GYTQVVAGTNYR.L

											775.3577	1548.7008	K.QANDELQYQSVVR.G
60S ribosomal protein	*Solanum lycopersicum*	Cytosol	97% to gi|76161008 *Solanum tuberosum*. E value: 9e-66	05.01-Protein synthesis/Ribosomal proteins	N	10.28 / 16920	20	148	16920	0.51	432.2404	862.4662	R.VALVNYGK.D
											551.7636	1101.5126	R.ALVDAPDMVR.S + Oxidation (M)
											624.8073	1247.6000	K.TLIAAMEAADVK.N + Oxidation (M)
Glycine-rich RNA binding protein	*Solanum tuberosum*	Nucleus	95% to gi|187373099 *Nicotiana tabacum*. E value: 8e-41	11.05-Disease/Defence/Stress responses	N	11.54 / 36051	11	143		NA	530.7712	1059.5278	R.LTLPVFNTR.S
											566.2648	1130.5150	R.NITVNEAQSR.G
											753.7990	1505.5834	R.DAIEGMNGQDLDGR.N + Oxidation (M)

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[a] *Zone N°*, zones label on the reference 1D-SDS-PAGE gel as shown in Figure 6;

[b] *Accession number*, accession number in NCBI database;

[c] *Organism*, organism in which the protein has been identified;

[d] *Protein name*, identified peptide names;

[e] *Cellular localization*, Sub-cellular localization of proteins was assigned based on database searches;

[f] *Matching criteria*, adopted criteria for the valuation of similarity for proteins identified after manual blast against current databases. Blank cells correspond to proteins readily identified without further blast;

[g] *Function category*, proteins ontologically classified into functional categories proposed by of Bevan et al., 1998, Nature 39, 1485-488;

[h] *Carbonylation status*, CC, candidate carbonylated; N, no;

[i] *Theoretical pI/Mw*, theoretical isoelectric point/molecular weight;

[j] *% Cov*, Mascot coverage %, percentage of sequence coverage obtained with identified peptides with Mascot software for the orthologous protein;

[k] *Score*, a minimum of two different peptides was used (score>46 for search in NCBI nr and score>63 when using the EST database); for proteins characterized by only one peptide, this peptide must contain at least five consecutive fragments (y or b) and yield a score >46;

[l] *Exponentially Modified Protein Abundance Index*: approximate, label-free, relative quantitation of the proteins in a mixture based on protein coverage by the peptide matches in a database search result (Ishihama et al., 2005, Molecular and Cellular Proteomics 4, 1265-1272);

[m] *Sequences*, list of peptides identified with Mascot software.

Supplementary Figure S1, Minas et al.

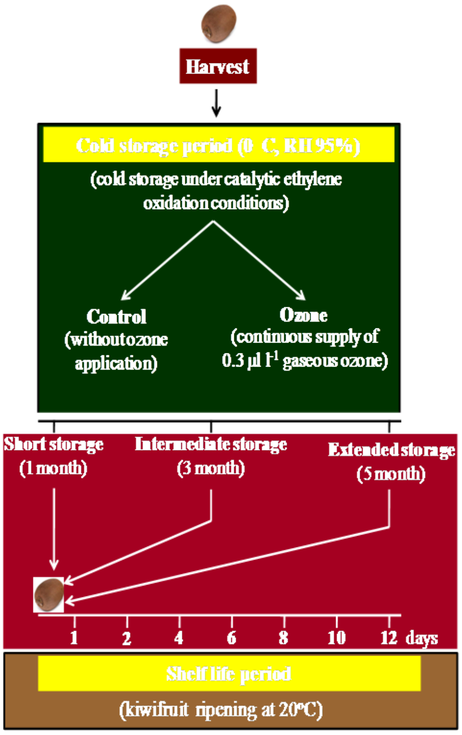

Figure S1. Scheme summarizing the experimental setup. Kiwifruits (cv. Hayward) were cold stored (0°C, 95% RH) for 1 month (short storage), 3 months (intermediate storage) or 5 months (extended storage) under catalytic ethylene oxidation conditions in the absence (control) or in the presence of 0.3 μl l^{-1} gaseous ozone (ozone treatment) followed by 12 days of ripening under shelf life conditions (20°C). Ethylene production and respiration were evaluated every 2 days of ripening whereas physicochemical (fruit firmness, soluble solids content and titratable acidity) and antioxidant (antioxidant capacity, ascorbic acid and phenolic contents) properties were analyzed at 1, 6 and 12 days of ripening under shelf life. The anti-radical activity of kiwifruit extracts was tested at 1 day shelf life following 1, 3 or 5 months of cold storage. 1D-SDS-PAGE and mass spectrometry analysis along with Oxyblot assays were conducted at 1, 6 or 12 days of shelf life after 5 months of cold storage.

Supplementary Figure S2, Minas et al.

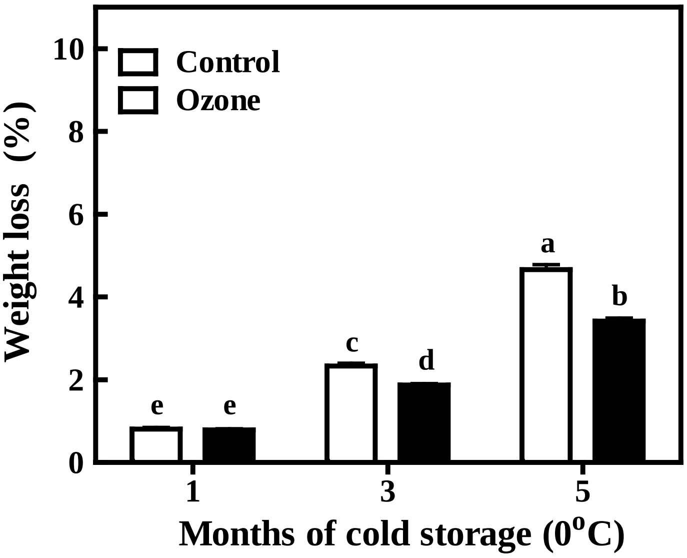

Figure S2. Weight loss (expressed as the percentage of the initial weight at harvest) of kiwifruits (cv. Hayward) after cold storage (0°C, 95% RH) in the absence (control) or in the presence of ozone (0.3 μl l^{-1}) for 1, 3 or 5 months plus 1 day of shelf life (20°C). Bars for followed by the same letter are not statistically significant according to Duncan's multiple range test ($P < 0.05$). Values are means ± SE ($n = 20$).

Supplementary Figure S3, Minas et al.

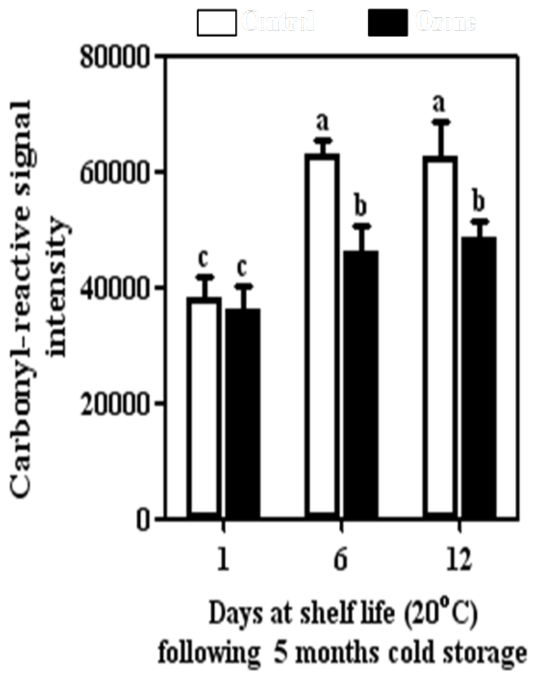

Figure S3. Relative abundance (arbitrary units) of carbonyl-reactive signal of the immunoblots in Figure 7A. Quantitative calculations were conducted using the calibrated densitometer and the Quantity One software for each entire gel lane. Bars followed by the same letter are not statistically significant according Duncans's multiple range test (*$P < 0.05$*). Values are means ± SE ($n = 3$).