

Table 1 Identification of 35 proteins in fresh-cut *Z. latifolia* stored for 3 and 5 d compared with the control at every corresponding storage time

Spot no. ^a	Accession no.	Protein name	Species	SCORE /Threshold	No. of peptides matched	Theoretical Mr(kDa)/pI	Observed Mr(kDa)/pI	Fold changes of spots % volume (<i>p</i> -0.05)				
								Whole (CK)		Fresh-cut		d
								0	3 d	5 d	3 d	
Signal transduction^b												
8	gi 115476520	Os08g0430500 (14-3-3-like protein)	<i>Oryza sativa</i>	420/42	5	29.0/4.78	32.1/4.81	1	0.56	0.68	0.45	0.22
10	gi 115477851	Os08g0562600 (C2 domain)	<i>Oryza sativa</i>	180/42	2	30.4/4.77	41.0/4.98	1	0.29	0.95	1.64	0.41
38	gi 16903082	Small Ras-related GTP-binding protein	<i>Triticum aestivum</i>	319/43	8	25.5/6.66	51.1/6.50	1	0.66	0.67	1.96	2.55
Metabolism^b												
6	gi 21698922	Adenosine kinase	<i>Oryza sativa</i>	217/43	3	32.6/5.29	45.0/4.47	1	0.85	0.57	1.35	0.25
14	gi 115474481	Os08g0113100 (Fructokinases)	<i>Oryza sativa</i>	396/44	4	36.7/5.97	41.5/5.37	1	0.74	1.46	1.05	0.53
17	gi 242090341	SORBIDRAFT_09g018750 (Glycosyl hydrolases family 17)	<i>Sorghum bicolor</i>	199/42	1	35.2/4.84	33.7/5.47	1	20.4	46.8	172.5	183.8
19	gi 115464537	Os05g0482700 (2,3-bisphosphoglycerate-independent phosphoglycerate mutase)	<i>Oryza sativa</i>	194/41	3	61.0/5.25	62.3/5.43	1	0.49	1.32	0.54	0.18
20	gi 2501354	Transketolase	<i>Craterostigma plantagineum</i>	49/43	1	73.9/6.16	76.0/5.48	1	0.13	0.28	0.48	0.32
26	gi 77556253	Diphosphonucleotide phosphatase 1	<i>Oryza sativa</i>	60/43	2	69.1/6.29	77.6/5.92	1	0.78	1.56	1.45	2.06
30	gi 90110845	Enolase	<i>Oryza sativa</i>	424/43	6	48.3/5.41	49.3/6.06	1	0.54	0.79	0.29	0.16
37	gi 115438939	Os01g0654500 (Isocitrate dehydrogenase NADP ⁺)	<i>Oryza sativa</i>	467/44	4	46.4/6.66	44.1/6.70	1	0.37	0.52	0.38	0.36
Cell Structure^b												
1	gi 115466468	Os06g0152100 (profilin)	<i>Oryza sativa</i>	167/43	2	14.3/4.73	12.1/4.53	1	2.65	25.3	1.48	8.65
18	gi 54035683	Actin	<i>Gossypium hirsutum</i>	792/43	10	41.9/5.31	46.3/5.45	1	0.80	0.71	0.90	0.20
27	gi 115455697	Os03g0780400 (Actin depolymerisation factor/cofilin - like domains)	<i>Oryza sativa</i>	392/43	5	16.8/5.65	17.6/5.97	1	0.47	0.25	0.11	0.18

Stress Response and Defense^b												
2	gi 242039265	SORBIDRAFT_01g018490 (Plant basic secretory protein)	<i>Sorghum bicolor</i>	67/43	2	24.5/6.96	26.3/4.62	1	0.28	0.36	7.89	11.3
3	gi 4097940	β-1,3-glucanase precursor	<i>Oryza sativa</i>	132/42	1	34.3/4.59	38.1/4.37	1	1.47	0.23	45.8	41.4
4	gi 167051	Glucan endo-1,3-beta-glucosidase	<i>Hordeum vulgare</i>	58/44	1	32.7/8.46	40.6/4.28	1	1.09	5.00	86.4	79.9
5	gi 4097940	β-1,3-glucanase precursor	<i>Oryza sativa</i>	132/42	1	34.3/4.59	39.5/4.26	1	4.22	34.3	116.1	241.2
12	gi 115462209	Universal stress protein family	<i>Oryza sativa</i>	158/42	2	18.2/5.22	17.2/5.09	1	0.98	3.26	1.61	3.02
21	gi 82621249	Thaumatococcus-like protein isoform 2	<i>Ficus pumila</i>	62/41	1	25.4/5.76	15.5/5.60	1	0.19	3.15	88.4	76.5
22	gi 56412207	Glutathione S-transferase	<i>Pennisetum glaucum</i>	163/43	2	24.0/5.57	28.4/5.65	1	0.58	3.10	4.15	5.82
24	gi 326504216	Predicted protein (Class III peroxidases)	<i>Hordeum vulgare</i>	117/43	2	34.9/6.93	34.9/5.80	1	0.10	0.08	2.01	1.53
28	gi 68250406	β-1,3-glucanase	<i>Triticum aestivum</i>	127/43	1	35.4/7.71	36.7/6.38	1	1.76	2.17	4.51	7.15
33	gi 28192421	Dehydroascorbate reductase	<i>Triticum aestivum</i>	166/43	2	23.5/5.88	20.1/6.80	1	0.47	0.47	0.22	0.07
34	gi 454269	Chitinase class I	<i>Oryza sativa</i>	92/42	2	34.7/6.82	20.9/6.56	1	0.68	0.94	0.05	0.09
Protein synthesis^b												
11	gi 50881454	Glycine-rich RNA-binding protein	<i>Oryza sativa</i>	241/44	3	15.9/6.29	13.3/5.42	1	0.16	0.36	0.16	0.02
13	gi 51090748	Putative chaperonin 21 precursor	<i>Oryza sativa</i>	125/42	1	26.4/7.71	26.5/5.28	1	0.52	0.48	0.53	0.18
15	gi 34393397	Putative ribosomal protein S12	<i>Oryza sativa</i>	146/43	4	15.1/5.33	37.6/5.43	1	0.45	0.62	0.76	0.28
31	gi 39545835	OSJNBb0060E08.6 (RNA recognition motif)	<i>Oryza sativa</i>	190/43	3	45.2/5.99	50.6/6.23	1	0.32	0.50	0.16	0.02
Senescence^b												
16	gi 50355623	Cysteine protease	<i>Daucus carota</i>	64/43	1	51.5/5.07	30.0/5.43	1	1.31	2.20	3.90	3.10
23	gi 194352762	Papain-like cysteine proteinase	<i>Hordeum vulgare</i>	112/43	1	40.2/6.84	30.6/5.60	1	1.81	1.61	2.74	1.67
Unclear functional proteins^b												
9	gi 115445585	Os02g0285300 (DREPP plasma membrane polypeptide)	<i>Oryza sativa</i>	119/42	2	24.0/4.73	39.8/4.97	1	0.42	0.48	0.32	0.42
29	gi 115439261	Os01g0686800 (WD40 domain)	<i>Oryza sativa</i>	271/43	3	36.7/5.97	41.5/6.34	1	0.78	0.55	0.41	0.10
35	gi 115473681	Os07g0642900 (LbH_gamma_CA_like)	<i>Oryza sativa</i>	246/43	6	29.7/6.42	37.4/6.65	1	0.52	0.14	3.40	4.64
36	gi 115434012	Os01g0104400 (RicinB_lectin_2)	<i>Oryza sativa</i>	177/43	3	30.4/6.27	34.2/6.80	1	0.23	0.27	0.61	0.37

^aSpot numbers refer to Figure 3.

^bFunctional classification.